

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2002, 10:35:59 : Search time 228.86 Seconds

(without alignments)
13,589 Million cell updates/sec

Title: US-09-544-664-55

Sequence: 1 KNLMANQRYGRELNRMSDEFEGSKLK 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A:Geneseq.032802:*
1: /SIDSL/gcgdata/hold-geneseq/genesep-emb1/AA1980.DAT:*
2: /SIDSL/gcgdata/hold-geneseq/genesep-emb1/AA1981.DAT:*
3: /SIDSL/gcgdata/hold-geneseq/genesep-emb1/AA1982.DAT:*
4: /SIDSL/gcgdata/hold-geneseq/genesep-emb1/AA1983.DAT:*
5: /SIDSL/gcgdata/hold-geneseq/genesep-emb1/AA1984.DAT:*
6: /SIDSL/gcgdata/hold-geneseq/genesep-emb1/AA1985.DAT:*
7: /SIDSL/gcgdata/hold-geneseq/genesep-emb1/AA1986.DAT:*
8: /SIDSL/gcgdata/hold-geneseq/genesep-emb1/AA1987.DAT:*
9: /SIDSL/gcgdata/hold-geneseq/genesep-emb1/AA1988.DAT:*
10: /SIDSL/gcgdata/hold-geneseq/genesep-emb1/AA1989.DAT:*
11: /SIDSL/gcgdata/hold-geneseq/genesep-emb1/AA1990.DAT:*
12: /SIDSL/gcgdata/hold-geneseq/genesep-emb1/AA1991.DAT:*
13: /SIDSL/gcgdata/hold-geneseq/genesep-emb1/AA1992.DAT:*
14: /SIDSL/gcgdata/hold-geneseq/genesep-emb1/AA1993.DAT:*
15: /SIDSL/gcgdata/hold-geneseq/genesep-emb1/AA1994.DAT:*
16: /SIDSL/gcgdata/hold-geneseq/genesep-emb1/AA1995.DAT:*
17: /SIDSL/gcgdata/hold-geneseq/genesep-emb1/AA1996.DAT:*
18: /SIDSL/gcgdata/hold-geneseq/genesep-emb1/AA1997.DAT:*
19: /SIDSL/gcgdata/hold-geneseq/genesep-emb1/AA1998.DAT:*
20: /SIDSL/gcgdata/hold-geneseq/genesep-emb1/AA1999.DAT:*
21: /SIDSL/gcgdata/hold-geneseq/genesep-emb1/AA2000.DAT:*
22: /SIDSL/gcgdata/hold-geneseq/genesep-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	148	100.0	28	21	AAAB37055
2	143	96.6	27	21	AAAB37056
3	138	93.2	26	21	AAAB37001
4	138	93.2	26	21	AAAB37002
5	138	93.2	27	21	AAAB37003
6	138	93.2	162	22	AAAB70370
7	138	93.2	204	17	AAAB95168
8	138	93.2	204	19	AAAB61315
9	138	93.2	204	19	AAAB61316
10	138	93.2	204	19	AAAB61317
11	138	93.2	204	19	AAAB61318

12	138	93.2	204	19	AAAB58832
13	138	93.2	204	22	AAAB70369
14	138	93.2	567	22	AAAB00220
15	114	77.0	166	18	AAAB32476
16	114	77.0	168	19	AAAB52779
17	114	77.0	168	21	AAAB35122
18	114	77.0	168	22	AAAB70368
19	114	77.0	168	22	AAAB48287
20	114	77.0	168	22	AAAB67688
21	113	76.4	23	17	AAAB95167
22	102	68.9	59	19	AAAB61319
23	102	68.9	59	19	AAAB61320
24	102	68.9	59	19	AAAB61321
25	102	68.9	59	19	AAAB61322
26	93	62.8	26	21	AAAB63241
27	93	62.8	26	22	AAAB70371
28	86	58.1	16	17	AAAB95163
29	86	58.1	16	20	AAAB95422
30	84	56.8	16	21	AAAB7028
31	73	49.3	16	20	AAAB05421
32	73	49.3	16	21	AAAB7029
33	72	48.6	18	22	AAAB70379
34	72	48.6	20	22	AAAB70380
35	51	34.5	125	21	AAAG25219
36	51	34.5	171	21	AAAG25218
37	51	34.5	181	21	AAAG25217
38	51	34.5	186	21	AAAG25578
39	51	34.5	186	21	AAAG54030
40	51	34.5	232	21	AAAG25577
41	51	34.5	232	21	AAAG54029
42	51	34.5	236	21	AAAG54679
43	51	34.5	241	21	AAAG54028
44	51	34.5	242	21	AAAG25576
45	51	34.5	682	22	ABAB52836

ALIGNMENTS

RESULT 1
ID ABAB7055 standard; peptide; 28 AA.
XX
MC ABAB7055:
XX
DT 28-FEB-2001 (first entry)
XX
XX Bcl2 polypeptide BH3 domain peptide #55.
DE
XX
XX Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;
KW caridiatic; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;
KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;
KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
stroke; myocardial infarction.
XX
XX
XX Homo sapiens.
OS
XX
XX WO200059526-A1.
FN
XX
XX 12-OCT-2000.
PD
XX
XX 06-APR-2000; 2000WO-US09352.
FF
XX
XX 07-APR-1999; 99US-0128202.
PR
XX
XX (UYTE-) UNIV JEFFERSON THOMAS.
PA
XX
XX Huang Z, Wang J, Zhang Z, Shan S, Lu Z;
PI
XX
XX WPI; 2000-679325/66.
DR
XX
XX New peptide conjugates for modulating apoptosis or for inhibiting B

cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer

Claim 18: Page 19; 74pp; English.

The invention relates to a peptide conjugate having the formula: (R-X)_n-peptide where n = 1-10; X = C=O, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is NH₂ or OH; or X = O or NH, when the R-X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COOH or CONH₂; and R = 2-18C alkyl or alkoxy, 2-14C alkenyl optionally containing one or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, phenyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples of the peptide portion of the conjugate. The peptides represent analogues of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of the Bcl-2 domain of the cell death agonist Bad. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of apoptosis in cancer cells. It is also useful for inhibiting Bcl-2 function. In particular, the peptide conjugate is useful for treating a subject afflicted with a cancer characterized by cancer cells that express Bcl-2. The cancer includes prostate, colorectal, gastric, or non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.

Sequence 28 AA:

Query Match 100.0%; Score 148; DB 21; Length 28;
Best Local Similarity 100.0%; Pred. No. 1e-15; Indels 0; Gaps 0;
Matches 28; Conservative 0; Mismatches 0;

OY 1 KNLMAORGRRLRMSDEFGSKGL 28
|||||
Db 1 knlwaagryrelrmsdefgskgl 28

RESULT 2
AAB37056 standard; peptide: 27 AA.

AC AAB37056;

DT 28-FEB-2001 (first entry)

DE Bcl2 polypeptide BH3 domain peptide #56.

Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS; stroke; myocardial infarction.

OS Homo sapiens.

XX WO200059526-A1.

PD 12-OCT-2000.

PP 06-APR-2000; 2000WO-US09352.

PR 07-APR-1999; 99US-0128202.

PA (UWJE-) UNIV JEPERSON THOMAS.

XX Huang Z, Wang J, Zhang Z, Shan S, Lu Z;

XX WPI: 2000-679325/66.

New peptide conjugates for modulating apoptosis or for inhibiting B cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer

Claim 18: Page 19; 74pp; English.

The invention relates to a peptide conjugate having the formula: (R-X)_n-peptide where n = 1-10; X = C=O, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is NH₂ or OH; or X = O or NH, when the R-X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COOH or CONH₂; and R = 2-18C alkyl or alkoxy, 2-14C alkenyl optionally containing one or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, phenyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples of the peptide portion of the conjugate. The peptides represent analogues of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of the Bcl-2 domain of the cell death agonist Bad. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of apoptosis in cancer cells. It is also useful for inhibiting Bcl-2 function. In particular, the peptide conjugate is useful for treating a subject afflicted with a cancer characterized by cancer cells that express Bcl-2. The cancer includes prostate, colorectal, gastric, or non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.

Sequence 27 AA:

Query Match 96.6%; Score 143; DB 21; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.7e-15;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KNLMAORGRRLRMSDEFGSKGL 27
|||||
Db 1 knlwaagryrelrmsdefgskgl 27

RESULT 3
AAB37001 standard; peptide: 26 AA.

AC AAB37001;

DT 28-FEB-2001 (first entry)

DE Bcl2 polypeptide BH3 domain peptide #1.

Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad; apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS; stroke; myocardial infarction.

OS Homo sapiens.

XX WO200059526-A1.

PD 12-OCT-2000.

PP 06-APR-2000; 2000WO-US09352.

PR 07-APR-1999; 99US-0128202.

XX WO200059526-A1.
 PN 12-OCT-2000.
 PD 06-APR-2000; 2000MC-US09352.
 PF 07-APR-1999; 99US-0128202.
 PR (UYJE-) UNIV JEFFERSON THOMAS.
 PA Huang Z, Wang J, Zhang Z, Shan S, Lu Z;
 PI WPI: 2000-679325/66.
 DR
 XX New peptide conjugates for modulating apoptosis or for inhibiting B
 PT cell lymphoma/leukemia 2 (bcl-2) function, especially useful for
 PL treating neurodegenerative disorders, stroke, or cancer.
 PS
 XX Claim 16: Page 17; 74pp; English.
 PS
 XX The invention relates to a peptide conjugate having the formula:
 CC (R-X)-peptide where R is a 1-10 X = C=O, when the R-X group is attached
 CC to the N-terminus of the peptide or a side chain of the peptide where
 CC the functional group of the side chain is NH2, and X is a peptide or a
 CC When the R-X group is attached to the C-terminus of the peptide, a
 CC side chain of the peptide, where the side chain functional group is COOH
 CC or CONH2; and R = 2-18C alkyl or alkoxy; 2-14C alkenyl optionally
 CC monosubstituted with a 1-5C straight or branched chain alkyl group;
 CC monosubstituted with a 1-5C straight or branched chain alkyl group;
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples
 CC of the peptide portion of the conjugate. The peptides represent analogues
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
 CC the Bcl-2 domain of the cell death agonist Bad. The peptide conjugate is
 CC useful for modulating apoptosis in the cells of a subject, or for
 CC reversing B cell lymphoma/leukemia 2 (bcl-2)-mediated blockage of
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
 CC function. In particular, the peptide conjugate is useful for treating a
 CC subject afflicted with a cancer characterized by cancer cells that
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric, or
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
 CC conjugate is also useful for treating disorders characterized by
 CC increased apoptosis, e.g., neurodegenerative disorders, acquired
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
 CC
 XX
 SO Sequence 27 AA;
 Query Match 93.2%; Score 138; DB 21; Length 27;
 Best Local Similarity 100.0%; Pred. NO. 3.4e-14;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NLMANQRYGRLRMSDEFGSFKGL 27
 DB 1 nlwaqrgyrelrrmsdefgsfkgl 26
 RESULT 6
 AAB70370 standard; protein: 162 AA.
 ID AAB70370;
 AC AAB70370;
 XX 02-MAY-2001 (first entry)
 DT
 DE Shorter murine BAD mutant amino acid sequence SEQ ID NO.3.
 XX
 XX Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
 KW immunosuppressive; neuroprotective; nontoxic; antileukemic; antiviral;
 KW cytoskeletal; antiviral; antiarthritic; antiinflammatory; wound healing;
 KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;

KW immunodeficiency disease; neurodegenerative disease; viral infection;
 KW ischemic cell death; reperfusion cell death; arthritis; infertility;
 KW lymphoproliferative condition; inflammation; autoimmune disease.
 OS Mus musculus.
 OS Synthetic.
 XX WO200110888-A1.
 PN 15-FEB-2001.
 PD 30-MAY-2000; 2000MC-US11864.
 PF 28-MAY-1999; 99US-0136783.
 PR (APOF-) APOPTOSIS TECHNOLOGY INC.
 PA Zhou X;
 PI WPI: 2001-138734/14.
 DR
 XX New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,
 XX useful for screening for candidate compounds which induce or inhibit
 XX apoptosis, comprises amino acid substitutions at Ser118, Ser135 or
 XX Ser113.
 PS
 XX Claim 7; Page 148-149; 157pp; English.
 PS
 XX The present invention describes an isolated or synthetic polypeptide
 CC (I) comprising a less than full length amino acid sequence of a mutant
 CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its
 CC fragment, which contains amino acid substitutions at Ser118 of a human
 CC BAD. Ser135 of a murine BAD (longer murine BAD) or Ser113 of a murine
 CC BAD (shorter murine BAD). (I) has immunosuppressive, neuroprotective,
 CC antitumor, antileukemic, antiviral, antiarthritic, antiinflammatory,
 CC nocotropic, antineoplastic, cytostatic, antiapoptotic, and
 CC immunosuppressive activities, and can be used as an apoptosis inducer or inhibitor. BAD polypeptides and
 CC polynucleotides can be used for screening candidate compounds and drugs
 CC for activity that promote cell survival or apoptosis. Other uses include
 CC inducing or inhibiting apoptosis in a cell. Candidate compounds
 CC identified and (mutant) BAD polypeptides are useful in treating
 CC immunodeficiency diseases, neurodegenerative diseases, ischemic cell
 CC death, reperfusion cell death, wound healing, cancer, viral infections,
 CC lymphoproliferative conditions, arthritis, infertility, inflammation and
 CC autoimmune diseases. The present sequence represents a specifically
 CC claimed shorter murine BAD mutant amino acid sequence from the present
 CC invention.
 CC
 XX
 SO Sequence 162 AA;
 Query Match 93.2%; Score 138; DB 22; Length 162;
 Best Local Similarity 100.0%; Pred. NO. 2.4e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NLMANQRYGRLRMSDEFGSFKGL 27
 DB 98 nlwaqrgyrelrrmsdefgsfkgl 123
 RESULT 7
 AAR95168 standard; protein: 204 AA.
 ID AAR95168;
 AC AAR95168;
 XX 06-JAN-1997 (first entry)
 DT
 DE bcl-x(l)/bcl-2 associated death promoter protein.
 XX
 XX Epitope; murine; bcl-x(l)/bcl-2 associated death promoter; Bad; stroke;
 KW polypeptide; bcl-x; cell death; regulator; BH2; apoptotic cell death;
 KW cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS;

KW neurodegenerative disease; senescence; ischemia; neoplasia.
 XX Mus musculus.
 OS
 XX
 PH Key Location/Qualifiers
 PH Region 147..149
 FT /note- "BH1 conserved amino acids"
 FT Region 191..192
 FT /note- "BH2 conserved amino acids"
 FT Domain 38..61
 FT /note- "PEST sequence"
 FT Domain 111..130
 FT /note- "PEST sequence"
 XX
 XX MO9613614-A1.
 XX
 XX 09-MAY-1996.
 XX
 XX 31-OCT-1995; 95WO-US14246.
 XX
 XX 31-OCT-1994; 94US-0333565.
 XX
 XX (UNITM) UNIV WASHINGTON.
 XX
 XX Kormeyer SJ;
 XX
 XX WPI: 1996-251465/25.
 XX N-PSDB: AAT29475.
 XX
 XX Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter -
 XX useful to treat neoplasia and apoptosis and to identify agents
 XX inhibiting its binding to bcl-2 or bcl-x(L) to form heterodimers
 XX
 XX
 XX Claim 3: Fig 1: 130pp: English.
 XX
 XX This sequence represents the murine bcl-x(L)/bcl-2 associated death
 XX promoter (bad) gene. Bad is a 22.1 kD protein which interacts with
 XX bcl-2 and bcl-x proteins and regulates cell death. It has homology
 XX to the bcl-2-related family clustered in the BH1 and BH2 domain. Bad
 XX has been found to hybridise to bcl-x(L) and bcl-2 in yeast two-hybrid
 XX assays and in vivo in mammalian cells. Overexpressed Bad counters the
 XX death inhibitory activity of bcl-x(L), but is much less effective at
 XX accelerating apoptotic cell death induced by cytokine deprivation in an
 XX IL-3 dependent cell line expressing bcl-x(L), and its also counters the
 XX bcl-2 dependent activity of bcl-x(L). Bad competes with Bax for binding
 XX binding to bcl-2 or bcl-x(L) to form heterodimers. Such agents may be
 XX used to treat neurodegenerative diseases, immunodeficiency diseases,
 XX e.g. AIDS, senescence or ischemia.
 XX
 XX Sequence 204 AA:
 SQ
 Query Match 93.2%; Score 138; DB 17; Length 204;
 Best Local Similarity 100.0%; Pred. No. 3, 2e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 NIMAAORYGRLRRKSDFFGSGFKL 27
 DB 140 nlwaagrygrelrrmsdelegsfkgl 165
 RESULT 8
 ID AAM61315 standard; Protein; 204 AA.
 XX
 XX AAM61315;
 XX
 XX 07-OCT-1998 (first entry)
 XX
 XX Murine BCL-XL/BCL-2 associated cell death regulator.

KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
 KW serine substituted mutant; apoptosis; cancer; viral infection.
 XX
 XX Mus sp.
 OS
 XX
 XX MO9817682-A1.
 XX
 XX 30-APR-1998.
 XX
 XX 17-OCT-1997; 97WO-US19175.
 XX
 XX 18-OCT-1996; 96US-0733505.
 XX
 XX (UNITM) UNIV WASHINGTON.
 XX
 XX Kormeyer SJ;
 XX
 XX WPI: 1998-261422/23.
 XX N-PSDB: AAV27833.
 XX
 XX New mutant BAD polypeptide with phosphorylatable serine replaced -
 XX useful for, e.g. treating reduced apoptosis such as in cancer or
 XX viral infection
 XX
 XX
 XX Claim 1: Fig 10: 95pp: English.
 XX
 XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
 XX death regulator) proteins, having an amino acid other than ser at
 XX position 112 and/or 116, relative to the murine Bcl-204 bad sequence. The
 XX present sequence is the murine BAD protein. Also described are (1)
 XX fragments of mutant BAD proteins in the heterologous polypeptide that
 XX fusion proteins and viral delivery. Mutant BAD proteins are used to treat
 XX or prevent diseases associated with reduced apoptosis, e.g. cancer.
 XX viral infection, lymphoproliferation, arthritis, infertility,
 XX inflammation and autoimmune disease. Polynucleotide sequences encoding
 XX mutant BAD proteins can be used similarly by gene therapy or to produce
 XX transgenic animals for use as disease models or in drug screening. BAD
 XX and inhibitors of serine-phosphatase. Inhibitors are potentially useful
 XX in treatment of excessive apoptosis such as AIDS, neurodegeneration,
 XX aging or ischemic cell death. The apoptotic status of cells is
 XX determined by measuring relative amounts of phosphorylated and non-
 XX phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
 XX greater death-promoting activity than wild-type BAD which can become
 XX phosphorylated on the specified ser, forming a product that does not
 XX heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
 XX proteins in the cytosol, thus promoting cell survival. The mutants with
 XX ser substituted cannot bind 14-3-3.
 XX
 XX Sequence 204 AA:
 SQ
 Query Match 93.2%; Score 138; DB 19; Length 204;
 Best Local Similarity 100.0%; Pred. No. 3, 2e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 NIMAAORYGRLRRKSDFFGSGFKL 27
 DB 140 nlwaagrygrelrrmsdelegsfkgl 165
 RESULT 9
 ID AAM61316 standard; Protein; 204 AA.
 XX
 XX AAM61316;
 XX
 XX 07-OCT-1998 (first entry)
 XX
 XX Mutant BCL-XL/BCL-2 associated cell death regulator #1.
 XX
 XX Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;

KW serine substituted mutant; apoptosis; cancer; viral infection.
 XX Mus sp.
 OS Synthetic.
 XX MO9817682-A1.
 XX 30-APR-1998.
 PD 17-OCT-1997: 97WO-US19175.
 PF 18-OCT-1996: 96US-0733505.
 PR (UNIT1) UNIV WASHINGTON.
 PA Korsmeyer SJ:
 XX WPI: 1998-261422/23.
 DR N-PSDB: AAV27834.
 XX New mutant BAD polypeptide with phosphorylatable serine replaced -
 PT useful for, e.g. treating reduced apoptosis such as in cancer or
 PT viral infection
 XX
 XX Claim 7: Page 59: 95pp: English.
 CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
 CC death regulator) proteins having an amino acid other than serine at
 CC position 112 and/or 116, relative to the murine BAD 204 aa sequence. The
 CC present sequence represents a mutant BAD protein. Also described are: (1)
 CC fragments of mutant BAD protein able to decrease cell viability; (2)
 CC fusion proteins of mutant BAD with a heterologous polypeptide that
 CC increases intracellular delivery. Mutant BAD proteins are used to treat
 CC or prevent diseases associated with reduced apoptosis, e.g. cancer,
 CC viral infection, lymphoproliferation, arthritis, infertility,
 CC inflammation and autoimmune disease. Polynucleotide sequences encoding
 CC mutant BAD proteins can be used similarly by gene therapy or to produce
 CC transgenic animals for use as disease models or in drug screening. BAD
 CC proteins phosphorylated at specified Ser are used to screen for enhancers
 CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful
 CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,
 CC aging or ischemic cell death. The apoptotic status of cells is
 CC determined by measuring relative amounts of phosphorylated and non-
 CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
 CC greater death-promoting activity than wild-type BAD which can become
 CC phosphorylated on the specified Ser, forming a product that does not
 CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
 CC proteins in the cytosol, thus promoting cell survival. The mutants with
 CC Ser substituted cannot bind 14-3-3.
 XX
 XX Sequence 204 AA:
 SQ
 Query Match 93.2%; Score 136; DB 19; Length 204;
 Best Local Similarity 100.0%; Pred. No. 3,2e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NIMAAORYRELRPMSPDEPGSFKGL 27
 |||
 Db 140 nlwaagrygrtelrmadefegsfkgl 165
 RESULT 10
 AAM61317
 ID AAM61317 standard; Protein: 204 AA.
 AC AAM61317;
 XX
 XX 07-OCT-1998 (first entry)
 DT
 XX Mutant BCL-XL/BCL-2 associated cell death regulator #2.
 DE
 XX Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
 KW

KW serine substituted mutant; apoptosis; cancer; viral infection.
 XX Mus sp.
 OS Synthetic.
 XX MO9817682-A1.
 XX 30-APR-1998.
 PD 17-OCT-1997: 97WO-US19175.
 PF 18-OCT-1996: 96US-0733505.
 PR (UNIT1) UNIV WASHINGTON.
 PA Korsmeyer SJ:
 XX WPI: 1998-261422/23.
 DR N-PSDB: AAV27835.
 XX New mutant BAD polypeptide with phosphorylatable serine replaced -
 PT useful for, e.g. treating reduced apoptosis such as in cancer or
 PT viral infection
 XX
 XX Claim 7: Page 60: 95pp: English.
 CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
 CC death regulator) proteins having an amino acid other than serine at
 CC position 112 and/or 116, relative to the murine BAD 204 aa sequence. The
 CC present sequence represents a mutant BAD protein. Also described are: (1)
 CC fragments of mutant BAD protein able to decrease cell viability; (2)
 CC fusion proteins of mutant BAD with a heterologous polypeptide that
 CC increases intracellular delivery. Mutant BAD proteins are used to treat
 CC or prevent diseases associated with reduced apoptosis, e.g. cancer,
 CC viral infection, lymphoproliferation, arthritis, infertility,
 CC inflammation and autoimmune disease. Polynucleotide sequences encoding
 CC mutant BAD proteins can be used similarly by gene therapy or to produce
 CC transgenic animals for use as disease models or in drug screening. BAD
 CC proteins phosphorylated at specified Ser are used to screen for enhancers
 CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful
 CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,
 CC aging or ischemic cell death. The apoptotic status of cells is
 CC determined by measuring relative amounts of phosphorylated and non-
 CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
 CC greater death-promoting activity than wild-type BAD which can become
 CC phosphorylated on the specified Ser, forming a product that does not
 CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
 CC proteins in the cytosol, thus promoting cell survival. The mutants with
 CC Ser substituted cannot bind 14-3-3.
 XX
 XX Sequence 204 AA:
 SQ
 Query Match 93.2%; Score 138; DB 19; Length 204;
 Best Local Similarity 100.0%; Pred. No. 3,2e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NIMAAORYRELRPMSPDEPGSFKGL 27
 |||
 Db 140 nlwaagrygrtelrmadefegsfkgl 165
 RESULT 11
 AAM61318
 ID AAM61318 standard; Protein: 204 AA.
 AC AAM61318;
 XX
 XX 07-OCT-1998 (first entry)
 DT
 XX Mutant BCL-XL/BCL-2 associated cell death regulator #3.
 DE
 XX Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
 KW

KM serine substituted mutant; apoptosis; cancer; viral infection.
 XX Mus sp.
 OS Synthetic.
 XX MO9817692-X1.
 XX 30-APR-1998.
 XX 17-OCT-1997; 97MO-US19175.
 XX 18-OCT-1996; 96US-0733505.
 XX (UNIW) UNIV WASHINGTON.
 PA Kormeyer SJ;
 PI WPI; 1998-261422/23.
 DR N-PSDB; AAV27836.
 XX New mutant BAD polypeptide with phosphorylatable serine replaced -
 PT useful for, e.g., treating reduced apoptosis such as in cancer or
 PT viral infection
 PS Claim 7; Page 60-61; 95pp; English.
 XX The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
 CC death regulatory) proteins, having an amino acid other than Ser at
 CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
 CC present sequence represents a mutant BAD protein. Also described are: (1)
 CC fragments of mutant BAD protein able to decrease cell viability; (2)
 CC fusion proteins of mutant BAD with a heterologous polypeptide that
 CC increases intracellular delivery. Mutant BAD proteins are used to treat
 CC various diseases, including, but not limited to, cancer, leukemia, AIDS,
 CC viral infection, immunodeficiency, lymphoproliferative disease, arthritis,
 CC inflammation and autoimmune disease. polynucleotide sequence encoding
 CC mutant BAD proteins can be used similarly by gene therapy or to produce
 CC transgenic animals for use as disease models or in drug screening. BAD
 CC proteins phosphorylated at specified Ser are used to screen for enhancers
 CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful
 CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,
 CC aging or ischemic cell death. The apoptotic status of cells is
 CC determined by measuring relative amounts of phosphorylated and non-
 CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
 CC greater death-promoting activity than wild-type BAD which can become
 CC phosphorylated on the specified Ser, forming a product that does not
 CC heterodimerize with BCL-2 or BCL-XL but instead binds to 14-3-3 family
 CC proteins in the cytosol, thus promoting cell survival. The mutants with
 CC Ser substituted cannot bind 14-3-3.
 XX
 XX
 SO Sequence 204 AA;
 OY
 Query Match 93.2%; Score 138; DB 19; Length 204;
 Best local similarity 100.0%; Pred. No. 3.2e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 2 NLMAOYRGRELRMSDEFGSGKGL 27
 140 nlwaagqygrellrmsdefgsfkgl 165
 RESULT 12
 AAB58832
 ID AAB58832 standard; protein: 204 AA.
 XX AAB58832;
 AC
 XX 23-JUL-1998 (first entry)
 DT
 XX Murine BAD protein.
 DE
 XX BAD protein; Bcl-XL/Bcl-2 associated cell death regulator; 14-3-3;

KM serine phosphorylation; post-translational modification; apoptosis;
 KM signal transduction regulator; phosphoserine phosphatase; senescence;
 KM immunodeficiency disease; neurodegenerative disease; infertility;
 KM cancer; viral infection; lymphoproliferative condition; arthritis;
 KM inflammation; autoimmune diseases.
 XX Mus sp.
 XX MO9809643-X1.
 XX 12-MAR-1998.
 XX 09-SEP-1997; 97MO-US15871.
 XX 09-SEP-1996; 96US-0707868.
 XX (UNIW) UNIV WASHINGTON.
 PA Kormeyer SJ;
 PI WPI; 1998-207049/18.
 XX Serine-phosphorylated Bcl-XL/Bcl-2 Associated cell death regulator
 PT polypeptide - useful for modulation of apoptosis associated with,
 PT e.g., cancer and immunodeficiency diseases
 PS Claim 3; Fig 8; 61pp; English.
 XX This sequence represents a novel serine-phosphorylated protein, BAD
 CC (Bcl-XL/Bcl-2 associated cell death regulator). The serine residue is
 CC phosphorylated in a post-translational modification and allows binding
 CC to the 14-3-3 protein which is a signal transduction regulator.
 CC Modulators of phosphorylated BAD, which act through inhibition/activation
 CC of phosphoserine phosphatase, are used to prevent or promote
 CC cell death. The invention also provides a method for screening agents
 CC to decrease immunodeficiency disease, senescence, neurodegenerative
 CC disease, ischemic cell death, reperfusion cell death, infertility and
 CC wound-healing. Decreased apoptosis may result from cancer, viral
 CC infection, lymphoproliferative conditions, arthritis, infertility,
 CC inflammation and autoimmune diseases. Measuring the amount of
 CC BAD in a cell is useful for determining the apoptotic state of a cell.
 XX
 XX
 SO Sequence 204 AA;
 OY
 Query Match 93.2%; Score 138; DB 19; Length 204;
 Best local similarity 100.0%; Pred. No. 3.2e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 2 NLMAOYRGRELRMSDEFGSGKGL 27
 140 nlwaagqygrellrmsdefgsfkgl 165
 RESULT 13
 AAB70369
 ID AAB70369 standard; protein: 204 AA.
 XX AAB70369;
 AC
 XX 02-MAY-2001 (first entry)
 DT
 XX Longer murine BAD mutant amino acid sequence SEQ ID NO:2.
 DE
 XX Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
 XX immunosuppressive; neuroprotective; neurotrophic; antiischemic; vulnary;
 XX cytoskeletal; antiviral; antiarthritis; antiinflammatory; wound healing;
 XX immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;
 KM immunodeficiency disease; neurodegenerative disease; viral infection;
 KM ischemic cell death; reperfusion cell death; arthritis; infertility;
 KM lymphoproliferative condition; inflammation; autoimmune disease.
 XX

OS Mus musculus.
 OS Synthetic.
 PN W0200110888-A1.
 PU 15-FEB-2001.
 PE 30-MAY-2000; 2000MO-US11864.
 PR 28-MAY-1999; 99US-0136783.
 PA (APOB-) APOPTOSIS TECHNOLOGY INC.
 PI Zhou X;
 DR WPI; 2001-138734/14.
 XX New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,
 PT useful for screening for candidate compounds which induce or inhibit
 PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
 PT Ser113.
 XX
 XX Claim 4; Page 148; 157pp; English.
 XX
 XX The present invention describes an isolated or synthetic polypeptide
 CC comprising a class of full length amino acid sequence of a mutant
 CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its
 CC fragment, which contains amino acid substitutions at Ser113 of a murine
 CC BAD. Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine
 CC BAD (shorter murine BAD). (i) has immunostimulant, neuroprotective,
 CC neurotropic, antischismic, vulnerrary, cytosstatic, antiviral,
 CC antitumoric, antiinflammatory and immunosuppressive activities, and
 CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and
 CC polynucleotides can be used for screening candidate compounds and drugs
 CC for activity that promote cell survival or apoptosis. Other uses include
 CC inducing or inhibiting apoptosis in a cell. Candidate compounds
 CC identified and (mutant) BAD polypeptides are useful in treating
 CC immunodeficiency diseases, neurodegenerative diseases, ischaemic cell
 CC death, reperfusion cell death, wound healing, cancer, viral infections,
 CC lymphoproliferative conditions, arthritis, infertility, inflammation and
 CC autoimmune diseases. The present sequence represents a specifically
 CC claimed longer murine BAD mutant amino acid sequence from the present
 CC invention.
 CC
 XX
 XX Sequence 204 AA:
 SQ
 Query Match 93.2%; Score 138; DB 22; Length 204;
 Best Local Similarity 100.0%; Pred. No. 3,2e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NLMNAORGRGLRMGDEPFGSRKGL 27
 DB 140 nlwaagrygrelrmdelegsfkgll 165

RESULT 14
 AAU00220
 ID AAU00220 standard; Protein: 567 AA.
 AC AAU00220:
 XX
 XX 31-MAY-2001 (first entry)
 DT
 XX
 XX Bad-PTFR apoptosis-modifying fusion protein.
 DE
 XX Mouse; Bad-PTFR; apoptosis; cancer; spinal muscular atrophy;
 KM diptheria toxin receptor binding domain; DTR; neoplasm; tumor;
 KM hyper-proliferation; Alzheimer's disease; neurodegenerative disorder;
 KM transient ischaemic neuronal injury; stroke; spinal cord injury;
 KM Huntington's disease.
 XX
 OS Chimeric - Mus sp.

OS Chimeric - Corynebacterium diptheriae.
 OS Synthetic.
 PN Key location/qualifiers
 FT 3..12
 FT Region /note="10x histidine tag"
 XX
 XX W0200112661-A2.
 PU 22-FEB-2001.
 PE 15-AUG-2000; 2000MO-US22293.
 PR 16-AUG-1999; 99US-0149220.
 PA (HARD) HARVARD COLLEGE.
 PA (USSR) US DEPT HEALTH & HUMAN SERVICES.
 PI Youle RJ, Liu X, Collier RJ;
 DR WPI; 2001-218343/22.
 XX N-PSDB; AAS00248.
 XX
 XX Novel fusion protein for modifying apoptosis in target cell and
 PT reducing apoptosis after transient ischaemic neuronal injury, has two
 PT domains which targets protein to a cell and modifies apoptotic response
 PT of cell.
 XX
 XX Claim 4; Page 59-61; 65pp; English.
 XX
 XX The sequence represents the amino acid sequence of Bad-PTFR apoptosis-
 CC modifying fusion protein comprising Bad gene sequence fused via a short
 CC linker to diptheria toxin translocation domain (DTR). The
 CC functional apoptosis-modifying fusion protein is capable of binding a
 CC target cell and integrating into or crossing a cellular membrane of the
 CC target cell. The apoptosis-modifying fusion protein comprises at least
 CC two domains: the DTR domain, which targets the fusion protein to the
 CC target cell and the Bcl-XL domain, which modifies an apoptotic response
 CC (inhibiting or enhancing) apoptosis in a target cell, such as neuron,
 CC lymphocyte, cancer, neoplasm, macrophage, epithelial, stem, tumor or
 CC hyper-proliferative cell or an adipocyte. It is also useful for reducing
 CC apoptosis in a subject after transient ischaemic neuronal injury,
 CC especially spinal cord injury. The fusion protein may be used to treat
 CC various diseases and injury conditions through inhibition or enhancement
 CC of apoptotic cellular response, including neurodegenerative disorders
 CC such as Alzheimer's disease, Huntington's disease, spinal muscular
 CC atrophy, stroke episodes and unregulated cell growth as in tumors and
 CC various cancers. The apoptosis-modifying fusion protein can be delivered
 CC effectively throughout the body and targeted to selective tissue and
 CC cells.
 CC
 XX
 XX Sequence 567 AA:
 SQ
 Query Match 93.2%; Score 138; DB 22; Length 567;
 Best Local Similarity 100.0%; Pred. No. 9,6e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NLMNAORGRGLRMGDEPFGSRKGL 27
 DB 161 nlwaagrygrelrmdelegsfkgll 186

RESULT 15
 AAM32476
 ID AAM32476 standard; Protein: 166 AA.
 AC AAM32476:
 XX
 XX 15-JAN-1998 (first entry)
 DT
 XX
 XX BBC6 protein for regulating cell death.

XX BRC6 gene; cell death; cell cycle; Bcl2; human.
 KW Homo sapiens.
 OS US5663316-A.
 XX 02-SEP-1997.
 PV 18-JUN-1996: 96US-0665617.
 XX 18-JUN-1996: 96US-0665617.
 XX 18-JUN-1996: 96US-0665617.
 XX (CLON-) CLONTECH LAB INC.
 BA Xudong Y;
 XX WPI: 1997-447980/41.
 XX N-PSDB: AAT91561.
 DR Isolated BRC6 gene - encodes a protein that regulates cell death
 XX through interaction with Bcl-2
 PS Claim 1: Column 11-12: 7pp: English.
 XX The present sequence represents a protein of 166 amino acids. The
 CC sequence is disclosed as being a protein called BRC6 which regulates
 CC cell death through interaction with Bcl-2. The DNA may be used for the
 CC production of the recombinant protein, which can be used in unspecified
 CC therapeutic or diagnostic procedures, as a molecular weight marker, and
 CC to raise antibodies that can be used in unspecified diagnostic or
 CC therapeutic applications and to reduce or eliminate the biological
 CC activity of the BRC6 protein in vivo.
 XX
 SQ Sequence 166 AA;

Query Match 77.0%; Score 114; DB 18: Length 166;
 Best Local Similarity 91.7%; Pred. No. 1.2e-09;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 NMAAORXYGPELRMSDFRGSFK 25
 ||||||||||||||||
 Db 101 nlwaagrygrelrmsdeivdsfk 124

Search completed: September 20, 2002, 10:35:59
 Job time: 427 sec

Fri Sep 20 11:03:16 2002

us-09-544-664-55.fai

Page 1

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2002, 10:37:21 : Search time 75.64 seconds
(without alignments)
9.042 Million cell updates/sec

Title: US-09-544-664-55
Perfect score: 148
Sequence: 1 KILMAORGRRLRMSDEFGSKGLK 28

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCMS.pep:*
6: /cgn2_6/ptodata/2/1aa/Backflist.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	138	93.2	204	1 US-08-333-565-2	Sequence 2, Appl1
2	138	93.2	204	2 US-08-661-479-2	Sequence 2, Appl1
3	138	93.2	204	3 US-08-717-123-2	Sequence 1, Appl1
4	138	93.2	204	4 US-08-723-505A-12	Sequence 1, Appl1
5	138	93.2	204	5 US-08-723-505A-13	Sequence 1, Appl1
6	138	93.2	204	6 US-08-723-505A-14	Sequence 1, Appl1
7	135	91.2	204	7 US-08-717-123-3	Sequence 3, Appl1
8	114	77.0	166	1 US-08-665-617-2	Sequence 2, Appl1
9	114	77.0	168	2 US-08-717-123-2	Sequence 1, Appl1
10	114	77.0	168	3 US-08-985-335-1	Sequence 7, Appl1
11	114	77.0	168	4 US-09-410-372-1	Sequence 1, Appl1
12	114	77.0	168	5 US-09-410-372-7	Sequence 7, Appl1
13	114	77.0	23	1 US-08-333-565-10	Sequence 10, Appl1
14	113	76.4	23	2 US-08-661-479-10	Sequence 10, Appl1
15	113	76.4	23	3 US-08-717-123-2	Sequence 10, Appl1
16	112	68.9	59	2 US-08-723-505A-25	Sequence 52, Appl1
17	112	68.9	59	3 US-08-723-505A-26	Sequence 57, Appl1
18	110	68.9	59	4 US-08-723-505A-27	Sequence 58, Appl1
19	102	68.9	59	5 US-08-723-505A-28	Sequence 59, Appl1
20	102	68.9	59	6 US-08-723-505A-29	Sequence 60, Appl1
21	86	58.1	16	1 US-08-333-565-26	Sequence 26, Appl1
22	86	58.1	16	2 US-08-661-479-26	Sequence 26, Appl1
23	86	58.1	16	3 US-08-723-505A-34	Sequence 34, Appl1
24	61	41.2	11	2 US-08-706-741B-69	Sequence 69, Appl1
25	61	41.2	11	3 US-08-924-695A-69	Sequence 69, Appl1
26	51	34.5	66	2 US-08-867-087B-40	Sequence 40, Appl1
27	46	31.1	946	4 US-09-074-579-3	Sequence 3, Appl1

28	44	29.7	263	4	US-09-651-656-27	Sequence 27, Appl1
29	43	29.1	281	3	US-09-407-737-10	Sequence 10, Appl1
30	43	29.1	213	4	US-08-716-726-18	Sequence 18, Appl1
31	43	29.1	213	4	US-09-221-844-18	Sequence 18, Appl1
32	43	29.1	380	1	US-08-153-848-40	Sequence 40, Appl1
33	43	29.1	380	3	US-09-299-843A-40	Sequence 40, Appl1
34	43	29.1	380	4	US-09-088-337B-40	Sequence 40, Appl1
35	43	29.1	380	5	PCT-US93-11153-40	Sequence 40, Appl1
36	42	28.4	322	4	US-09-359-161-7	Sequence 7, Appl1
37	42	28.4	348	2	US-08-997-080-170	Sequence 170, App
38	42	28.4	348	2	US-08-997-362-170	Sequence 170, App
39	42	28.4	348	4	US-09-095-895-170	Sequence 170, App
40	42	28.4	348	4	US-09-324-542-170	Sequence 170, App
41	42	28.4	393	2	US-08-997-080-94	Sequence 94, Appl1
42	42	28.4	393	3	US-08-997-362-94	Sequence 94, Appl1
43	42	28.4	393	3	US-08-873-970-94	Sequence 94, Appl1
44	42	28.4	393	3	US-09-095-895-94	Sequence 94, Appl1
45	42	28.4	393	4	US-09-324-542-94	Sequence 94, Appl1

ALIGNMENTS

RESULT 1
US-08-333-565-2
Sequence 2, Application US/08333565
Patent No. 5622892
GENERAL INFORMATION:
APPLICANT: KORMEYER, Stanley J.
TITLE OF INVENTION: BCL-2/BCL-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 39
KNOWLEDGE OF SEQUENCES: 39
ADDRESS: 3799 Townsend Drive
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,565
FILING DATE: 31-Oct-1994
CLASSIFICATION: A61K31/00
INVENTOR: Smith, William M.
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15/26A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
FAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
NOISE TYPE: Protein
FEATURES:
NAME/KEY: Protein
LOCATION: 1..204
OTHER INFORMATION: /note="Reduced amino acid sequence of mouse RAD."

Query Match 93.2% Score 138 DB 1: Length 204:
Best Local Similarity 100.0% Pred. No. 1e-13:
Matches 26: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 NLMANRYGRELIRMSDEFGSFGL 27
 |||||||||||||||||||
 Db 140 NLMANRYGRELIRMSDEFGSFGL 165

RESULT 2
 US-08-661-479-2
 : Sequence 2, Application US/08661479
 : Patent No. 5834209
 : GENERAL INFORMATION:
 : APPLICANT: KORSMEYER, Stanley J.
 : TITLE OF INVENTION: BCL-X/BCL-2 ASSOCIATED CELL DEATH
 : NUMBER OF INVENTIONS: 1
 : NUMBER OF CLAIMS: 19
 : CORRESPONDENCE ADDRESS:
 : ATTORNEY/AGENT INFORMATION:
 : STREET: 379 Lytton Avenue
 : CITY: Palo Alto
 : STATE: California
 : COUNTRY: US
 : ZIP: 94301
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : FILING DATE: 11-JUN-1995
 : PRIORITY DATE: 11-JUN-1995
 : PRIORITY APPLICATION DATA:
 : APPLICATION NUMBER: US 08/333,565
 : FILING DATE: 31-OCT-1994
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Smith, William M.
 : REGISTRATION NUMBER: 30,223
 : REFERENCE/DOCKET NUMBER: 15726A-000700
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (415) 326-2400
 : TELEFAX: (415) 326-2422
 : INFORMATION FOR SEQ ID NO: 2:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 204 amino acids
 : STRANDEDNESS: linear
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : FEATURE:
 : NAME/KEY: Protein
 : LOCATION: 1..204
 : OTHER INFORMATION: /note="Deduced amino acid sequence
 : OTHER INFORMATION: of mouse BAD."*
 US-08-661-479-2

Query Match 93.2%; Score 138; DB 2; Length 204;
 Best Local Similarity 100.0%; Pred. No. 1e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NLMANRYGRELIRMSDEFGSFGL 27
 |||||||||||||||||||
 Db 140 NLMANRYGRELIRMSDEFGSFGL 165

RESULT 3
 US-08-733-505A-1
 : Sequence 1, Application US/08733505A
 : Patent No. 5856445
 : GENERAL INFORMATION:
 : APPLICANT: KORSMEYER, Stanley J.
 : TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
 : TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR

NUMBER OF SEQUENCES: 60
 CORRESPONDENCE ADDRESS:
 ADDRESS: HOWELL & HAFERKAMP, L.C.
 STREET: 7733 FORSYTH BLVD., SUITE 1400
 CITY: ST. LOUIS
 STATE: MISSOURI
 COUNTRY: USA
 ZIP: 63105
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/733,505A
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: HOLLAND, DONALD R.
 REGISTRATION NUMBER: 35,197
 REFERENCE/DOCKET NUMBER: 965458
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (314) 727-5188
 TELEFAX: (314) 727-6092
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 204 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-733-505A-1

Query Match 93.2%; Score 138; DB 2; Length 204;
 Best Local Similarity 100.0%; Pred. No. 1e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NLMANRYGRELIRMSDEFGSFGL 27
 |||||||||||||||||||
 Db 140 NLMANRYGRELIRMSDEFGSFGL 165

RESULT 4
 US-08-733-505A-12
 : Sequence 12, Application US/08733505A
 : Patent No. 5856445
 : GENERAL INFORMATION:
 : APPLICANT: KORSMEYER, Stanley J.
 : TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
 : NUMBER OF SEQUENCES: 60
 : CORRESPONDENCE ADDRESS:
 ADDRESS: HOWELL & HAFERKAMP, L.C.
 STREET: 7733 FORSYTH BLVD., SUITE 1400
 CITY: ST. LOUIS
 STATE: MISSOURI
 COUNTRY: USA
 ZIP: 63105
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/733,505A
 FILING DATE:
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: HOLLAND, DONALD R.
 REGISTRATION NUMBER: 35,197
 REFERENCE/DOCKET NUMBER: 965458
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-505A-12

Query Match 93.2%; Score 138; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 NIMAORYGRELRRMSDEFGSFKGL 27
|||||
DB 140 NIMAORYGRELRRMSDEFGSFKGL 165

RESULT 5
US-08-733-505A-13
Sequence 13, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSER: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-505A-13

Query Match 93.2%; Score 138; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 NIMAORYGRELRRMSDEFGSFKGL 27
|||||
DB 140 NIMAORYGRELRRMSDEFGSFKGL 165

RESULT 6

US-08-733-505A-14
Sequence 14, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSER: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-505A-14

Query Match 93.2%; Score 138; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 NIMAORYGRELRRMSDEFGSFKGL 27
|||||
DB 140 NIMAORYGRELRRMSDEFGSFKGL 165

RESULT 7
US-08-717-123-3
Sequence 3, Application US/08717123
Patent No. 5965703
GENERAL INFORMATION:
APPLICANT: Horne, William A.
TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
ACIDS AND METHODS OF USE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

```

: APPLICATION NUMBER: US/08/717,123
: FILING DATE: 20-SEP-1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Campbell, Cathryn A.
: REGISTRATION NUMBER: 31,815
: REFERENCE/DOCKET NUMBER: P-ID 1929
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 535-9001
: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 204 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
:
: US-08-717-123-3

Query Match          91.2% Score 135; DB 2; Length 204;
Best Local Similarity 96.2%; Pred. No. 2,9e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      2 NLMAAORYGRLRMSDEFGSFKL 27
DB      140 NLMAAORYGRLRMSDEFGSFKL 165

RESULT      8
US-08-665-617-2
: Sequence 2, Application US/08665617
: Patent No. 5663316
: GENERAL INFORMATION:
: APPLICANT: Hudson, Yin
: REGISTRATION NUMBER: 31,815
: REFERENCE/DOCKET NUMBER: P-ID 1929
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 535-9001
: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 168 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
:
: MOLECULE TYPE: protein
:
: US-08-665-617-2

Query Match          77.0% Score 114; DB 1; Length 168;
Best Local Similarity 91.7%; Pred. No. 3.7e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      2 NLMAAORYGRLRMSDEFGSFK 25
```

```

DB      101 NLMAAORYGRLRMSDEFGSFK 124

RESULT      9
US-08-717-123-2
: Sequence 2, Application US/08717123
: Patent No. 5965703
: GENERAL INFORMATION:
: APPLICANT: Horne, William A.
: REGISTRATION NUMBER: 31,815
: REFERENCE/DOCKET NUMBER: P-ID 1929
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 535-9001
: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 168 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
:
: MOLECULE TYPE: protein
:
: US-08-717-123-2

Query Match          77.0% Score 114; DB 2; Length 168;
Best Local Similarity 91.7%; Pred. No. 3.8e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      2 NLMAAORYGRLRMSDEFGSFK 25
DB      103 NLMAAORYGRLRMSDEFGSFK 126

RESULT      10
US-08-985-335-1
: Sequence 1, Application US/08985335
: Patent No. 6080847
: GENERAL INFORMATION:
: APPLICANT: Hillman, Jennifer L.
: REGISTRATION NUMBER: 31,794
: REFERENCE/DOCKET NUMBER: CL-8
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (352) 372-5800
: TELEFAX: (352) 372-5800
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 166 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: MOLECULE TYPE: protein
:
: US-08-665-617-2

Query Match          77.0% Score 114; DB 1; Length 166;
Best Local Similarity 91.7%; Pred. No. 3.7e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      2 NLMAAORYGRLRMSDEFGSFK 25
```

```

? COUNTRY: USA
? ZIP: 94304
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FASTSEQ for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/985,335
? FILING DATE: Filed Herewith
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Billings, Lucy J.
? REGISTRATION NUMBER: 36,749
? REFERENCE/DOCKET NUMBER: PF-0421 US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 650-845-4166
? TELEFAX: 650-845-0555
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 168 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? IMMEDIATE SOURCE:
? LIBRARY: SYNORAB01
? CLONE: 358673
? US-08-985-335-1

Query Match 77.0%; Score 114; DB 3; Length 168;
Best Local Similarity 91.7%; Pred. No. 3,8e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 NMAAORRGRLRMSDFEVSFK 25
DB 103 NMAAORRGRLRMSDFEVSFK 126

RESULT 11
US-08-985-335-7
? Sequence 7, Application US/08985335
? Patent No. 6080847
? GENERAL INFORMATION:
? APPLICANT: Hillman, Jennifer L.
? APPLICANT: Yue, Henry
? APPLICANT: Lal, Preeti
? APPLICANT: Shah, Purni
? APPLICANT: Corley, Neil C.
? TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
? TITLE OF INVENTION: PROLIFERATION
? NUMBER OF SEQUENCES: 9
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Incyte Pharmaceuticals, Inc.
? STREET: 3174 Porter Dr.
? CITY: Palo Alto
? STATE: CA
? COUNTRY: USA
? ZIP: 94304
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? OPERATING SYSTEM: DOS
? SOFTWARE: FASTSEQ for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/985,335
? FILING DATE: Filed Herewith
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:

```

```

? NAME: Billings, Lucy J.
? REGISTRATION NUMBER: 36,749
? REFERENCE/DOCKET NUMBER: PF-0421 US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 650-845-0555
? TELEFAX: 650-845-4166
? INFORMATION FOR SEQ ID NO: 7:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 168 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? IMMEDIATE SOURCE:
? LIBRARY: Genbank
? CLONE: 1683637
? US-08-985-335-7

Query Match 77.0%; Score 114; DB 3; Length 168;
Best Local Similarity 91.7%; Pred. No. 3,8e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 NMAAORRGRLRMSDFEVSFK 25
DB 103 NMAAORRGRLRMSDFEVSFK 126

RESULT 12
US-09-410-372-1
? Sequence 1, Application US/09410372
? Patent No. 6281334
? GENERAL INFORMATION:
? APPLICANT: Hillman, Jennifer L.
? APPLICANT: Yue, Henry
? APPLICANT: Lal, Preeti
? APPLICANT: Shah, Purni
? APPLICANT: Corley, Neil C.
? TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
? TITLE OF INVENTION: PROLIFERATION
? NUMBER OF SEQUENCES: 9
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Incyte Pharmaceuticals, Inc.
? STREET: 3174 Porter Dr.
? CITY: Palo Alto
? STATE: CA
? COUNTRY: USA
? ZIP: 94304
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? OPERATING SYSTEM: DOS
? SOFTWARE: FASTSEQ for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/410,372
? FILING DATE:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/985,335
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Billings, Lucy J.
? REGISTRATION NUMBER: 36,749
? REFERENCE/DOCKET NUMBER: PF-0421 US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 650-845-0555
? TELEFAX: 650-845-4166
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 168 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? IMMEDIATE SOURCE:
? LIBRARY: SYNORAB01

```

CLONE: 358673
US-09-410-372-1

Query Match 77.0%; Score 114; DB 4; Length 168;
Best Local Similarity 91.7%; Pred. No. 3.8e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 N1MAA0RYGRELRRMSDFEFGSK 25
DB 103 N1MAA0RYGRELRRMSDFEFGSK 126

RESULT 13

US-09-410-372-7
Sequence 7, Application US/09410372
Patent No. 6281334
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yse, Henry
APPLICANT: Lai, Preeti
APPLICANT: Shih, Puyi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASTESD for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410.372
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985.335
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-845-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1683637
US-09-410-372-7

Query Match 77.0%; Score 114; DB 4; Length 168;
Best Local Similarity 91.7%; Pred. No. 3.8e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 N1MAA0RYGRELRRMSDFEFGSK 25
DB 103 N1MAA0RYGRELRRMSDFEFGSK 126

RESULT 14

US-08-333-565-10
Sequence 10, Application US/08333565
Patent No. 5622852
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-X/Bcl-2 ASSOCIATED CELL DEATH
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333.565
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-333-565-10

Query Match 76.4%; Score 113; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 6.1e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 N1MAA0RYGRELRRMSDFEG 22
DB 3 N1MAA0RYGRELRRMSDFEG 23

RESULT 15

US-08-661-479-10
Sequence 10, Application US/08661479
Patent No. 5634209
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-X/Bcl-2 ASSOCIATED CELL DEATH
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661.479

Fri Sep 20 11:03:16 2002

us-09-544-664-55.rail

Page 7

```

1      ILIING DATE: 11-JUN-1995
2
3      CLASSIFICATION: 435
4
5      PRIOR APPLICATION DATA:
6
7      APPLICATION NUMBER: US 08/333,565
8
9      FILING DATE: 31-OCT-1994
10
11     ATTORNEY/AGENT INFORMATION:
12
13     NAME: Smith, William M
14
15     REGISTRATION NUMBER: 30,223
16
17     REFERENCE/DOCKEN NUMBER: 15726A-0007000
18
19     TEL/COMMUNICATION INFORMATION:
20
21     TELEPHONE: (415) 326-2400
22
23     FAX: (415) 326-2422
24
25     INFORMATION FOR SEO ID NO.: 10:
26
27     SEQUENCE CHARACTERISTICS:
28
29     LENGTH: 23 amino acids
30
31     TYPE: alpha acid
32
33     STRANDEDNESS: single
34
35     TOPOLOGY: linear
36
37     MOLECULE TYPE: peptide
38
39     US-08-661-479-10

```

```

Query Match      76.44; Score 113; DB 2; length 23;
Best Local Similarity 100.0%; Pred. No. 6 le-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
Qy      2  NMAAORTGRELRLMSDFEG 22
         |||||
Db      3  NMAAORTGRELRLMSDFEG 23

```

Search completed: September 20, 2002, 10:37:21
Job time: 409 sec

Page 7

• • •

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2002, 10:39:12 : Search time 95.59 Seconds
(without alignments)
28.146 Million cell updates/sec

Title: US-09-544-664-55

Percent score: 148

Sequence: 1 KNMAAGRGRLRMSDFECSFKLK 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR71.*
2: PIR1.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	138	93.2	204	2	bad protein - mouse
2	54	36.5	946	2	inter-alpha-trypt
3	53	35.8	223	2	hypothetical prote
4	53	35.8	946	2	inter-alpha-inhibi
5	52	35.1	370	2	2-dehydro-3-deoxy
6	51	34.5	232	2	floral homeotic pr
7	50	33.8	374	2	spermidine/nitric
8	50	33.8	516	2	probable threonine
9	50	33.8	1378	2	DNA-directed RNA p
10	49.5	33.4	127	2	glycerol-3-phospho
11	49	33.1	453	2	conserved hypotet
12	48.5	32.8	134	2	ER517
13	48.5	32.8	314	2	transforming prote
14	48	32.4	266	2	transferrin p15 - maiz
15	48	32.4	220	2	oxidoreductase, so
16	48	32.4	526	2	threonine synthase
17	48	32.4	1164	2	hypothetical prote
18	47.5	32.1	334	2	Arthro-Famide neur
19	47.5	32.1	1140	2	hypothetical prote
20	47	31.8	287	2	neuropeptide pol-R
21	47	31.8	597	2	oxalacetate decar
22	47	31.8	967	2	oxoglutarate dehyd
23	47	31.8	5138	2	hypothetical prote
24	46.5	31.4	314	2	anemxin P33 - maiz
25	46.5	31.4	435	2	Arthro-Famide prec
26	46	31.1	165	2	chloroformin chai
27	46	31.1	399	2	probable polyamine
28	46	31.1	946	1	inter-alpha-trypt
29	45.5	30.7	261	2	conserved hypotet

30	45.5	30.7	327	2	D97636	probable secreted
31	45.5	30.7	327	2	A62839	conserved hypotet
32	45.3	30.7	562	2	C71473	hypothetical prote
33	45.3	30.7	805	2	G88314	NADH dehydrogenase
34	45.3	30.7	1014	2	F38091	exonuclease ABC c
35	45	30.4	273	2	S08726	phosphatase 11 by
36	45	30.4	273	2	A62267	mannanase stabiliz
37	45	30.4	295	2	F85201	conserved hypotet
38	45	30.4	346	2	B93106	hypothetical prote
39	45	30.4	486	2	T31224	conserved hypotet
40	45	30.4	521	2	B46105	sodium ion pump
41	45	30.4	591	2	A68029	oxalacetate decar
42	45	30.4	596	2	A28088	oxalacetate decar
43	45	30.4	715	2	A25575	probable membrane
44	45	30.4	804	1	VCL064	env polypeptide
45	45	30.4	804	1	VCL064	env polypeptide

ALIGNMENTS

Result 1
A:55671
bad protein - mouse
C:Species: Mus musculus (house mouse)
C:Accession: A55671
C:Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 05-Nov-1999
R:Yang B, Zha U, Jockel, J., Boise, L.H., Thompson, C.B., Korsmeyer, S.J.
Cell 80, 285-291, 1995
A:Title: Bad a heterodimeric partner for bcl-x-L and bcl-2, displaces Bax and promot
A:Reference number: A55671; MUID:95136561
A:Accession: A55671
A:Status: Preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-204 <YAN>
A:Cross-references: GB:I37296; NID:9639778; PIDN:AAA6465.1; PID:9639779
C:Keywords: heterodimer

Query Match 93.2% Score 138; DB 2; length 204;
Best local similarity 100.0%; Pred. No. 1.2e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 KNMAAGRGRLRMSDFECSFKLK 27
DB 140 KNMAAGRGRLRMSDFECSFKLK 165
Result 2
JCS575
inter-alpha-tryptin inhibitor heavy chain 2 - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
A:Accession: JCS575; PC4485
R:Nakatsuji, T.; Suzuki, Y.; Yamamoto, T.; Shinohara, H.
J. Biochem. 122, 71-82, 1997
A:Title: Molecular cloning and sequencing of cDNAs encoding three heavy-chain precurs
sin inhibitor heavy chain family
A:Reference number: JCS575; MUID:97420688
A:Accession: JCS575
A:Molecule type: mRNA
A:Residues: 1-946 <NKA>
A:Cross-references: DDBJ:D89286; NID:91694689; PIDN:BAVA1393.1; PID:91694690
A:Experimental source: Liver
A:Accession: PC4485
A:Molecule type: protein
A:Residues: 55-64,140-146,151-156,424-447,500-528,577-605 <NKA>
C:Comment: In the plasma three inter-alpha-tryptin inhibitor heavy chains 1, 2 and 3
that the complexes play important role for pancreatic cancer.
C:Superfamily: inter-alpha-tryptin inhibitor complex component II
F:261-264,717-916/Disulfide bonds: #status predicted


```

A:Title: The homeotic gene ABP1AAL3 of Arabidopsis thaliana encodes a MADS box and is e
A:Reference number: AA2095; MUID:92154682
A:Accession: AA2095
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-232 <JAC>
A:Cross-references: GB:M86357; NID:g166607; PIDN:AAA32740.1; PID:g166608
A:Experimental source: petals, stamens
A:Note: Sequence extracted from NCBI backbone (NCBIN:82520, NCBIPI:82521)
R:Okamoto, H.; Yano, A.; Shiraiishi, H.; Okada, K.; Shimura, Y.
Plant Mol. Biol. 26, 465-472, 1994
A:Title: Genetic complementation of a floral homeotic mutation, apetala3, with an Arabid
A:Reference number: S52633; MUID:95036018
A:Accession: S52633
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-63 <OKA>
A:Cross-references: GB:D21125
R:Blocker, H.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quettler, F.; Salanoubat M.Mewes
Submitted to the Protein Sequence Database, March 2000
A:Accession: Y47593
A:Reference number: Z24469
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-232 <BL0>
A:Cross-references: EMBL:AL132971
A:Experimental source: cultivar Columbia; BAC clone T12E18
C:Genetics:
A:Map position: 3
A:Introns: 63/2; 85/3; 106/2; 139/3; 153/3; 166/3
A:Note: T12E18.30
C:Superfamily: Transcription factor squa; serum response factor DNA-binding domain homol
C:Keywords: DNA binding; nucleus; transcription regulation
F:2-57/Domain: serum response factor DNA-binding domain homology <SRF>

Query Match      34.5%; Score 51; DB 2; Length 232;
Best Local Similarity 44.4%; Pred. No. 7.3;
Matches 12; Conservative 3; Mismatches 4; Indels 0; Gaps 1;

OY      7 ORYG-----RELRLMSDFECSFK 25
Db      107 QRIQELDLIDLTQIRLRLEDEMENTFR 133

RESULT      7
CBA4338
Spermidine/putrescine ABC transporter [imported] - Halobacterium sp. NRC-1.
C:Species: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: CBA4338
R:Leibhauser, B.; Keller, K.; Guiz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabbid
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebdhardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: AB4160; MUID:20504483
A:Accession: CBA4338
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-374 <STO>
A:Cross-references: GB:AE004437; NID:g1059314; PIDN:AAG20071.1; GSPDB:GN00138
C:Genetics:
A:Gene: polA2

Query Match      33.8%; Score 50; DB 2; Length 374;
Best Local Similarity 76.9%; Pred. No. 17;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY      12 ELRRMSDFECSF 24
|||||  ||||

```

[illegible]

glycerol-3-phosphate cytidyltransferase (gct), CDP-glycerol pyrophosphorylase (telchd)
 C:Species: Listeria monocytogenes
 C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
 C:Accession: A11210
 R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, J.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Ertlan, K.D.; Fathl, H.; Jones, L.M.; Karel, U.
 Science 294, 849-852, 2001
 A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurepatic, G.; Maduno, E.; Maltournam, A.; Mok, C.; Schlueter, T.; Simoes, N.; Terrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.
 A>Title: Comparative genomics of *Listeria* species.
 A:Reference number: AB1077; MUID:2157279; PMID:11679669
 A:Accession: A11210
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 11127 <GLN>
 A:Cross-References: GB:NC_003210; PIDN:CA09167.1; PID:g16410491; GSPDB:GN0177
 A:Experimental source: strain Ecd-e
 C:Genetics:
 A:Gene: tagd

Query Match 33.4%, Score 49.5; DB 2; Length 127;
 Best Local Similarity 36.4%; Pred. No. 6;
 Matches 12; Conservative 6; Mismatches 10; Indels 5; Gaps 1;
 Oy 1 KNLMAOR-----YGRRLRMSDEFGSRKGLK 28,
 Db 71 ENMDEKNDLEKIGIDIVKMDDEDFDLK 103

RESULT 11
 E83517
 conserved hypothetical protein PA1031 (imported) - *Pseudomonas aeruginosa* (strain PA01)
 C:Species: *Pseudomonas aeruginosa*
 C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: E83517
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B. Adman, S.; Yun, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kass, A.; Lathig, K.; Lim, J.; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A>Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen.
 A:Reference number: AB2950; MUID:20437337
 A:Accession: E83517
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1453 <STO>
 A:Cross-References: GB:AE004535; GB:AE004091; MID:g9946936; PIDN:AA04420.1; GSPDB:GN001
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA1031

Query Match 33.1%, Score 49; DB 2; Length 453;
 Best Local Similarity 55.6%; Pred. No. 28;
 Matches 10; Conservative 4; Mismatches 2; Indels 2; Gaps 1;
 Oy 4 MAOARYGR-ELRMSDE 19
 Db 65 WASERGREELRLASE 82

RESULT 12
 S40376
 Ig kappa chain - human
 C:Species: Homo sapiens (man)
 C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C:Accession: S40376
 R:Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A>Title: Expressed human immunoglobulin chl genes and their hypermutation.
 A:Reference number: S40312; MUID:9408091
 A:Accession: S40376

A>Status: preliminary; translation not shown
 A:Molecule type: RNA
 A:Residues: 1-134 <LE>
 A:Cross-References: EMBL:X72486; MID:g441440; PIDN:CA03154.1; PID:g441441
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:34-113/Domain: immunoglobulin homology <IMX>

Query Match 32.8%; Score 48.5; DB 2; Length 134;
 Best Local Similarity 38.2%; Pred. No. 9;
 Matches 13; Conservative 1; Mismatches 9; Indels 11; Gaps 1;
 Oy 4 MAOARYGR-ELRMSDEFGSRK 26
 Db 58 WROPRGSRFRRLIYNVSKRDSGVSDRFGSG 91

RESULT 13
 T02975
 annexin p35 - maize
 C:Species: Zea mays (maize)
 C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
 C:Accession: T02975
 R:Battley, N.H.; James, N.C.; Greenland, A.J.
 Plant Physiol. 112, 1391-1396, 1996
 A>Title: cDNA isolation and gene expression of maize annexin p35 and p35.
 A:Reference number: Z14796; MUID:97092863
 A:Accession: T02975
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-314 <KMT>
 A:Cross-References: EMBL:X8245; MID:g1370602; PIDN:CAA6690.1; PID:g1370603
 A:Experimental source: cultivar GILPEER; root LIP
 C:Superfamily: annexin I; annexin repeat homology
 F:14-85/Domain: annexin repeat homology <AXR>

Query Match 32.8%; Score 48.5; DB 2; Length 314;
 Best Local Similarity 47.8%; Pred. No. 23;
 Matches 10; Conservative 4; Mismatches 6; Indels 1; Gaps 1;
 Oy 6 NORVGR-IPRMSDFGSRK 25
 Db 54 AYAYGRRLALGDFIRKFE 74

RESULT 14
 C36365
 transforming protein homolog MRAS3 - *Rhizomucor racemosus*
 C:Species: *Rhizomucor racemosus*
 C>Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 19-Jan-2001
 C:Accession: C36365
 R:Casale, W.L.; McConnell, D.G.; Wang, S.Y.; Lee, Y.J.; Linz, J.E.
 Mol. Cell. Biol. 10, 6654-6663, 1990
 A>Title: Expression of a gene family in the dimorphic fungus *Mucor racemosus* which ex
 A:Reference number: A36365; MUID:91061774
 A:Accession: C36365
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-206 <CAS>
 A:Cross-References: GB:M55177
 C:Superfamily: ras transforming protein; translation elongation factor Tu homology
 C:Keywords: GTP binding; nucleotide binding; P-loop
 F:11-126/Domain: translation elongation factor Tu homology <ETU>
 F:117-126/Region: nucleotide-binding motif A (P-loop)
 F:153-155/Region: GTP-binding NKX/L motif
 F:153-155/Region: GTP-binding SAK/L motif
 F:23,24,42,123,124,126,153/Binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser) #

Query Match 32.4%; Score 48; DB 2; Length 206;
 Best Local Similarity 62.5%; Pred. No. 18;

•
•
•
•

•
•

•

•

•

•

•
•

•

GenCote version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2002, 11:04:34 ; Search time 44.99 seconds

(without alignments)
24.098 Million cell updates/sec

Title: US-09-544-664-55

Sequence: 1 KNMAAORYGRELRLMSDEFGSKGLK 28

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_40.*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	138	93.2	204	1	BAD_MOUSE
2	138	93.2	205	1	BAD_MOUSE
3	114	77.0	168	1	BAD_HUMAN
4	54	36.5	946	1	ITIH2_MOUSE
5	52	35.8	946	1	ITIH2_MOUSE
6	52	35.1	370	1	AROG_YEAST
7	51	34.5	232	1	AP3_ARATH
8	50	33.8	1378	1	PROB_CAMEL
9	49	33.1	453	1	RMUC_PSEAE
10	48	32.4	205	1	RAS3_HIRPA
11	48	32.4	220	1	6PGC_THIEMO
12	48	32.4	519	1	6PGC_THIEMO
13	48	32.4	526	1	THRC_SOLTU
14	47.5	32.1	334	1	FMRA_CALPA
15	47	31.8	198	1	BIM_HUMAN
16	47	31.8	287	1	PRFA_POLPE
17	46.5	31.4	429	1	FMRI_AYTEL
18	46.5	31.4	435	1	FMRI_AYTEL
19	46	31.1	946	1	ITIH2_HUMAN
20	45.5	30.7	1014	1	UVRA-STROO
21	45	30.4	273	1	PSBO_AVASP
22	45	30.4	328	1	SNF4_KLULA
23	45	30.4	590	1	DCOA_SALTY
24	45	30.4	593	1	DCOA_KLEPN
25	45	30.4	653	1	HTV2_HUMAN
26	45	30.4	865	1	HTV2_HUMAN
27	45	30.4	1557	1	LMJ1_CHEBL
28	44.5	30.1	907	1	NOOG_ECOLI
29	44.5	30.1	907	1	NOOG_ECOLI
30	44	29.7	196	1	BIM_MOUSE
31	44	29.7	196	1	BIM_MOUSE
32	44	29.7	262	1	ENDB_ECOLI
33	44	29.7	629	1	SYM_THIEMO

34	44	29.7	768	1	ENV_SIVAI
35	44	29.7	877	1	ENV_SIVAG
36	44	29.7	978	1	RA50_AQUAE
37	44	29.7	1790	1	USOL_YEAST
38	44	29.7	1966	1	MYSB_CAEEL
39	43.5	29.4	217	1	UREF_SYNY3
40	43.5	29.4	1200	1	DPG1_XENLA
41	43	29.1	377	1	APJ_MOUSE
42	43	29.1	380	1	APJ_HUMAN
43	43	29.1	380	1	APJ_MOUSE
44	43	29.1	453	1	DHAP_MOUSE
45	43	29.1	463	1	Y030_NPVAC

ALIGNMENTS

RESULT	1	STANDARD	PCT	204 AA.
BAD_MOUSE				
ID	BAD_MOUSE			
AC	061337			
DT	01-NOV-1997 (rel. 35, Created)			
DT	01-NOV-1997 (rel. 35, Last sequence update)			
DT	01-MAR-2002 (rel. 41, Last annotation update)			
DE	Bcl2 antagonist of cell death (BAD) (Bcl-2 binding component			
DE	6) (bcl-xl/bcl-2 associated death promoter).			
OS	BAD OR BbC6.			
OS	mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI-TaxID=10090;			
RN	1			
RF	SEQUENCE FROM N.A.			
RF	TRISUP-BRAIN AND THYMUS:			
RA	MEDLINE=95136361; PubMed=7834748;			
RA	Yang E, Zhai J, Jockel J, Bolse L.H., Thompson C.B., Korsmeyer S.J.;			
RT	*Bad*, heterodimeric partner for Bcl-XL and Bcl-2, displaces Bax and			
RT	promotes cell death *.			
RL	Cell 80:285-291(1995).			
RN	[2]			
RP	PHOSPHORYLATION, AND MUTAGENESIS OF SER-112 AND SER-136.			
RX	MEDLINE=98022381; PubMed=9381178;			
RA	Del Peso L., Gonzalez-Garcia M., Page C., Herrera R., Nunez G.;			
RT	*Interleukin-3-induced phosphorylation of BAD through the protein			
RT	kinase Akt*.			
RL	Science 278:687-689(1997).			
RN	[3]			
RP	MUTAGENESIS OF SERINE RESIDUES.			
RA	MEDLINE=20403302; PubMed=10949026;			
RA	Datta S.R., Kato A., Hu L., Petros A., Fesik S.W., Yaffe M.B.;			
RT	*14-3-3 proteins and survival kinases cooperate to inactivate BAD by			
RT	BH3 domain phosphorylation*.			
RL	Mol. Cell 6:41-51(2000).			
CC	-1- FUNCTION: Promotes cell death. Successfully competes for the			
CC	binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level			
CC	of heterodimerization of these proteins with BAX. Can reverse the			
CC	death repressor activity of Bcl-x(L), but not that of Bcl-2.			
CC	Appears to act as a link between growth factor receptor signaling			
CC	and the apoptotic pathways.			
CC	-1- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-			
CC	x(L), Bcl-2 and Bcl-w. Also binds Bcl-2 (by similarity).			
CC	The Ser-112/Ser-136 phosphorylated form binds 14-3-3 proteins.			
CC	-1- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon			
CC	phosphorylation, localizes to the cytoplasm.			
CC	-1- DOMAIN: Inactive BH3 domain is required by BIR, BID, BAK, BAD AND			
CC	BAX for their pro-apoptotic activity and for their interaction			
CC	with anti-apoptotic members of the Bcl-2 family.			
CC	-1- PTM: Phosphorylated on Ser-112 in response to survival stimuli.			
CC	Subsequent phosphorylation on Ser-136 promotes heterodimerization			
CC	with 14-3-3 proteins. This interaction then facilitates the			
CC	phosphorylation at Ser-155, a site within the BH3 domain, leading			
CC	to the release of Bcl-x(L) and the promotion of cell survival.			

CC Ser-136 is the major site of AKT/PKB phosphorylation. Ser-135 the
 CC major site of apoptosis kinase A (GSK-3) phosphorylation.
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: L37296; AAA64465.1; -
 CC DR MGD: MGI:1096330; Bad.
 CC DR InterPro: IPR000712; FALSE_NEG.
 CC DR PROSITE: PS01259; BH3; FALSE_NEG.
 CC KM Apoptosis; Phosphorylation.
 CC FT DOMAIN 147 161 BH3.
 CC FT MOD_RES 112 112 PHOSPHORYLATION (BY CAPK AND PKB).
 CC FT MOD_RES 136 136 PHOSPHORYLATION (BY CAPK AND PKB).
 CC FT MOD_RES 155 155 PHOSPHORYLATION (BY CAPK AND PKB).
 CC FT MUTAGEN 112 112 S->A: NO PHOSPHORYLATION.
 CC FT MUTAGEN 136 136 S->A: NO PHOSPHORYLATION.
 CC FT MUTAGEN 155 155 S->A: NO PHOSPHORYLATION.
 CC FT INTERACTS WITH BCL-X(L).
 CC SEQUENCE 204 AA: 22080 MW: 6C2BA910205053F7 CRC64:
 SO
 Query Match 93.2%; Score 138; DB 1; Length 204;
 Best Local Similarity 100.0%; Pred. No. 17e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 2 N1MAAGRYCRLRMDEPESFGKL 27
 Db 140 N1MAAGRYCRLRMDEPESFGKL 165
 ID BAD_RAT STANDARD: PRT; 205 AA.
 AC 035147; C70256; 09YHX1;
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DE 01-MAR-2002 (Rel. 41; Last annotation update)
 DE Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component
 DE 6) (Bcl-XL/Bcl-2 associated death promoter).
 GN BAD.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF SER-113 AND SER-137.
 RC TISSUE=Ovary;
 RC MEDLINE=98034386; PubMed=9369453;
 RA Hsu S.-Y., Karpila A., Zhu L., Hsueh A.-J.W.;
 RA "Inference of BAD (Bcl-XL/Bcl-2-associated death promoter)-induced
 RA apoptosis in mammalian cells by 14-3-3 isoforms and P11";
 RL Mol. Endocrinol. 11:1858-1867(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RC MEDLINE=98194755; PubMed=9535132;
 RA Nigam V., Magro G., Trevall S., Musco S., Cavallaro S.;
 RA "Cloning and expression of the programmed cell death regulator BAD in
 RA the rat brain";
 RL Neurosci. Lett. 243:137-140(1998).
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
 RC TISSUE=Brain;
 RX MEDLINE=21109372; PubMed=11161472;
 RX Hammer S., Arumae U., Yu L.-Y., Sun Y.-F., Saarna M., Lindholm D.;

RM *Functional characterization of two splice variants of rat BAD and
 RM their interaction with Bcl-X(L) sympathetic neurons.*
 RM Mol. Endocrinol. 17:97-104(2001)
 CC -1- FUNCTION: Bcl-2 and Bcl-X(L) are fully competent for the
 CC binding to Bcl-X(L). Bcl-2 and Bcl-X(L) thereby affecting the level
 CC of heterodimerization of these proteins with BAX can reverse the
 CC death repressor activity of Bcl-X(L) but not that of Bcl-2 (by
 CC similarity). Appears to act as a link between growth factor
 CC receptor signaling and the apoptotic pathways.
 CC -1- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-
 CC X(L), Bcl-2 and Bcl-W. Also binds protein S100A10. The Ser-
 CC 113/Ser-137 phosphorylated form binds 14-3-3 proteins.
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon
 CC phosphorylation, localizes to the cytoplasm (by similarity).
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; alpha (shown here) and beta; are
 CC produced by alternative splicing. They differ only in their C-
 CC terminal regions.
 CC -1- TISSUE SPECIFICITY: Expressed in all tissues tested, including
 CC brain, liver, spleen and heart. In the brain, restricted to
 CC epithelial cells of the choroid plexus. Isoform alpha is the more
 CC abundant form.
 CC -1- DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND
 CC BAX for their pro-apoptotic activity and for their interaction
 CC with anti-apoptotic members of the Bcl-2 family.
 CC -1- PTM: Phosphorylated on Ser-113 in response to survival stimuli.
 CC Subsequent phosphorylation on Ser-137 promotes heterodimerization
 CC with 14-3-3 proteins. This interaction then facilitates the
 CC phosphorylation at Ser-156, a site within the BH3 domain, leading
 CC to the release of Bcl-X(L) and the promotion of cell survival.
 CC Ser-137 is the major site of AKT/PKB phosphorylation. Ser-156 the
 CC major site of protein kinase A (CAPK) phosphorylation (by
 CC similarity).
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF003523; AAC53374.1; -
 CC DR EMBL: AF031227; AAC15100.1; -
 CC DR EMBL: AF279910; AAF91427.1; -
 CC DR EMBL: AF279911; AAF91428.1; -
 CC DR InterPro: IPR000712; BCL-2.
 CC DR PROSITE: PS01259; BH3; FALSE_NEG.
 CC KM Apoptosis; Phosphorylation; Alternative splicing.
 CC FT DOMAIN 148 162 BH3.
 CC FT MOD_RES 113 113 PHOSPHORYLATION (BY CAPK AND PKB) (BY
 CC SIMILARITY).
 CC FT MOD_RES 137 137 PHOSPHORYLATION (BY CAPK AND PKB) (BY
 CC SIMILARITY).
 CC FT MOD_RES 156 156 PHOSPHORYLATION (BY CAPK AND PKB) (BY
 CC SIMILARITY).
 CC FT VARSPLIC 166 205 LPRPSAGYATQKQSNWRTIISQWDRNUGSGSTPSQ
 CC -> EELTYSVEELKALNEMSLPLNLSRQSPPTPTP
 CC EVAMPKRWTLALRLC (IN ISOFORM BETA).
 CC S->A: NO EFFECT ON HETERODIMERIZATION
 CC WITH 14-3-3 PROTEINS.
 CC FT MUTAGEN 113 113 WITH 14-3-3 PROTEINS.
 CC FT MUTAGEN 137 137 WITH 14-3-3 PROTEINS.
 CC FT MUTAGEN 156 156 WITH 14-3-3 PROTEINS.
 CC FT NO HETERODIMERIZATION WITH 14-3-3
 CC PROTEINS. NO EFFECT ON HETERODIMERIZATION
 CC WITH BCL2 NOR WITH PROTEIN P11.
 CC FT NO HETERODIMERIZATION WITH BCL2
 CC NOR WITH PROTEIN P11.
 CC CONFLICT 29 34 SHONG > BAKER (INFER. 1).
 SO SEQUENCE 205 AA: 22228 MW: 7A9A1DNEC94AD1 CRC64:
 Query Match 93.2%; Score 138; DB 1; Length 205;
 Best Local Similarity 100.0%; Pred. No. 1.7e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XY	2	NLMAORGRELRMSDEPESFGL 27
Db	141	NLMAORGRELRMSDEPESFGL 166
	RESULT 3	
	BAD_HUMAN	
TD	BAD_HUMAN	STANDARD; PRT; 168 AA.
AC	092934; 014803;	
DT	01-NOV-1997 (Rel. 35, Created)	
DT	16-OCT-2002 (Rel. 47, Last sequence update)	
DT	01-MAR-2002 (Rel. 41, Last annotation update)	
DE	Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component 6) (Bcl-xL/Bcl-2 associated death promoter).	
GN	BAD OR BIRC6 OR BCL2L8.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	
OX	NCBI_Taxid:9606;	
LN	11]	
RP	SEQUENCE FROM N.A.	
RP	Yin D.X., Li Z., Huang B., Chen S., Zhou H.;	
RT	"A human protein that interacts with Bcl-2 and have homology to mouse BAD."	
RL	Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.	
RN	12]	
RP	SEQUENCE FROM N.A., AND PHOSPHORYLATION BY RAF-1.	
RX	MEDLINE:97083574; PubMed:8929533;	
RA	Wang H.-G., Rapp U.R., Reed J.C.;	
RT	"Bcl-2 targets the protein kinase Raf-1 to mitochondria."	
RL	Cell 87:629-638(1996).	
RN	13]	
RP	SEQUENCE FROM N.A.	
RP	Takayama S., Reed J.C.;	
RL	Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.	
RN	14]	
RP	SEQUENCE FROM N.A., AND DIMERIZATION.	
RX	TISSUE-Bone marrow;	
RA	MEDLINE:98049594; PubMed:9398232;	
RT	Ottelle S., Diaz J.-L., Horne N., Chang J., Wang Y., Wilson G., Chang S., Weeks S., Fritz L.C., Oldendorf T.;	
RL	Dimetrization properties of human BAD.?	
RN	J Biol. Chem. 272:30866-30872(1997).	
RN	15]	
RP	SEQUENCE FROM N.A.	
RX	TISSUE-Lung;	
RA	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.	
RL	16]	
RP	STRUCTURE BY NMR OF 103-127.	
RX	MEDLINE:21073561; PubMed:11206074;	
RA	Petros A.M., Nettesheim D.G., Wang Y., Olejniczak E.T., Meadows R.P., Mack J., Swift K., Matuyoshi E.D., Zhang H., Thompson C.B., Fesk S.W.;	
RT	"Rationale for Bcl-xL/Bad peptide complex formation from structure, mutagenesis, and biophysical studies."	
RL	Protein Sci. 9:2528-2534(2000).	
CC	-1- FUNCTION: Promotes cell death. Successfully competes for the binding to Bcl-xL, Bcl-2 and Bcl-w, thereby affecting the level of heterodimerization of these proteins with BAX. Can reverse the death repressor activity of Bcl-xL, but not that of Bcl-2 (by similarity). Appears to act as a link between growth factor receptor signaling and the apoptotic pathways.	
CC	-1- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-xL, Bcl-2 and Bcl-w. Also binds protein S100A10 (By similarity).	
CC	The Ser-75/Ser-99 phosphorylated form binds 14-3-3 proteins (By similarity).	
CC	-1- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon phosphorylation, localizes to the cytoplasm.	
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.	
CC	-1- DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, AND BAX for their pro-apoptotic activity and for their interaction with anti-apoptotic members of the Bcl-2 family.	

```

CC -1- p1m Phosphorylation on Ser-75 in response to survival stimuli.
CC Subsequent phosphorylation on Ser-99 promotes heterodimerization
CC CC14-3-3 proteins. This interaction then facilitates the
CC phosphorylation at Ser-118, a site within the BH3 domain, leading
CC to the release of Bcl-2(l), and the promotion of cell survival.
CC Ser-99 is the major site of AKT/PKB phosphorylation, Ser-118 the
CC major site of protein kinase A (CAK) phosphorylation (by
CC similarity).
CC -1- SIMILARITY: CONTAINS 1 BCL-3 HOMOLOGY DOMAIN 3 (BH3).
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation in
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U66879; AAB36516.1; -.
CC DR EMBL; AF021792; AAB72092.1; -.
CC DR EMBL; AF031523; AAB88124.1; -.
CC DR EMBL; BC001901; AAH01901.1; -.
CC PDB; 1G57; 07-FEB-01.
CC MIM; 603167; -.
CC DR InterPro; IPR000712; BCL-2.
CC DR PROSITE; PS01259; BH3; FALSE_NEG.
CC KW Apoptosis; Phosphorylation; 3D-structure.
CC FM DOMAIN 110 124
CC FM MOD_RES 75 75
CC FM MOD_RES 99 99
CC FM MOD_RES 118 118
CC FM MOD_RES 118 118
CC FM CONFLICT 64 91
CC FM EFT AGAVERNSRSTSPAGTDEDECKGEERS -> RRGCGDPSS
CC EFT POLDPKGGGGRKDDGGGQ (IN REF. 1).
CC EFT SO SEQUENCE 168 AA; 18392 MW; 65PDB027DDBE3241 CRC04.

```

```

RL J. Blochem. 122:71-82(1997).
RN [2]
RP SEQUENCE OF 55-64; 140-146; 151-156; 424-447; 500-528 AND 577-605,
RD AND SUBUNIT.
RC TISSUE:Plasma;
RX MEDLINE-97018241; Pubmed-8864857;
RA Yamamoto T., Yamamoto K., Sinohe H.;
RT "Inter-alpha-trypsin inhibitor and its related proteins in Syrian
hamster urine and plasma.";
RL Blochem. 120:145-152(1996).
CC -1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
CC SIMILARITY).
CC -1- SUBUNIT: I-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,
CC BIKUNIN, INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2
CC AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND
CC BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.
CC -1- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
CC 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ITIH FAMILY.
CC -1- SIMILARITY: CONTAINS 1 WFPA DOMAIN.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: D89286; BA13939.1;
DR InterPro: IPR02035; WFPA.
DR Pfam: PF00092; vwa; 1.
DR SMART: SM00327; VWA; 1.
DR PROSITE: PS50234; VWFA; 1.
KW Serine protease inhibitor; Repeat; signal; Multigene family;
KM Glycoprotein.
FT SIGNAL 1 18
FT PROPEP 19 54
FT CHAIN 55 702
FT PT
FT PROPEP 703 946
FT DOMAIN 308 468
FT CARBOHYD 118 118
FT CARBOHYD 263 263
FT CARBOHYD 445 445
FT CARBOHYD 578 578
FT BINDING 702 702
FT PT
FT CONFLICT 510 510
FT CONFLICT 595 595
FT SEQUENCE 946 AA; 106580 MW; CA8BP565458E7B2E CRC64;

Query Match 36.5%; Score 54; DB 1; Length 946;
Best Local Similarity 34.6%; Pred. No. 3.4;
Matches 9; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

OY 2 N1MAAQRVGRRLRMSDEFGSGFL 27
|:| : | | | | |
Db 212 NWATVELOGMRLHVPDFEGHFGCV 237

RESULT 5
ITR2_MOUSE STANDARD; PRT; 946 AA.
AC 061703;
DT 15-JUL-1998 (rel. 36, created)

```

```

DT 15-JUL-1998 (rel. 36, last sequence update)
DT 15-JUL-1999 (rel. 38, last annotation update)
DE Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy
DE chain H2).
GN ITR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID:10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6N; TISSUE-Liver;
RX MEDLINE-95194326; Pubmed-7534067;
RA Chan P., Risler J.-L., Raguenez G., Saller J.-P.;
RT "The three heavy-chain precursors for the Inter-alpha-inhibitor
RT family in mouse: new members of the multicopper oxidase protein group
RT with differential transcription in liver and brain.";
RL Blochem. J. 306:505-512(1995).
CC -1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
CC SIMILARITY).
CC -1- SUBUNIT: I-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,
CC BIKUNIN, INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2
CC AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND
CC BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BOTH LIVER AND BRAIN.
CC -1- PTM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
CC 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY
CC SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ITIH FAMILY.
CC -1- SIMILARITY: CONTAINS 1 WFPA DOMAIN.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X70392; CAA49842.1;
DR MGD: MGI:96619; Itih2.
DR InterPro: IPR02035; WFPA.
DR Pfam: PF00092; vwa; 1.
DR SMART: SM00327; VWA; 1.
DR PROSITE: PS50234; VWFA; 1.
KW Serine protease inhibitor; Repeat; signal; Multigene family;
KM Glycoprotein.
FT SIGNAL 1 18
FT PROPEP 19 54
FT CHAIN 55 702
FT PT
FT PROPEP 703 946
FT DOMAIN 308 468
FT CARBOHYD 118 118
FT CARBOHYD 263 263
FT CARBOHYD 445 445
FT BINDING 702 702
FT PT
FT SEQUENCE 946 AA; 105927 MW; 40DB6716433BD9DC CRC64;

Query Match 35.8%; Score 53; DB 1; Length 946;
Best Local Similarity 34.6%; Pred. No. 4.8;
Matches 9; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

OY 2 N1MAAQRVGRRLRMSDEFGSGFL 27
|:| : | | | | |
Db 212 NWATVELOGMRLHVPDFEGHFGCV 237

```

RESULT 6
 AROG_YEAST STANDARD; PRT: 370 AA.
 ID AROG_YEAST
 AC P32449;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Phospho-2-dehydro-3-deoxyheptone aldolase, tyrosine-inhibited
 DE (EC 4.1.2.15) (Phospho-2-keclo-3-deoxyheptone aldolase) (DAHP
 synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase).
 GN ARO4 OR YBR249C OR YBR1701.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxId=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9225349; PubMed=1348177;
 RA Kuenzler M., Parayiclini G., Egli C., Irniger S., Braus G.H.;
 RT "Cloning, primary structure and regulation of the ARO4 gene, encoding
 RT the tyrosine-inhibited 3-deoxy-D-arabino-heptulosonate-7-phosphate
 RT synthase from Saccharomyces cerevisiae.";
 RL Gene 113:67-74(1992).
 RN [2]
 RP REVISIONS TO 205-207.
 RA Kuenzler M.;
 RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN=5288C;
 RX MEDLINE=94078675; PubMed=8256322;
 RA Doughton F., Bletau N., Aigle M., Grouzet M.;
 RT "The complete sequence of a 6794 bp segment located on the right arm
 RT of chromosome II of Saccharomyces cerevisiae. Finding of a putative
 RT dorfase in a yeast."
 RL Genbank 51131-1137(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX STRAIN=5288C;
 RA Aljhoric G., Pohl F.M., Pohl T.M.;
 RT Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: STEREOSPECIFIC CONDENSATION OF PHOSPHOENOLPYRUVATE (PEP)
 CC AND D-ERYTHROSE-4-PHOSPHATE (E4P) GIVING RISE TO 3-DIOXY-D-
 CC ARABINO-HEPTULOSONATE-7-PHOSPHATE (DAHP).
 CC -1- CATALYTIC ACTIVITY: 2-dehydro-3-deoxy-D-arabino-heptonate 7-
 CC phosphate + phosphate -> phosphoenolpyruvate + D-erythrose 4-
 CC phosphate + H(2)O.
 CC -1- ENZYME REGULATION: INHIBITED BY TYROSINE.
 CC -1- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN
 CC THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).
 CC -1- INDUCTION: BY AMINO ACID STARVATION.
 CC -1- SIMILARITY: BELONGS TO CLASS-1 DAHP SYNTHETASE FAMILY.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation at
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X61107; CAA43419.1; -;
 DR EMBL: L20286; AAA65607.1; -;
 DR EMBL: Z66118; CAA8212.1; -;
 DR PIR: S38185; S38185;
 DR HSSP: P00886; 1087;
 DR SGD: S0000453; ARO4.
 DR InterPro: IPR001285; DAHP_synth_1.
 DR Pfam: PF00793; DAHP_synth_1; 1.
 DR Prodom: PD005060; DAHP_synth_1; 1.
 KW Aromatic amino acid biosynthesis; Lyase; Multigene family.

SQ SEQUENCE 370 AA; 39749 MW; 594ED4BF24175979 CMC64;
 Query Match 35.18; Score 52; DB 1; Length 370;
 Best Local Similarity 47.68; Pred. NO. 2.4;
 Matches 10; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 Oy 2 NMAAGRCGRLRMSDEFEQ 22
 Db 80 DLEAGVRLRLKRLSDLEIK 100
 : 1 1 1 1 : 1 1 1 1 : 1
 RESULT 7
 AP3_ARATH STANDARD; PRT: 232 AA.
 ID AP3_ARATH
 AC P35632; Q39003;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Floral homeotic protein APTAL3.
 GN AP3 OR AY3654340 OR TL2E18.30.
 OS Arabidopsis thaliana (Mouse ear cress).
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Eukaryota; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eucosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxId=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Petal;
 RX MEDLINE=92154682; PubMed=1346756;
 RA Jack T., Brockman L.L., Meyerowitz E.M.;
 RT "The homeotic gene APTAL3 of Arabidopsis thaliana encodes a MADS
 RT box and is expressed in petals and stamens.";
 RL Cell 68:683-697(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=CV ANDSPERG ERCTN;
 RX MEDLINE=95036018; PubMed=7948893;
 RA Okamoto H., Yano A., Shirahashi H., Okada K., Shimura Y.;
 RT "Genetic complementation of a floral homeotic mutation, aptal3,
 RT with an Arabidopsis thaliana gene homologous to DEFICIENS of
 RT Antirrhinum majus.";
 RL Plant Mol. Biol. 26:465-472(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN-VARIOUS STRAINS;
 RX MEDLINE=99126449; PubMed=9927474;
 RA Purugganan M.D., Sudlith J.I.;
 RT "Molecular population genetics of floral homeotic loci. Departures
 RT from the equilibrium-neutral model at the APTAL3 and PISTILLATA
 RL genes of Arabidopsis thaliana.";
 RL Genetics 151:839-848(1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX STRAIN=CV, COLUMBIA;
 RX MEDLINE=21016720; PubMed=1130713;
 RA Salinoubat M., Lemcke K., Rieger M., Ansoorge W., Unselid M.,
 RA Farmanou B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
 RA Delany M., Boutry M., Grivell L.A., Macho R., Puigdomenech P.,
 RA De Simone V., Choisne N., Artiguenave F., Robert C., Buetler P.,
 RA Wincker P., Catholico L., Weissbach J., Saurin W., Queller F.,
 RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
 RA Wurmbach E., Ditzion B., Erfle H., Jordan N., Brandt S.,
 RA Wiedemann R., Kranz H., Voss H., Holland N., Brandt S.,
 RA Vezzi A., D'Angelo M., Pallavicini A., Toppi S., Simonati B.,
 RA Contat A., Hornschuetter K., Kaner G., Loehner T.-H., Nordstiek G.,
 RA Reichelt J., Scharte M., Schoen O., Barques M., Terol J., Clement J.,
 RA Navarro P., Collado C., Perez-Perez A., Ottenweilner B., Duchemin D.,
 RA Cooke R., Laudie M., Berger-Llauro C., Punelle B., Maury D.,
 RA de Haan M., Marise A.C., Alcaraz J.-P., Collet A., Casacubeta E.,
 RA Montfort A., Argillogio A., Flores M., Lignori R., Vitale D.,
 RA Manhaupt G., Haese D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
 RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.

```

RA R0097Y.T, Rlizo B., Malt A., Uteback T., Fujii C.Y., Shea T.P.,
RA Cressy T.H., Haas B., Melt R., Wu D., Peterson J., Van Aken S.,
RA Pal G., Milltacher J., Sellers P., Gill J.E., Feldblum T.V.,
RA Preiss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneo K., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kinura T., Idegawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara N., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,
RA Matnobe A., Yamada M., Yasuda M., Tabata S.,
RA "Sequence and analysis of chromosome 3 of the plant Arabidopsis
RA thaliana."
RL Mature 408:8-822(2000).
CC - FUNCTION: TRANSCRIPTION FACTOR INVOLVED IN THE GENETIC CONTROL OF
CC FLOWER DEVELOPMENT.
CC - SUBUNIT FORMS AN HETERODIMER WITH PISTILLATA.
CC - SUBCELLULAR LOCATION: Nuclear.
CC - TISSUE SPECIFICITY: EXPRESSED IN PETALS AND STAMENS.
CC - MISCELLANEOUS: MUTATIONS IN AP3 CAUSE TRANSFORMATION OF PETALS
CC INTO SEEDS AND STAMINA INTO CARPELS.
CC - SIMILARITY: BELONGS TO THE MAD5 DOMAIN FAMILY OF TRANSCRIPTION
CC FACTORS.
CC - SIMILARITY: CONTAINS A PROBABLE DIMERIZATION DOMAIN FOUND IN
CC SRP-TYPE TRANSCRIPTION FACTORS (K-BOX).
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires explicit license agreement (See http://www.isb-sib.ch/announce/,
CC o_send_en_email@isb-sib.ch).
CC -----
DR EMBL: M66397; AA33740.1; -
DR EMBL: D21125; BA00465.1; -
DR EMBL: AF115798; AD051888.1; -
DR EMBL: AF115800; AD051889.1; -
DR EMBL: AF115802; AD051891.1; -
DR EMBL: AF115804; AD051893.1; -
DR EMBL: AF115811; AD051900.1; -
DR EMBL: AF115814; AD051903.1; -
DR EMBL: AL132971; CAB81799.1; -
DR PIR: A42095; A42095.
DR HSSP: P11746; 1MMN.
DR TRANSFAC: T01176; -.
DR InterPro: IPR002487; K-box.
DR InterPro: IPR002100; MAD5-box.
DR Pfam: PF01486; K-box_1.
DR Pfam: PF00319; SRP-TF_1.
DR PRINTS: PR00404; MAD5DOMAIN.
DR SMART: SM00437; MAD5_1.
DR PROSITE: PS00350; MAD5_BOX_1.
DR PROSITE: PS50066; MAD5_BOX_2.
KW Transcription regulation; DNA-binding; Activator; Nuclear protein;
KW Developmental protein.
KT DOMAIN 3 57 MAD5.
KT DOMAIN 3 165 K-BOX.
FT CONFLICT 199 199 A -> R (IN REF. 2).
PT FT DOMAIN 199 199 A -> R (IN REF. 2).
SQ SEQUENCE 232 AA: 27341 MW: 669070319F9857C3 CRC64:
QY Query Match 34.5% Score 51; DB 1; Length 232;
Db Best Local Similarity 44.4%; Pred. No. 2;
Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1.
QY 7 QRYG-----RELRRNSDEFCSFK 25
II I :||||: |||: |||: ||
Db 107 ORLGCTDLDIDQLRLRLEDEMTEPK 133
RESULT 8
RPOB_CAMJ6 STANDARD: PRT: 1378 AA.
CD 046124; Q9P131;

```

```

DT DT 01-NOV-1997 (Rel. 35, Created)
BT BT 16-OCT-2001 (Rel. 40, Last sequence update)
DE DE 16-OCT-2001 (Rel. 40, Last annotation update)
DR DR DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase
GN beta chain) (RNA polymerase beta subunit).
NC RPOB OR C3D478.
CC Campylobacter jejuni.
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OX Campylobacter.
XX NCBI_TaxID=197;
RA RA SEQUENCE FROM N.A.
RP RP STRAIN=NCIC 11165;
RC RC MEDLINE=PM1505912; PubMed=10688204;
RD RD Parishall J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
RE RE Basham D., Chillingworth T., Davies R.M., Felwell T., Holtoyd S.,
RF RF Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RG RG Quail M.A., Rajandream M.A., Rutherford K.M., Van Vliet A.H.M.,
RH RH Whitehead S., Barrett B.G.;
RI RI "The genome sequence of the food-borne pathogen Campylobacter jejuni
RJ RJ reveals hypervariable sequences."
RK RK Nature 403:665-668(2000).
RL RL [2]
RM RM SEQUENCE OF 338-1031 FROM N.A.
RN RN MEDLINE=J6084944; PubMed=748986;
RX RX Buschmanne V.H., Puente J.L., Sanchez-Lopez F., Bobadilla M.,
RY RY Calva E.;
RA RA Identification of Campylobacter jejuni and C. coli using the rpoB
RT RT gene and a cyclic DNA fragment from C. jejuni.*
RU RU -1. POSITION OF DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
RV RV OF CAMPYLOBACTER RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
RW RW SUBSTRATES
RX RX -1. CATALYTIC ACTIVITY: N nucleoside triphosphate -> N diphosphate +
RY RY (PPA)(H2O)
RZ RZ -1. SUMMARY: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
S1 S1 ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
S2 S2 BETA' CHAIN.
S3 S3 -1. SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY
S4 S4 -----
S5 S5 This Swiss-Prot entry is copyright. It is produced through a collaboration
S6 S6 between the Swiss Institute of Bioinformatics and the EMBL outstation at
S7 S7 the European Bioinformatics Institute. There are no restrictions on its
S8 S8 use by non-profit institutions as long as its content is in no way
S9 S9 modified and this statement is not removed. Usage by and for commercial
S10 S10 entities requires a license agreement (See http://www.isb-sdb.ch/announce/
S11 S11 or send an email to license@sdb.cb).
S12 S12 -----
S13 S13 EMBL: AL139075; CAH75116.1; -.
S14 S14 EMBL: X77304; CAAS4509.1; -.
S15 S15 DR InterPro: IPRO01572; RNA_POL.B.
S16 S16 Pfam: PF00562; RNA_POL_B.1.
S17 S17 DR PROSITE: PS01166; RNA_POL_BFAM.1.
S18 S18 KW Transferase; Transcription; DNA-directed RNA polymerase;
S19 S19 Complete proteome.
S20 S20 FT CONFLICT 338 347 NLAAGVDAA->MTWMLALMQP (IN REF. 2).
S21 S21 FT CONFLICT 558 558 A->R (IN REF. 2).
S22 S22 FT CONFLICT 671 671 C->S (IN REF. 2).
S23 S23 FT CONFLICT 691 691 A->R (IN REF. 2).
S24 S24 FT CONFLICT 691 691 C->T (IN REF. 2).
S25 S25 SO SEQUENCE 1378 AA; 155915 MW; AB7467C305028EB5 CRC64;
QY QY 3 LMAAQRYG--RELRRM---SDEFEGSPFGK 28
DB DB 1306 VMALLEYGARTLRKEMTKIKSDVDGEGRFAVK 1337
RESULT 9
INFO PSBAE

```

[illegible]

```
CC CC -1 ENZYME REGULATION: ALTERNATE BETWEEN AN INACTIVE FORM BOUND TO GDP  
CC CC AND AN ACTIVE FORM BOUND TO GTP. ACTIVATED BY A GUANINE  
CC CC NUCLEOTIDE-EXCHANGE FACTOR (GEF) AND INACTIVATED BY A GTPASE-  
CC CC ACTIVATING PROTEIN (GAP).  
CC CC -1 SUBCELLULAR LOCATION: PLASMA MEMBRANE.  
CC CC -1 DEVELOPMENTAL STAGE: IN SPOROBLAST MYCELIA AND MUCH LESS IN  
CC CC GAMMATAPE AND YEAST.  
CC CC -1 SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. HAS FAMILY  
CC CC THIS SWISS-PROT entry is copyright, it is produced through a collaboration  
CC CC between the swiss institute of Bioinformatics and the EMBL outstation  
CC CC the European Bioinformatics Institute. There are no restrictions on its  
CC CC use by non-profit institutions as long as its content is in no way  
CC CC modified and this statement is not removed. Usage by and for commercial  
CC CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
CC CC or send an email to license@isb-sib.ch).  
CC CC -----  
DR DR EMBL, MS5177; AAA83379.1; .  
DR DR PIR, C63465; C63636.  
DR DR HSSP, P01112; IPLL.  
DR DR InterPro: IPR001877; Ras_Lrrnsfmmg.  
DR DR Pfam, PF00072; F001897.1 Ras_Lrrnsfmng.  
DR DR PRINTS, PR00449; RASTRNSFMNG.  
DR DR SMART, SM00173; RAS; 1.  
KW KWP GTP-binding; Prenylation; Lipoprotein.  
FT FT NP_BIND 16 67 GTP (BY SIMILARITY).  
FT FT NP_BIND 63 67 GTP (BY SIMILARITY).  
FT FT NP_BIND 122 125 GTP (BY SIMILARITY).  
FT FT DOMAIN 38 46 EFFECTOR REGION (PROBABLE).  
FT FT LIPID 202 202 FARNSYL (BY SIMILARITY).  
SQ SQ SEQUENCE 205 AA; 23408 MW; DBF06466f905f50 CRC64;  
  
Query Match 32.4%; Score 48; DB 1; Length 205;  
Batch Local Similarity 62.5%; Pred No 4.9;  
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
  
OY OY 11 RELRRMSDEFGSPFK 26  
DB DB 168 REIRRNRKEDGRSK 183  
|||:|||:  
  
RESULT 11  
6 PGLI.THEMA STANDARD: PRT: 220 AA.  
ID ID 6PGLI.THEMA  
CN CN OXNONE:  
RN RN 30 MAY-2000 (Rel. 39, Created)  
RP RP 10 MAY-2000 (Rel. 39, Last sequence update)  
DT DT 10 OCT-2000 (Rel. 39, Last annotation update)  
DN DN 6-phosphogluconate dehydratase (EC 3.1.1.31) (pfcl).  
GC GC PGL OR DEVB OR TML154.  
CS CS Thermotoga maritima.  
OC OC Bacteria; Thermotogales; Thermotoga.  
NCBI_TaxId=2336;  
[1]  
RA RA STRAIN=MSB8 / DSM 3109;  
RX RX MEDLINE=99287316; PubMed=10360571;  
FA FA Half D.H., Hickey R.K., Peterson J.D., Nelson W.G., Ketchum K.A.,  
RA McDonald L., Utherback T.R., Malek J.A., Linher K.D., Garrett M.M.,  
RA Steiwert A.M., Sutton W.D., Pratt M.S., Phillips C.A., Richardson D.,  
RA Kleiberberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,  
RA Rabinberg S.L., Smith R.O., Fraser J.C., Fraser C.H., Greenleaf  
RT RT genome sequence of Thermotoga maritima.";  
RL RL Mature 399:323-329(1999).  
CL CL -1 FUNCTION: HYDROLYSIS OF 6-PHOSPHOGUCONOLACTONE TO 6-  
CC CC PHOSPHOGUCONATE.  
CC CC -1 CATALYTIC ACTIVITY: 6-phospho-D-glucono-1,5-lactone + H(2O) = 6-  
CC CC phospho-D-gluconate.  
CC CC -1 PATHWAY: SECOND STEP IN PENTOSE PHOSPHATE PATHWAY.
```


RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
 RA Kramer J., Pulcin L., Maris E., Dante M., Pepin K., Hillier L.,
 RA Nelson J., Spieth J., Ryan E., Andrews S., Giesel C., Layman D.,
 RA Du H., Ali J., Benight A., Jones K., Drone K., Cotton M., Joshi C.,
 RA Antoniou B., Zidane M., Strong K., Sun H., Lamar B., Jordan C.,
 RA Ma F., Zhong J., Preston R., Vill D., Sheker M., Matero A., Shah R.,
 RA Sway I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Gill S.,
 RA Gratt S., Shordy N., Hasegawa A., Hamed A., Lochi M., Johnson A.,
 RA Chen E., Marra M., Martensen R., McCombie W.R.,
 RA Sequence and analysis of chromosome 4 of the plant Arabidopsis
 thaliana. Nature 402:769-777(1999).
 RL Mature 402:769-777(1999).
 RN (3)
 RP SEQUENCE OF 2-526 FROM N.A. AND CHARACTERIZATION.
 RC STRAIN=cv. Columbia;
 RX PubMed:8706836;
 RA Curten G., Dumas R., Ravanel S., Douce R.,
 RT "Characterization of an Arabidopsis thaliana cDNA encoding an
 RT s-adenosylmethionine-sensitive threonine synthase. Threonine synthase
 RT from higher plants." FEBS Lett. 390:85-90(1996).
 RL FEBS Lett. 390:85-90(1996).
 RN (4)
 RP CHARACTERIZATION.
 RC PubMed:9748328;
 RA Curten G., Job D., Douce R., Dumas R.,
 RT "Allosteric activation of Arabidopsis threonine synthase by
 RT s-adenosylmethionine." Biochemistry 37:13212-13221(1998).
 RL Biochemistry 37:13212-13221(1998).
 RN (5)
 RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 41-526.
 RA Thomazeau K., Curten G., Dumas R., Bion V.,
 RT "Crystal structure of threonine synthase from Arabidopsis thaliana." J.
 RT Protein Sci. 10:638-648(2001).
 RL Protein Sci. 10:638-648(2001).
 CC -1- CATALYTIC ACTIVITY: O-phospho-L-homoserine + H(2)O -> L-threonine +
 CC phosphate.
 CC -1- COFACTOR: Pyridoxal phosphate.
 CC -1- ENZYME REGULATION: Allosterically activated up to 20-fold by S-
 CC adenosyl-methionine (SAM).
 CC -1- PATHWAY: Threonine biosynthesis; last step.
 CC -1- SUBUNIT: Homodimer biosynthesis; last step.
 CC -1- SUBCELLULAR LOCATION: Chloroplast.
 CC -1- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
 CC CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC CC
 CC EMBL: AB027151; BAA77707.1; -;
 CC EMBL: AL050352; CAB3659.1; -;
 CC EMBL: AL161575; CAB79742.1; -;
 CC EMBL: L41666; MAB04607.1; -;
 CC PDB: 1E5X; 02-AUG-01.
 DR InterPro: IPR001926; PALP.
 DR Pfam: PF00291; PALP.1.
 DR PROSITE: PS00165; DEHYDRATASE_SER_THR.1.
 KW Threonine biosynthesis; Lyase; Pyridoxal phosphate; Allosteric enzyme;
 FT Chloroplast; Transl. peptide; 3D-structure.
 FT TRANSIT 1 40 CHLOROPLAST.
 FT CHAIN 41 526 THREONINE SYNTHASE.
 FT BINDING 203 203 PYRIDOXAL PHOSPHATE.
 FT CONFLICT 2 2 A->L (IN REF. 3).
 FT SEQUENCE 526 AA; 57776 MW; B27787A57B8832AD0 CRC64;

QY 2 NUNA0RYGRELRRMSD-----EFGSGFGL 27
 DB 172 NFWAERBKKOFLGMNDLVKHCISHTGSRFDL 205
 ID FMRA-CALPA STANDARD; PRT; 334 AA.
 AC 001133;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, last sequence update)
 DT 01-MAR-2002 (Rel. 41, last annotation update)
 DE Antho-Ramide neuropeptides precursor.
 OS Calliactis parasitica (sea anemone)
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zantharia; Actinaria;
 OC Nyantheae; Hormathiidae; Calliactes.
 ON NCBI_TaxID=6114;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE:91172845; PubMed:1706527;
 RA Damer D., Schmitz C., Diekhoff D., Grimmelikhuisen C.J.P.,
 RT "Primary structure of the precursor for the sea anemone neuropeptide
 RT Antho-Ramide (Gda-GlyArg-Phe-NH2)." J.
 RL Proc. Natl. Acad. Sci. U.S.A. 88:2353-2359(1991).
 CC -1- FUNCTION: NOT KNOWN BUT IT COULD ACT AS A TRANSMITTER AT
 CC NEUROKOSCUCLAR SYNAPSES.
 CC -1- TISSUE SPECIFICITY: NEURONS ASSOCIATED WITH SMOOTH MUSCLE FIBERS.
 CC CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC CC
 CC EMBL: M59166; AAA27878.1; -;
 CC PIR: A39172; A39172.
 DR InterPro: IPR002544; FARP.
 DR Pfam: PF01581; FARP; 15.
 KW Neuropeptide; Amidation; Repeat; Signal.
 FT SIGNAL 1 26
 FT PEPTIDE 117 120 POTENTIAL.
 FT PEPTIDE 126 129 ANTHO-REFAMIDE.
 FT PEPTIDE 135 138 ANTHO-REFAMIDE.
 FT PEPTIDE 143 146 ANTHO-REFAMIDE.
 FT PEPTIDE 152 155 ANTHO-REFAMIDE.
 FT PEPTIDE 161 164 ANTHO-REFAMIDE.
 FT PEPTIDE 170 173 ANTHO-REFAMIDE.
 FT PEPTIDE 179 182 ANTHO-REFAMIDE.
 FT PEPTIDE 188 191 ANTHO-REFAMIDE.
 FT PEPTIDE 197 200 ANTHO-REFAMIDE.
 FT PEPTIDE 206 209 ANTHO-REFAMIDE.
 FT PEPTIDE 215 218 ANTHO-REFAMIDE.
 FT PEPTIDE 224 227 ANTHO-REFAMIDE.
 FT PEPTIDE 234 237 ANTHO-REFAMIDE.
 FT PEPTIDE 243 246 ANTHO-REFAMIDE.
 FT PEPTIDE 253 256 ANTHO-REFAMIDE.
 FT PEPTIDE 263 266 ANTHO-REFAMIDE.
 FT PEPTIDE 272 275 ANTHO-REFAMIDE.
 FT PEPTIDE 281 284 ANTHO-REFAMIDE.
 FT MOD. RES 120 120 AMIDATION (G-12) PROVIDE AMIDE GROUP).
 FT MOD. RES 129 129 AMIDATION (G-13) PROVIDE AMIDE GROUP).
 FT MOD. RES 138 138 AMIDATION (G-14) PROVIDE AMIDE GROUP).
 FT MOD. RES 146 146 AMIDATION (G-15) PROVIDE AMIDE GROUP).
 FT MOD. RES 155 155 AMIDATION (G-16) PROVIDE AMIDE GROUP).
 FT MOD. RES 164 164 AMIDATION (G-17) PROVIDE AMIDE GROUP).
 FT MOD. RES 173 173 AMIDATION (G-18) PROVIDE AMIDE GROUP).
 FT MOD. RES 182 182 AMIDATION (G-19) PROVIDE AMIDE GROUP).
 FT MOD. RES 191 191 AMIDATION (G-20) PROVIDE AMIDE GROUP).
 FT MOD. RES 200 200 AMIDATION (G-21) PROVIDE AMIDE GROUP).
 FT MOD. RES 209 209 AMIDATION (G-22) PROVIDE AMIDE GROUP).
 FT MOD. RES 218 218 AMIDATION (G-23) PROVIDE AMIDE GROUP).

Query Match
Best Local Similarity 44.0%; Pred. No. 9.9;
Matches 11; Conservative 3; Mismatches 10; Indels 1; Gaps 1;

Query 1 KNLMAQRYGRELRLRMSDEFEGSF 24
DB 89 KRYVPGRGREGFGREGFGGR 113

Result 15

B1M_HUMAN
ID O43521; STANDARD; PRT; 198 AA.
AC 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE BCL2-like protein 11 (Bcl2 interacting mediator of cell death).
DE BCL2L1 OR B1M.
GN Homo sapiens (human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, AND ALTERNATIVE SPLICING.
RC TISSUE=Peripheral blood, and spleen;
RX MEDLINE=98094360; PubMed=9430630;
RA O'Connor L., Strasser A., O'Reilly L.A., Hausmann G., Adams J.M., Cory S., Huang D.C.S.;
RA B1m: a novel member of the Bcl-2 family that promotes apoptosis.";
RL EMBD J. 17:384-395(1998).
CC -1- FUNCTION: INDUCES APOPTOSIS. ISOFORM B1M IS MORE POTENT THAN ISOFORM B1MEL.
CC -1- SUBUNIT: FORMS HETERODIMERS WITH A NUMBER OF ANTIAPOPTOTIC BCL-2 PROTEINS INCLUDING MCL-1, BCL-2, BCL-XL, BFL-1, AND BHRF-1. DOES NOT HETERODIMERIZE WITH PROAPOPTOTIC PROTEINS SUCH AS BAD, BOK, BAX OR BAK (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: ASSOCIATED WITH INTRACITOPLASMIC MEMBRANES (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: B1MEL (SHOWN HERE) AND B1ML; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- DOMAIN: THE BH3 DOMAIN IS REQUIRED FOR BCL-2 BINDING AND CYTOTOXICITY.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 3 (BH3).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@sib-sib.ch).
CC
CC EMBL: AF032457; AAC39593.1; -;
CC EMBL: AF032456; AAC39594.1; -;
CC DR MIM: 603827; -;
CC DR InterPro: IPR000712; BCL2.
CC DR PROSITE: PS01259; BH3; FALSE NEG.
CC DR Apoptosis: Alternative splicing; Membrane.
CC KM DOMAIN 148 162 BH3
CC FT VARSPLC 148 101 MISSING (IN ISOFORM B1ML).
CC SO SEQUENCE 198 AA; 22171 MW; D75735E469CA6997 CRC64;

Query Match
Best Local Similarity 45.5%; Score 47; DB 1; Length 198;
Matches 10; Conservative 3; Mismatches 5; Indels 4; Gaps 1;

Query 3 LMAQRYGRELRLRMSDEFEGSF 24
DB 146 IWIAD---ELRRIDDEFNAY 163

Search completed: September 20, 2002, 11:04:35
Job time: 1632 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OK protein - protein search, using sw model

Run on: September 20, 2002, 11:03:47 : Search time 172.19 Seconds
(without alignments)
28.131 Million cell updates/sec

Title: US-09-544-664-55

Sequence: 1 KMLAAQYGRGLRMSDEFGSKGLK 28

Scoring table: BLOSUM62
Gapop 10.0 , gapext 0.5

Searched: 562222 seqs, 17294929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.insecta:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.rbc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.potent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archaeap:*

Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	91	61.5	146	13 Q919N2	Q919N2 bradydantio
2	53	35.8	223	16 Q10843	Q10843 menziesia c
3	52.5	35.5	505	8 Q47148	Q47148 rhododendro
4	52.5	35.5	506	8 Q63960	Q63960 rhododendro
5	52.5	35.5	506	8 Q62972	Q62972 rhododendro
6	52.5	35.5	506	8 Q62973	Q62973 rhododendro
7	52.5	35.5	506	8 Q62974	Q62974 rhododendro
8	52.5	35.5	506	8 Q62975	Q62975 rhododendro
9	52.5	35.5	506	8 Q62977	Q62977 rhododendro
10	52.5	35.5	506	8 Q62978	Q62978 rhododendro
11	52.5	35.5	506	8 Q62980	Q62980 rhododendro
12	52.5	35.5	506	8 Q62981	Q62981 rhododendro
13	52.5	35.5	506	8 Q62982	Q62982 rhododendro
14	52.5	35.5	506	8 Q62983	Q62983 rhododendro
15	52.5	35.5	506	8 Q62984	Q62984 rhododendro
16	52.5	35.5	506	8 Q62988	Q62988 rhododendro

17	52.5	35.5	506	8 Q62989	Q62989 rhododendro
18	52.5	35.5	506	8 Q62990	Q62990 rhododendro
19	52.5	35.5	506	8 Q62991	Q62991 rhododendro
20	52.5	35.5	506	8 Q62992	Q62992 rhododendro
21	52.5	35.5	506	8 Q62993	Q62993 menziesia m
22	52.5	35.5	506	8 Q47149	Q47149 rhododendro
23	52.5	35.5	506	8 Q47152	Q47152 rhododendro
24	52.5	35.5	506	8 Q47155	Q47155 rhododendro
25	52.5	35.5	506	8 Q47158	Q47158 menziesia p
26	52.5	35.5	506	8 Q47170	Q47170 rhododendro
27	52.5	35.5	506	8 Q47171	Q47171 rhododendro
28	52.5	35.5	506	8 Q47172	Q47172 rhododendro
29	52.5	35.5	506	8 Q47173	Q47173 rhododendro
30	52.5	35.5	506	8 Q47174	Q47174 rhododendro
31	52.5	35.5	507	8 Q62985	Q62985 rhododendro
32	52.5	35.5	507	8 Q62986	Q62986 rhododendro
33	52.5	35.5	508	8 Q62979	Q62979 rhododendro
34	51.5	34.8	506	8 Q47153	Q47153 rhododendro
35	51.5	34.8	506	8 Q47160	Q47160 rhododendro
36	51	34.5	231	10 Q9S830	Q9S830 arabidopsis
37	51	34.5	232	10 Q9S703	Q9S703 arabidopsis
38	51	34.5	232	10 Q9S022	Q9S022 arabidopsis
39	51	34.5	232	10 Q9S021	Q9S021 arabidopsis
40	51	34.5	232	10 Q9S020	Q9S020 arabidopsis
41	51	34.5	232	10 Q9S019	Q9S019 arabidopsis
42	51	34.5	232	10 Q9S018	Q9S018 arabidopsis
43	51	34.5	232	10 Q9S017	Q9S017 arabidopsis
44	51	34.5	232	10 Q9S016	Q9S016 arabidopsis
45	51	34.5	232	10 Q9S015	Q9S015 arabidopsis

ALIGNMENTS

RESULT 1	PRELIMINARY:	PRF:	146 AA.
ID Q919N2			
AC Q919N2			
DT 01-OCT-2000 (TREMBLrel. 15, Created)			
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)			
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)			
DE BAD.			
GN BAD.			
OS Brachydanio rerio (zebrafish) (zebra danio).			
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;			
OC Cypriniformes; Cyprinidae; Danio.			
OX NCBI_TaxID=7935;			
RN 111 SOURCE FROM N.A.			
RS 111 MEDLINE=20373792; PubMed=10917738;			
RA Inohara N. Nucc G.;			
RT "Genes with homology to mammalian apoptosis regulators identified in zebrafish."			
RT Cell Death Differ. 7:509-510(2000).			
DR EMBL; AF21017; AAF66962.2;			
SQ SEQUENCE 146 AA; 16546 MW; 28A5650B85D7ECB CRC64;			
QY 3 LMAAQRGRGLRMSDEFGSKGLK 28			
DB 89 LMAAQRGRGLRMSDEFGSKGLK 114			
QY 3 LMAAQRGRGLRMSDEFGSKGLK 28			
DB 89 LMAAQRGRGLRMSDEFGSKGLK 114			
RESULT 2			
ID Q10843			
AC Q10843			
DT 01-NOV-1998 (TREMBLrel. 06, Created)			
PRF:	223 AA.		
Query Match	61.5%;	Score 91;	DB 13;
Best Local Similarity	61.5%;	Pred. No. 1.3e-05;	
Matches 16;	Conservative 6;	Mismatches 4;	Indels 0;
Gaps 0;			

DT 01-NOV-1998 (TREMBLrel. 08, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE HYPOHETICAL. 24.1 KDA PROTEIN C19.03C.
 GN RV2014 OR MYC39.03C.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 CC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxId=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RC MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Deakin K., Felwell T., Gentles S., Hamlin R., Holroyd S.,
 RA Kersey R., Kerec J., Krogan J., McLean J., Moule S., Murphy L.,
 RA Butler S., Selsman K., Skellern S., Starmer S., Young R., Rogers J.,
 RA Stubbins J.P., Taylor K., Whitehead S., Barrett B.G.,
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence."
 RT Nature 393:537-544(1998).
 CC -1- SIMILARITY: TO M.PARATUBERCULOSIS IS900.
 DR EMBL: 274025; CAAG8415.1; -.
 DR Tuberculis; RV2014; -.
 DR InterPro: IPR003346; Transposase-20.
 DR Pfam: PF02371; Transposase-20; 1.
 DR Hypothetical protein; Complete proteome.
 KW SEQUENCE 223 AA; 24132 MW; 70456750017EEF37 CRC64;
 SQ

Query Match 35.88; Score 53; DB 16; Length 223;
 Best Local Similarity 38.88; Pred. No. 7.6;
 Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 OY 2 NINAAAGYGRGLRMSD 18
 DB 165 NINAAADRYRAIRAGHD 181

RESULT 3
 ID 047148 PRELIMINARY; PRT; 505 AA.
 AC 047148; 06; Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-MAY-2001 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RIBOSOMAL MATURASE (FRAGMENT).
 GN MATK.
 OS Menziesia ciliolicalyx.
 OC Chloroplast.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Ericales; Ericaceae; Menziesia.
 OX NCBI_TaxId=49154;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Kron K.A.;
 RT "Phylogenetics of Rhododendroideae (Ericaceae)."
 RT Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 RL EMBL: U61331; AAC15245.2; -.
 DR InterPro: IPR000442; Intron_maturase2.
 DR InterPro: IPR002866; MatK_N.
 DR Pfam: PF01348; Intron_maturase2; 1.
 DR EMBL: U61331; MatK_N; 1.
 KW Chloroplast.
 FT NON-TER
 SQ SEQUENCE 505 AA; 60233 MW; E55F927AD2E57DE5 CRC64;
 Query Match 35.58; Score 52.5; DB 8; Length 505;
 Best Local Similarity 37.58; Pred. No. 23;

Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;
 OY 1 KINMAA-----QRYGRGLRMSDEFGSFK 25
 DB 390 KPYMAALSDSDIERFRGIRYRLSHYSSSLK 421

RESULT 4
 ID 063960 PRELIMINARY; PRT; 506 AA.
 AC 063960;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DE RIBOSOMAL MATURASE.
 GN RCT14 OR MATK.
 OS Rhododendron latifolium, and
 OC Rhododendron latifolium.
 CC Chloroplast.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Ericales; Ericaceae; Rhododendron.
 OX NCBI_TaxId=75582, 75580;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kuraishi Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
 RA Yukawa T.;
 RL J. Jpn. Bot. 0:0-0(1998).
 DR EMBL: AB012749; BAA25870.1; -.
 DR EMBL: AB012745; BAA25866.1; -.
 DR InterPro: IPR000442; Intron_maturase2.
 DR InterPro: IPR002866; MatK_N.
 DR Pfam: PF01348; Intron_maturase2; 1.
 DR Pfam: PF01348; MatK_N; 1.
 KW Chloroplast.
 SQ SEQUENCE 506 AA; 60389 MW; DE0C07AE608B787 CRC64;
 Query Match 35.5%; Score 52.5; DB 8; Length 506;
 Best Local Similarity 37.58; Pred. No. 23;
 Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

OY 1 KINMAA-----QRYGRGLRMSDEFGSFK 25
 DB 391 KPYMAALSDSDIERFRGIRYRLSHYSSSLK 422
 RESULT 5
 ID 062972 PRELIMINARY; PRT; 506 AA.
 AC 062972;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RIBOSOMAL MATURASE.
 GN MATK.
 OS Rhododendron ovatum.
 CC Chloroplast.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Ericales; Ericaceae; Rhododendron.
 OX NCBI_TaxId=49169;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Kuraishi Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
 RA Yukawa T.;
 RT "Investigation of Sectional Relationships in the Genus
 RT Rhododendron(Ericaceae) based on matk Sequences".
 RL J. Jpn. Bot. 0:0-0(1998).
 DR EMBL: AB012729; BAA25850.1; -.
 DR InterPro: IPR000442; Intron_maturase2.
 DR InterPro: IPR002866; MatK_N.
 DR Pfam: PF01348; Intron_maturase2; 1.

DR Pfam: PF01824; MatK_N: 1.
 KW Chloroplast.
 SQ SEQUENCE 506 AA; 60493 MW; D230E54B8C20FEF0 CRC64;

Query Match 35.5%; Score 52.5; DB 8; Length 506;
 Best Local Similarity 37.5%; Pred. No. 23;
 Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

OY 1 KNLMIA-----ORYGRELIRMSDEFGSFK 25
 | : ||| | : | : |||
 Db 391 KPVMALSDSDIERGRYRNLSHYSGSLK 422

RESULT 6
 ID 062973 PRELIMINARY; PRT; 506 AA.

AC 062973;
 DT 01-AUG-1998 (TREMblrel. 07, Created)
 DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE RIBOSOMAL MATURASE.
 GN MATK.
 OS Rhododendron stamineum.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Ericales; Ericaceae; Rhododendron.
 OX NCBI_TaxId=75375;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Kutsashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
 RA Yukewa T.;
 RT Investigation of Sectional Relationships in the Genus
 RT Rhododendron (Ericaceae) based on matk Sequences.;
 RL J. Jpn. Bot. 0:0-0(1998).
 DR EMBL: AB012730; BAA25851.1;
 DR InterPro: IPR000442; Intron_mature2.
 DR InterPro: IPR002866; MatK_N.
 DR Pfam: PF01348; Intron_mature2; 1.
 DR Pfam: PF01824; MatK_N: 1.
 DR Chloroplast.
 KW SEQUENCE 506 AA; 60611 MW; 53FA367CD99483C CRC64;

Query Match 35.5%; Score 52.5; DB 8; Length 506;
 Best Local Similarity 37.5%; Pred. No. 23;
 Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

OY 1 KNLMIA-----ORYGRELIRMSDEFGSFK 25
 | : ||| | : | : |||
 Db 391 KPVMALSDSDIERGRYRNLSHYSGSLK 422

RESULT 7
 ID 062974 PRELIMINARY; PRT; 506 AA.

AC 062974;
 DT 01-AUG-1998 (TREMblrel. 07, Created)
 DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE RIBOSOMAL MATURASE.
 GN MATK.
 OS Rhododendron albiflorum.

OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Ericales; Ericaceae; Rhododendron.
 OX NCBI_TaxId=49161;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Kutsashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
 RA Yukewa T.;

RT *Investigation of Sectional Relationships in the Genus
 RT Rhododendron (Ericaceae) based on matk Sequences.;

RL J. Jpn. Bot. 0:0-0(1998).
 DR EMBL: AB012731; BAA25852.1;
 DR InterPro: IPR000442; Intron_mature2.
 DR InterPro: IPR002866; MatK_N.
 DR Pfam: PF01348; Intron_mature2; 1.
 DR Pfam: PF01824; MatK_N: 1.
 KW Chloroplast.

SQ SEQUENCE 506 AA; 60491 MW; 3CC930385B12DBC CRC64;

Query Match 35.5%; Score 52.5; DB 8; Length 506;
 Best Local Similarity 37.5%; Pred. No. 23;
 Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

OY 1 KNLMIA-----ORYGRELIRMSDEFGSFK 25
 | : ||| | : | : |||
 Db 391 KPVMALSDSDIERGRYRNLSHYSGSLK 422

RESULT 8
 ID 062975 PRELIMINARY; PRT; 506 AA.

AC 062975;
 DT 01-AUG-1998 (TREMblrel. 07, Created)
 DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE RIBOSOMAL MATURASE.
 GN MATK.
 OS Rhododendron ponticum.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Ericales; Ericaceae; Rhododendron.
 OX NCBI_TaxId=49628;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Kutsashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
 RA Yukewa T.;
 RT Investigation of Sectional Relationships in the Genus
 RT Rhododendron (Ericaceae) based on matk Sequences.;
 RL J. Jpn. Bot. 0:0-0(1998).
 DR EMBL: AB012732; BAA25853.1;
 DR InterPro: IPR000442; Intron_mature2.
 DR InterPro: IPR002866; MatK_N.
 DR Pfam: PF01348; Intron_mature2; 1.
 DR Pfam: PF01824; MatK_N: 1.
 DR Chloroplast.
 KW SEQUENCE 506 AA; 60449 MW; 21PF700B071B5B8 CRC64;

Query Match 35.5%; Score 52.5; DB 8; Length 506;
 Best Local Similarity 37.5%; Pred. No. 23;
 Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

OY 1 KNLMIA-----ORYGRELIRMSDEFGSFK 25
 | : ||| | : | : |||
 Db 391 KPVMALSDSDIERGRYRNLSHYSGSLK 422

RESULT 9
 ID 062977 PRELIMINARY; PRT; 506 AA.

AC 062977;
 DT 01-AUG-1998 (TREMblrel. 07, Created)
 DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE RIBOSOMAL MATURASE.
 GN MATK.
 OS Rhododendron luteum.

OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Ericales; Ericaceae; Rhododendron.
 ON NCBI_TaxID=49467;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
 RA Yukawa T.;
 RT "Investigation of Sectional Relationships in the Genus
 Rhododendron(Ericaceae) based on matk Sequences.";
 RL J. Jpn. Bot. 0:0-0(1998).
 DR EMBL: AB012734; BAA25855.1; -
 DR InterPro: IPR000442; Intron_mature2.
 DR InterPro: IPR002866; MatK_N.
 DR Pfam: PF01348; Intron_mature2; 1.
 DR Pfam: PF01824; MatK_N; 1.
 KW Chloroplast.
 SO SEQUENCE 506 AA; 60359 MW; F2B1DCA4BF91A609 CRC64;

Query Match 35.5%; Score 52.5; DB 8; Length 506;
 Best Local Similarity 37.5%; Pred. No. 23;
 Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

OY 1 KNLMMA-----ORYGRELRRMSDEFGSFK 25
 | : ||| | : ||| | : ||| | : ||| |
 Db 391 KPVMALSDSDIIEFGRIYRNLSHYSGSLK 422

RESULT 10
 ID 062978 PRELIMINARY; PRT; 506 AA.
 AC 062978;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RIBOSOMAL MATURASE.
 GN MATK.
 OS Rhododendron canadense.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Ericales; Ericaceae; Rhododendron.
 ON NCBI_TaxID=49465;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
 RA Yukawa T.;
 RT "Investigation of Sectional Relationships in the Genus
 Rhododendron(Ericaceae) based on matk Sequences.";
 RL J. Jpn. Bot. 0:0-0(1998).
 DR EMBL: AB012735; BAA25856.1; -
 DR InterPro: IPR000442; Intron_mature2.
 DR InterPro: IPR002866; MatK_N.
 DR Pfam: PF01348; Intron_mature2; 1.
 DR Pfam: PF01824; MatK_N; 1.
 KW Chloroplast.
 SO SEQUENCE 506 AA; 60350 MW; 5E832589ED64EA25 CRC64;

Query Match 35.5%; Score 52.5; DB 8; Length 506;
 Best Local Similarity 37.5%; Pred. No. 23;
 Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;
 OY 1 KNLMMA-----ORYGRELRRMSDEFGSFK 25
 | : ||| | : ||| | : ||| | : ||| |
 Db 391 KPVMALSDSDIIEFGRIYRNLSHYSGSLK 422

RESULT 11
 ID 062980 PRELIMINARY; PRT; 506 AA.
 AC 062980;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RIBOSOMAL MATURASE.
 GN MATK.
 OS Rhododendron albrechtii.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Ericales; Ericaceae; Rhododendron.
 ON NCBI_TaxID=49463;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
 RA Yukawa T.;
 RT "Investigation of Sectional Relationships in the Genus
 Rhododendron(Ericaceae) based on matk Sequences.";
 RL J. Jpn. Bot. 0:0-0(1998).
 DR EMBL: AB012737; BAA25858.1; -
 DR InterPro: IPR000442; Intron_mature2.
 DR InterPro: IPR002866; MatK_N.
 DR Pfam: PF01348; Intron_mature2; 1.
 DR Pfam: PF01824; MatK_N; 1.
 KW Chloroplast.
 SO SEQUENCE 506 AA; 60301 MW; 9D5877E063E856CB CRC64;

Query Match 35.5%; Score 52.5; DB 8; Length 506;
 Best Local Similarity 37.5%; Pred. No. 23;
 Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

OY 1 KNLMMA-----ORYGRELRRMSDEFGSFK 25
 | : ||| | : ||| | : ||| | : ||| |
 Db 391 KPVMALSDSDIIEFGRIYRNLSHYSGSLK 422

RESULT 12
 ID 062981 PRELIMINARY; PRT; 506 AA.
 AC 062981;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RIBOSOMAL MATURASE.
 GN MATK.
 OS Rhododendron pentaphyllum.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Ericales; Ericaceae; Rhododendron.
 ON NCBI_TaxID=75576;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
 RA Yukawa T.;
 RT "Investigation of Sectional Relationships in the Genus
 Rhododendron(Ericaceae) based on matk Sequences.";
 RL J. Jpn. Bot. 0:0-0(1998).
 DR EMBL: AB012738; BAA25859.1; -
 DR InterPro: IPR000442; Intron_mature2.
 DR InterPro: IPR002866; MatK_N.
 DR Pfam: PF01348; Intron_mature2; 1.
 DR Pfam: PF01824; MatK_N; 1.
 KW Chloroplast.
 SO SEQUENCE 506 AA; 60449 MW; B138208746D99258 CRC64;

Query Match 35.5%; Score 52.5; DB 8; Length 506;
 Best Local Similarity 37.5%; Pred. No. 23;
 Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;
 OY 1 KNLMMA-----ORYGRELRRMSDEFGSFK 25
 | : ||| | : ||| | : ||| | : ||| |
 Db 391 KPVMALSDSDIIEFGRIYRNLSHYSGSLK 422

RESULT 13
062982 PRELIMINARY; PRT: 506 AA.
AC 062982;
DT 01-AUG-1998 (TREMblrel. 07, Created)
DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
OS RIBOSOMAL MATURASE.
OC Rhododendron nipponicum.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Ericales; Ericaceae; Rhododendron.
OX NCBI_TaxID=75577;
RN (1)
RP SEQUENCE FROM N.A.
RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
RA Yikawa T.,
RT Investigation of Sectional Relationships in the Genus
KT Rhododendron(Ericaceae) based on matk Sequences."
RL J. Jpn. Bot. 0:0-0(1998).
DR EMBL; AB012739; BAA25860.1; "
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01348; Intron_maturase2; 1.
DR Pfam; PF01824; MatK_N; 1.
KW Chloroplast.
SQ SEQUENCE 506 AA: 60419 MW: 1P95132C6P4F6B40 CRC64;

Query Match 35.5%; Score 52.5; DB 8; Length 506;
Best Local Similarity 37.5%; Pred. No. 23;
Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;
QY 1 KNIMAA-----QRYGRLRMSDEFGSGFK 25
DB 391 KPWWALSDSDIIERFGRIYRNLSHYSGSLK 422

RESULT 14
062983 PRELIMINARY; PRT: 506 AA.
AC 062983;
DT 01-AUG-1998 (TREMblrel. 07, Created)
DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
OS RIBOSOMAL MATURASE.
CN MATK.
OS Rhododendron primuliflorum.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Ericales; Ericaceae; Rhododendron.
OX NCBI_TaxID=75578;
RN (1)
RP SEQUENCE FROM N.A.
RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
RA Yikawa T.,
RT Investigation of Sectional Relationships in the Genus
KT Rhododendron(Ericaceae) based on matk Sequences."
RL J. Jpn. Bot. 0:0-0(1998).
DR EMBL; AB012740; BAA25861.1; "
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01348; Intron_maturase2; 1.
DR Pfam; PF01824; MatK_N; 1.
KW Chloroplast.
SQ SEQUENCE 506 AA: 60393 MW: DAAB47A759CFPC46 CRC64;

Query Match 35.5%; Score 52.5; DB 8; Length 506;

Best Local Similarity 37.5%; Pred. No. 23;
Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

QY 1 KNIMAA-----QRYGRLRMSDEFGSGFK 25
DB 391 KPWWALSDSDIIERFGRIYRNLSHYSGSLK 422
RESULT 15
062984 PRELIMINARY; PRT: 506 AA.
AC 062984;
DT 01-AUG-1998 (TREMblrel. 07, Created)
DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
OS RIBOSOMAL MATURASE.
CN MATK.
OS Rhododendron ferrugineum (Alpenrose).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Ericales; Ericaceae; Rhododendron.
OX NCBI_TaxID=49622;
RN (1)
RP SEQUENCE FROM N.A.
RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
RA Yikawa T.,
RT Investigation of Sectional Relationships in the Genus
KT Rhododendron(Ericaceae) based on matk Sequences."
RL J. Jpn. Bot. 0:0-0(1998).
DR EMBL; AB012741; BAA25862.1; "
DR InterPro; IPR000442; Intron_maturase2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01348; Intron_maturase2; 1.
DR Pfam; PF01824; MatK_N; 1.
KW Chloroplast.
SQ SEQUENCE 506 AA: 60534 MW: ADA44B25E92436E8 CRC64;

Query Match 35.5%; Score 52.5; DB 8; Length 506;
Best Local Similarity 37.5%; Pred. No. 23;
Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;
QY 1 KNIMAA-----QRYGRLRMSDEFGSGFK 25
DB 391 KPWWALSDSDIIERFGRIYRNLSHYSGSLK 422

Search completed: September 20, 2002, 11:03:47
Job time: 1664 sec

cell lymphoma/leukemia 2 (bc1-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer

Claim 18: Page 19: 74pp: English.

The invention relates to a peptide conjugate having the formula:
 (R-X)-peptide where n = 1-10; X = C=O, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is NH₂ or OH; or X = O or NH, when the R-X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COOH or CONH₂; and R = 2-18c alkyl or alkoxy, 2-14c alkenyl optionally or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally or a phenyl group substituted with a 1-5c straight or branched chain alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples of a bc1-2 superfamily polypeptide corresponding to amino acids 72-97 of the BH3 domain of the cell death agonist Bad. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphoma/leukemia 2 (bc1-2)-mediated blockage of apoptosis in cancer cells. It is also useful for inhibiting bc1-2 function in cancer cells. The peptide conjugate is useful for treating a subject afflicted with a cancer characterized by overexpression of bc1-2, acute or chronic lymphocytic and non-lymphocytic leukemia, melanoma, or non-small lung, renal or thyroid cancers, neuroblastoma, gastric, or acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.

Sequence 27 AA:

Query Match 100.0%; Score 143; DB 21; Length 27;
 Best Local Similarity 100.0%; Pred. No. 5, 1e-15;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KNIWAAGRYGRLTIRMSDEFSGSKGL 27
 DB 1 KNIWAAGRYGRLTIRMSDEFSGSKGL 27

RESULT 2
 ID AAB37055 standard; peptide: 28 AA.
 AC AAB37055;
 DT 28-FEB-2001 (first entry)
 XX
 XX Bcl2 polypeptide BH3 domain peptide #55.
 XX
 KW Cytostatic; neuroprotective; anti-HIV; antiviral; cerebroprotective;
 KW cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;
 KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
 KW stroke; myocardial infarction.
 XX
 KW Homo sapiens.
 XX
 XX M0200059526-A1.
 XX
 XX 12-OCT-2000.
 XX
 XX 06-APR-2000; 2000MO-US09352.
 XX
 XX 07-APR-1999; 99US-0128202.
 XX
 XX (UIJE-) UNIV JEFFERSON THOMAS.
 XX
 XX Huang Z, Wang J, Zhang Z, Shan S, Lu Z.
 XX
 XX

New peptide conjugates for modulating apoptosis or for inhibiting B cell lymphoma/leukemia 2 (bc1-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer

Claim 18: Page 19: 74pp: English.

The invention relates to a peptide conjugate having the formula:
 (R-X)-peptide where n = 1-10; X = C=O, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is NH₂ or OH; or X = O or NH, when the R-X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COOH or CONH₂; and R = 2-18c alkyl or alkoxy, 2-14c alkenyl optionally or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally or a phenyl group substituted with a 1-5c straight or branched chain alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples of a bc1-2 superfamily polypeptide corresponding to amino acids 72-97 of the BH3 domain of the cell death agonist Bad. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphoma/leukemia 2 (bc1-2)-mediated blockage of apoptosis in cancer cells. It is also useful for inhibiting bc1-2 function in cancer cells. The peptide conjugate is useful for treating a subject afflicted with a cancer characterized by cancer cells that overexpress bc1-2, acute or chronic lymphocytic and non-lymphocytic leukemia, melanoma, or non-small lung, renal or thyroid cancers, neuroblastoma, gastric, or acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.

Sequence 28 AA:

Query Match 100.0%; Score 143; DB 21; Length 28;
 Best Local Similarity 100.0%; Pred. No. 5, 3e-15;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KNIWAAGRYGRLTIRMSDEFSGSKGL 27
 DB 1 KNIWAAGRYGRLTIRMSDEFSGSKGL 27

RESULT 3
 ID AAB37001 standard; peptide: 26 AA.
 AC AAB37001;
 DT 28-FEB-2001 (first entry)
 XX
 XX Bcl2 polypeptide BH3 domain peptide #1.
 XX
 KW Cytostatic; neuroprotective; anti-HIV; antiviral; cerebroprotective;
 KW cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;
 KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
 KW stroke; myocardial infarction.
 XX
 KW Homo sapiens.
 XX
 XX M0200059526-A1.
 XX
 XX 12-OCT-2000.
 XX
 XX 06-APR-2000; 2000MO-US09352.
 XX
 XX 07-APR-1999; 99US-0128202.
 XX
 XX

XX (UYJE-) UNIV JEFFERSON THOMAS.
 XX
 XX Huang Z, Wang J, Zhang Z, Shan S, Lu Z;
 XX
 XX WPI: 2000-679325/66.
 XX
 XX New peptide conjugates for modulating apoptosis or for inhibiting B
 PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
 PT treating neurodegenerative disorders, stroke, or cancer
 XX
 XX Claim 18; Page 17; 74pp; English.
 XX
 XX The invention relates to a peptide conjugate having the formula:
 CC (R-X)n peptide where n = 1-10; X = C=O, when the R-X group is attached
 CC to the N-terminus of the peptide, or a side chain of the peptide where
 CC the R-X group is attached to the C-terminus of the peptide; n is
 CC when the R-X group is attached to the side chain of the peptide, n is
 CC side chain of the peptide, where the side chain functional group is COOH
 CC or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl optionally
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl containing one
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples
 CC of the peptide portion of the conjugate. The peptides represent analogues
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
 CC the Bcl-2 domain of the cell death agonist Bad. The peptide conjugate is
 CC useful for modulating apoptosis in the cells of a subject, or for
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
 CC function. In particular, the peptide conjugate is useful for treating a
 CC subject afflicted with a cancer characterized by cancer cells that
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
 CC conjugate is also useful for treating disorders characterized by
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
 CC
 XX Sequence 26 AA:
 SO
 Query Match 96.5%; Score 138; DB 21; Length 26;
 Best Local Similarity 100.0%; Pred. No. 2.9e-14;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NIMAAORYGRELIRMSDEFSGSFQKL 27
 DB 1 nlwaagrygrelrimsdefsgsfqkl 26
 RESULT 4
 AAB37002 standard; peptide; 26 AA.
 XX
 XX AAB37002;
 AC
 XX 28-FEB-2001 (first entry)
 DT
 XX Bcl2 polypeptide Bcl2 domain peptide #2.
 XX
 XX Cytostatic; neuroprotective; anti-HIV; virocidic; cerebroprotective;
 KW cardiant; Bcl-2 superfamily; Bcl2 domain; cell death agonist; Bad;
 KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
 KW stroke; myocardial infarction.
 XX
 XX Homo sapiens.
 OS
 XX W0200059526-A1.
 PN
 XX
 XX 12-OCT-2000.
 PD

XX 06-APR-2000; 2000OMO-US09352.
 PF
 XX
 XX 07-APR-1999; 99US-0128202.
 XX
 XX (UYJE-) UNIV JEFFERSON THOMAS.
 XX
 XX Huang Z, Wang J, Zhang Z, Shan S, Lu Z;
 XX
 XX WPI: 2000-679325/66.
 XX
 XX New peptide conjugates for modulating apoptosis or for inhibiting B
 PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
 PT treating neurodegenerative disorders, stroke, or cancer
 XX
 XX Claim 18; Page 17; 74pp; English.
 XX
 XX The invention relates to a peptide conjugate having the formula:
 CC (R-X)n peptide where n = 1-10; X = C=O, when the R-X group is attached
 CC to the N-terminus of the peptide, or a side chain of the peptide where
 CC the functional group of the side chain is NH2 or OH; or X = O or NH;
 CC when the R-X group is attached to the C-terminus of the peptide, or a
 CC side chain of the peptide, where the side chain functional group is COOH
 CC or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkylenyl containing one
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain
 CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples
 CC of the peptide portion of the conjugate. The peptides represent analogues
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
 CC the Bcl-2 domain of the cell death agonist Bad. The peptide conjugate is
 CC useful for modulating apoptosis in the cells of a subject, or for
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
 CC function. In particular, the peptide conjugate is useful for treating a
 CC subject afflicted with a cancer characterized by cancer cells that
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
 CC conjugate is also useful for treating disorders characterized by
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
 CC
 XX Sequence 26 AA:
 SO
 Query Match 96.5%; Score 138; DB 21; Length 26;
 Best Local Similarity 100.0%; Pred. No. 2.9e-14;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NIMAAORYGRELIRMSDEFSGSFQKL 27
 DB 1 nlwaagrygrelrimsdefsgsfqkl 26
 RESULT 5
 AAB37003 standard; peptide; 27 AA.
 XX
 XX AAB37003;
 AC
 XX 28-FEB-2001 (first entry)
 DT
 XX Bcl2 polypeptide Bcl2 domain peptide #3.
 XX
 XX Cytostatic; neuroprotective; anti-HIV; virocidic; cerebroprotective;
 KW cardiant; Bcl-2 superfamily; Bcl2 domain; cell death agonist; Bad;
 KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
 KW stroke; myocardial infarction.
 XX
 XX Homo sapiens.
 OS

XX MOZ00059536-A1.

XX 12-OCT-2000.

XX 06-APR-2000; 2000MO-US09352.

XX 07-APR-1999; 99US-0128202.

XX (UYJE-) UNIT JEFFERSON THOMAS.

XX Huang Z, Wang J, Zhang Z, Shan S, Lu Z;

XX WPI: 2000-679325/66.

XX New peptide conjugates for modulating apoptosis or for inhibiting B
PT cell lymphoma/leukemia 2 (bcl-2) function, especially useful for
PT treating neurodegenerative disorders, stroke, or cancer

XX Claim 18; Page 17; 74pp; English.

XX The invention relates to a peptide conjugate having the formula:
XX (R-X)n peptide where n = 1-10, X = C=O, when the R-X group is attached
XX to the peptide, a side chain of the peptide where
XX the functional group of the side chain is attached to the C-terminus of the peptide, or a
XX side chain of the peptide, where the side chain functional group is COOH
XX or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkenyl optionally
XX containing one or two double bonds, cyclohexyl, cyclopentyl, cyclohexyl optionally
XX monosubstituted with a 1-5C straight or branched chain alkyl group,
XX phenyl optionally monosubstituted with a 1-5C straight or branched chain
XX alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples
XX of the peptide portion of the conjugate. The peptides represent analogues
XX of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
XX the Bcl-2 domain of the cell death agonist Bad. The peptide conjugate is
XX useful for modulating apoptosis in the cells of a subject, or for
XX reversing B cell lymphoma/leukemia 2 (bcl-2)-mediated blockage of
XX apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
XX function. In particular, the peptide conjugate is useful for treating a
XX subject afflicted with a cancer characterized by cancer cells that
XX express Bcl-2. The cancer includes prostate, colorectal, gastric,
XX non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
XX acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
XX conjugate is also useful for treating disorders characterized by
XX increased apoptosis, e.g., neurodegenerative disorders, acquired
XX immunodeficiency syndrome (AIDS), stroke or myocardial infarction.

XX Sequence 27 AA:

Query Match 96.5%; Score 138; DA 21; Length 27;

Best Local Similarity 100.0%; Pred. No. 36-14;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 NLMAAQRGRELRRMSDEFGSKGL 27

DB 1 nlwaagrygrelrrmsdefgskgl 26

RESULT 6

AAB70370 AAB70370 standard; protein; 162 AA.

XX AAB70370:

XX 02-MAY-2001 (first entry)

XX Shorter murine BAD mutant amino acid sequence SEQ ID NO:3.

XX Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
XX immunostimulant; neuroprotective; nootropic; antischismic; vulnery;
XX cytosolic; antiviral; antiarthritic; antiinflammatory; wound healing;
XX immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;

KW immunodeficiency disease; neurodegenerative disease; viral infection;
KW ischemic cell death; reperfusion cell death; arthritis; infertility;
KW lymphoproliferative condition; inflammation; autoimmune disease.

XX Mus musculus.

XX Synthetic.

XX MOZ00110888-A1.

XX 15-FEB-2001.

XX 30-MAY-2000; 2000MO-US11864.

XX 28-MAY-1999; 99US-0136783.

XX (APOE-) APOPTOSIS TECHNOLOGY INC.

XX Zhou X;

XX WPI: 2001-138734/14.

XX New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,
PT useful for screening for candidate compounds which induce or inhibit
PT apoptosis, comprises amino acid substitutions at Ser118, Ser135 or
PT Ser113

XX Claim 7; Page 148-149; 157pp; English.

XX The present invention describes an isolated or synthetic polypeptide
XX (1) comprising a less than full length amino acid sequence of a mutant
XX Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its
XX fragment, which contains amino acid substitutions at Ser118 of a human
XX BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine
XX BAD (shorter murine BAD). (1) has immunostimulant, neuroprotective,
XX nootropic, antischismic, vulnery, cytosolic, antiviral,
XX antiarthritic, antiinflammatory and immunosuppressive activities, and
XX can be used as an apoptosis inducer or inhibitor. BAD polypeptides and
XX polynucleotides can be used for screening candidate compounds and drugs
XX for activity that promote cell survival or apoptosis. Other uses include
XX inducing or inhibiting apoptosis in a cell. Candidate compounds
XX identified and (mutant) BAD polypeptides are useful in treating
XX immunodeficiency diseases, neurodegenerative diseases, ischemic cell
XX death, reperfusion cell death, wound healing, cancer, viral infections,
XX lymphoproliferative conditions, arthritis, infertility, inflammation and
XX autoimmune diseases. The present sequence represents a specifically
XX claimed shorter murine BAD mutant amino acid sequence from the present
XX invention.

XX Sequence 162 AA:

Query Match 96.5%; Score 138; DA 22; Length 162;

Best Local Similarity 100.0%; Pred. No. 2-2e-13;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 NLMAAQRGRELRRMSDEFGSKGL 27

DB 98 nlwaagrygrelrrmsdefgskgl 123

RESULT 7

AAR95168 AAR95168 standard; protein; 204 AA.

XX AAR95168:

XX 05-JAN-1997 (first entry)

XX bcl-X(L)/bcl-2 associated death promoter protein.

XX Epitope; murine; bcl-X(L)/bcl-2 associated death promoter; Bad; stroke;
XX polypeptide; bcl-X; cell death; regulator; Bcl-2; apoptotic cell death;
XX cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS;

XX neurodegenerative disease; senescence; ischaemia; neoplasia.
 XX Mus musculus.
 OS
 XX Key Location/Organisms
 XX Region 147..149
 XX Region /note= "BHL conserved amino acids"
 XX Region 191..192
 XX Domain /note= "BH2 conserved amino acids"
 XX Domain 38...61
 XX Domain /note= "PEST sequence"
 XX Domain 111..130
 XX /note= "PEST sequence"
 PD W096J3614-A1.
 PN
 PD 09-MAY-1996.
 XX
 XX 31-OCT-1995. 95M0-US14246.
 XX
 XX 31-OCT-1994. 94US-0333565.
 XX
 XX (UNIT) UNIT WASHINGTON.
 PA
 PI Korsmeyer SJ;
 DR WP1: 1996-251465/25.
 DR N-FSDB: A879479.
 PT polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter -
 PS useful to treat neoplasia and apoptosis and to identify agents
 PS inhibiting its binding to bcl-2 or bcl-x(L) to form heterodimers
 PS
 PS Claim 3: Fig 1: 130pp: English.

CC This sequence represents the murine bcl-x(L)/bcl-2 associated death
 CC promoter (BD) gene product which encodes a protein that has homology
 CC to bcl-2. Bcl-2 is a proto-oncogene that regulates cell death. It has homology
 CC to the bcl-2-related family clustered in the BHL and BH2 domain. Bad
 CC has been found to hybridize to bcl-x(L) and bcl-2 in yeast two-hybrid
 CC assays and in vivo in mammalian cells. Overexpressed bad counters the
 CC death inhibitory activity of bcl-x(L), but is much less effective at
 CC counteracting the death inhibitory activity of bcl-2. Bad expression can
 CC accelerate apoptotic cell death induced by cytokine deprivation in an
 CC bcl-2 dependent manner. Bad also competes with Bax for binding to the
 CC death-inhibitory activity of bcl-x(L) and competes with Bax for binding
 CC to bcl-x(L). Bad may be used to identify agents which inhibit its
 CC binding to bcl-2 or bcl-x(L) to form heterodimers. Such agents may be
 CC used to treat neurodegenerative diseases, immunodeficiency diseases,
 CC e.g. AIDS, senescence or Ischaemia.

CC CC
 CC Sequence 204 AA:
 SO

Query Match 96.5%; Score 138; DB 17; Length 204;
 Best Local Similarity 100.0%; Pred. No. 2.8e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

YY (2) NMMAAGTGRRLRMSDFDSFGKGL (27)
 YY | ||||| ||||| ||||| ||||| |||||
 DB 140 ntatgacgtgatcttattttatggatgaagtgtagt 165

RESULT 8
 AAAM61315
 ID AAAM61315 standard; Protein: 204 AA.
 XX
 XX AAAM61315;
 XX
 DT 07-OCT-1998 (first entry)
 XX
 XX Murine BCL-XL/BCL-2 associated cell death regulator.

```
KM Mutine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein  
KM serine substituted mutant; apoptosis; cancer; viral infection.  
  
XX Mus sp.  
OS W09817682-AI.  
PN 30-Apr-1998.  
PD 17-OCT-1997: 97WO-USU19175.  
PE 18-OCT-1996: 96US-07J33505,  
FR (UNIW ) UNTV WASHINGTON.  
XR Korsmeyer SJ:  
XN WPL1: 1998-261422/23.  
DR N-PDB: AAV27833.  
PP New mutant BAD polypeptide with phosphorylatable serine replaced -  
PT used by Ser-9' treating reduced apoptosis such as in cancer or  
PR viral infection  
PS Claim 1: Fig 10; 95pp; English.  
CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell  
CC death regultor) proteins, having an amino acid other than Ser at  
CC position 112 and/or 136, related to the mutants described above. The  
CC fragments of mutant BAD protein able to decrease cell viability; (2)  
CC fusion proteins of mutant BAD with a heterologous polypeptide that  
CC increases intracellular delivery. Mutant BAD proteins are used to treat  
CC or prevent diseases associated with reduced apoptosis, e.g. cancer,  
CC viral infection, lymphoproliferation, arthritis, infertility, aneoding  
CC inflammation and autoimmune disease. Polynucleotide sequences encoding  
CC mutant BAD proteins can be used directly as probes or in drug screening. BAD  
CC proteins phosphorylated at specified ser are used to screen for enhancers  
CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful  
CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,  
CC aging or ischemic cell death. The apoptotic status of cells is  
CC determined by measuring relative amounts of phosphorylated and non-  
CC phosphorylated BAD, by usual immunoblotting methods. Mutant BAD which become  
CC phosphorylated from the specified Ser forming a product that does not  
CC heterodimerize with BCL-2 or BCL-Xl but instead binds to 14-3-3 family  
CC proteins in the cytosol, thus promoting cell survival. The mutants with  
CC Ser substituted cannot bind 14-3-3.  
CX Sequence 204 AA:
```

KW serine substituted mutant; apoptosis; cancer; viral infection.
 OS Mus sp.
 OS Synthetic.
 XX W09817682-AL.
 XX 30-Apr-1998.
 PD 30-Apr-1998.
 XX 17-Oct-1997: 97WO-US19175.
 XX 18-Oct-1996: 96US-0735505.
 XX (UNIM) UNIT WASHINGTON.
 XX Koremeyer SJ.
 PI
 XX MPI: 1998-261422/23.
 DR N-PSDB: AAW27834.
 XX New mutant BAD polypeptide with phosphorylatable serine replaced -
 PF useful for, e.g. treating reduced apoptosis such as in cancer or
 PP viral infection
 XX
 XX Claim 7: Page 59; 95pp: English.
 XX
 CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
 CC death regulator) proteins, having an amino acid other than Ser at
 CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
 CC present sequence represents a mutant BAD protein. Also described are: (1)
 CC fragments of mutant BAD protein able to decrease cell viability; (2)
 CC fusion proteins of mutant BAD with heterologous polypeptides that treat
 CC infection, such as HIV, hepatitis B virus, hepatitis C virus, and
 CC or prevent diseases associated with reduced apoptosis, e.g. cancer, treat
 CC viral infection, lymphoproliferation, arthritis, infertility,
 CC inflammation and autoimmune disease. Polynucleotide sequences encoding
 CC mutant BAD proteins can be used similarly by gene therapy or to produce
 CC transgenic animals for use as disease models or in drug screening. BAD
 CC proteins phosphorylated at specified Ser are used to screen for enhancers
 CC and inhibitors of apoptosis, such as AIDS and endometriosis, useful
 CC in treatment of excessive apoptosis, such as AIDS and endometriosis,
 CC aging or ischemic cell death. The apoptotic status of cells is
 CC determined by measuring relative amounts of phosphorylated and non-
 CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
 CC greater death-promoting activity than wild-type BAD which can become
 CC phosphorylated on the specified Ser, forming a product that does not
 CC heterodimerize with BCL-2 or BCL-XL but instead binds to 14-3-3 family
 CC proteins in the cytosol, thus promoting cell survival. The mutants with
 CC Ser substituted cannot bind 14-3-3.
 XX
 XX Sequence 204 AA:
 SO
 Query Match 96.5%; Score 138; DB 19; Length 204;
 Best Local Similarity 100.0%; Pred. NO. 2.8e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 NMAAQRGRLRNKSPDEGSPKGL 27
 DB 140 nlmadqyrceltrmsdecegsfkgl 165
 RESULT 10
 AAW61317
 ID AAW61317 standard; Protein: 204 AA.
 AC AAW61317:
 XX 07-Oct-1998 (first entry)
 XX Mutant BCL-XL/BCL-2 associated cell death regulator #2.
 DE
 XX
 KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;

KW serine substituted mutant; apoptosis; cancer; viral infection.
 OS Mus sp.
 OS Synthetic.
 XX W09817682-AL.
 XX 30-Apr-1998.
 PD 30-Apr-1998.
 XX 17-Oct-1997: 97WO-US19175.
 XX 18-Oct-1996: 96US-0735505.
 XX (UNIM) UNIT WASHINGTON.
 XX Koremeyer SJ.
 PI
 XX MPI: 1998-261422/23.
 DR N-PSDB: AAW27835.
 XX New mutant BAD polypeptide with phosphorylatable serine replaced -
 PF useful for, e.g. treating reduced apoptosis such as in cancer or
 PP viral infection
 XX
 XX Claim 7: Page 60; 95pp: English.
 XX
 CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
 CC death regulator) proteins, having an amino acid other than Ser at
 CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
 CC present sequence represents a mutant BAD protein. Also described are: (1)
 CC fragments of mutant BAD protein able to decrease cell viability; (2)
 CC fusion proteins of mutant BAD with heterologous polypeptides that treat
 CC infection, such as HIV, hepatitis B virus, hepatitis C virus, and
 CC or prevent diseases associated with reduced apoptosis, e.g. cancer, treat
 CC viral infection, lymphoproliferation, arthritis, infertility,
 CC inflammation and autoimmune disease. Polynucleotide sequences encoding
 CC mutant BAD proteins can be used similarly by gene therapy or to produce
 CC transgenic animals for use as disease models or in drug screening. BAD
 CC proteins phosphorylated at specified Ser are used to screen for enhancers
 CC and inhibitors of apoptosis, such as AIDS and endometriosis, useful
 CC in treatment of excessive apoptosis, such as AIDS and endometriosis,
 CC aging or ischemic cell death. The apoptotic status of cells is
 CC determined by measuring relative amounts of phosphorylated and non-
 CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
 CC greater death-promoting activity than wild-type BAD which can become
 CC phosphorylated on the specified Ser, forming a product that does not
 CC heterodimerize with BCL-2 or BCL-XL but instead binds to 14-3-3 family
 CC proteins in the cytosol, thus promoting cell survival. The mutants with
 CC Ser substituted cannot bind 14-3-3.
 XX
 XX Sequence 204 AA:
 SO
 Query Match 96.5%; Score 138; DB 19; Length 204;
 Best Local Similarity 100.0%; Pred. NO. 2.8e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 NMAAQRGRLRNKSPDEGSPKGL 27
 DB 140 nlmadqyrceltrmsdecegsfkgl 165
 RESULT 11
 AAW61318
 ID AAW61318 standard; Protein: 204 AA.
 AC AAW61318:
 XX 07-Oct-1998 (first entry)
 XX Mutant BCL-XL/BCL-2 associated cell death regulator #3.
 DE
 XX
 KW Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;

XX BRC6 gene; cell death; cell cycle; Bcl2; human.
 KW Homo sapiens.
 OS US5663316-A.
 PN 02-SEP-1997.
 PD 18-JUN-1996; 96US-0665617.
 PF 18-JUN-1996; 96US-0665617.
 PR 18-JUN-1996; 96US-0665617.
 PA (CLON-) CLONTECH LAB INC.
 XX Xudong Y;
 PI WPI; 1997-447980/41.
 DR N-PSDB; AAT91561.
 XX
 PT Isolated BRC6 gene - encodes a protein that regulates cell death
 through interaction with Bcl-2
 PS Claim 1; Column 11-12; 7pp; English.
 XX
 CC The present sequence represents a protein of 166 amino acids. The
 sequence is disclosed as being a protein called BRC6 which regulates
 cell death through interaction with Bcl-2. The DNA may be used for the
 production of the recombinant protein, which can be used in unspecified
 therapeutic or diagnostic procedures, as a molecular weight marker, and
 to raise antibodies that can be used in unspecified diagnostic or
 therapeutic applications and to reduce or eliminate the biological
 activity of the BRC6 protein in vivo.
 CC
 SQ Sequence 166 AA:

Query Match 79.7%; Score 114; DB 18; Length 166;
 Best local similarity 91.7%; pred. No. 1, le-09;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 NMAAGRYGELRRMSDFEGSFK 25
 DB 101 nlwaagrygrellrmaelrdsfk 124

Search completed: September 20, 2002, 10:35:59
 Job time: 427 sec



GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2002, 10:37:21 | search time 75.64 seconds
(without alignments)
8,719 Million cell updates/sec

Title: US-09-544-664-56

Perfect score: 143

Sequence: 1 KRLNAAQRYGRELRLRMDSDFGSPKGL 27

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Issued Patents: AA*

1: /cgn2_6/p/ctdata/2/1aa/5A.COM6.pep:*
2: /cgn2_6/p/ctdata/2/1aa/5B.COM6.pep:*
3: /cgn2_6/p/ctdata/2/1aa/5A.COM6.pep:*
4: /cgn2_6/p/ctdata/2/1aa/5B.COM6.pep:*
5: /cgn2_6/p/ctdata/2/1aa/5C.COM6.pep:*
6: /cgn2_6/p/ctdata/2/1aa/5D.COM6.pep:*
7: /cgn2_6/p/ctdata/2/1aa/5E.COM6.pep:*
8: /cgn2_6/p/ctdata/2/1aa/5F.COM6.pep:*
9: /cgn2_6/p/ctdata/2/1aa/5G.COM6.pep:*
10: /cgn2_6/p/ctdata/2/1aa/5H.COM6.pep:*
11: /cgn2_6/p/ctdata/2/1aa/5I.COM6.pep:*
12: /cgn2_6/p/ctdata/2/1aa/5J.COM6.pep:*
13: /cgn2_6/p/ctdata/2/1aa/5K.COM6.pep:*
14: /cgn2_6/p/ctdata/2/1aa/5L.COM6.pep:*
15: /cgn2_6/p/ctdata/2/1aa/5M.COM6.pep:*
16: /cgn2_6/p/ctdata/2/1aa/5N.COM6.pep:*
17: /cgn2_6/p/ctdata/2/1aa/5O.COM6.pep:*
18: /cgn2_6/p/ctdata/2/1aa/5P.COM6.pep:*
19: /cgn2_6/p/ctdata/2/1aa/5Q.COM6.pep:*
20: /cgn2_6/p/ctdata/2/1aa/5R.COM6.pep:*
21: /cgn2_6/p/ctdata/2/1aa/5S.COM6.pep:*
22: /cgn2_6/p/ctdata/2/1aa/5T.COM6.pep:*
23: /cgn2_6/p/ctdata/2/1aa/5U.COM6.pep:*
24: /cgn2_6/p/ctdata/2/1aa/5V.COM6.pep:*
25: /cgn2_6/p/ctdata/2/1aa/5W.COM6.pep:*
26: /cgn2_6/p/ctdata/2/1aa/5X.COM6.pep:*
27: /cgn2_6/p/ctdata/2/1aa/5Y.COM6.pep:*
28: /cgn2_6/p/ctdata/2/1aa/5Z.COM6.pep:*

Print No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	138	96.5	204	1	US-08-333-565-2
2	138	96.5	204	2	US-08-661-479-2
3	138	96.5	204	2	US-08-733-505A-1
4	138	96.5	204	2	US-08-733-505A-12
5	138	96.5	204	2	US-08-733-505A-13
6	138	96.5	204	2	US-08-733-505A-14
7	138	96.5	204	2	US-08-733-505A-15
8	138	96.5	204	2	US-08-733-505A-16
9	138	96.5	204	2	US-08-733-505A-17
10	138	96.5	204	2	US-08-733-505A-18
11	138	96.5	204	2	US-08-733-505A-19
12	138	96.5	204	2	US-08-733-505A-20
13	138	96.5	204	2	US-08-733-505A-21
14	138	96.5	204	2	US-08-733-505A-22
15	138	96.5	204	2	US-08-733-505A-23
16	138	96.5	204	2	US-08-733-505A-24
17	138	96.5	204	2	US-08-733-505A-25
18	138	96.5	204	2	US-08-733-505A-26
19	138	96.5	204	2	US-08-733-505A-27
20	138	96.5	204	2	US-08-733-505A-28
21	138	96.5	204	2	US-08-733-505A-29
22	138	96.5	204	2	US-08-733-505A-30
23	138	96.5	204	2	US-08-733-505A-31
24	138	96.5	204	2	US-08-733-505A-32
25	138	96.5	204	2	US-08-733-505A-33
26	138	96.5	204	2	US-08-733-505A-34
27	138	96.5	204	2	US-08-733-505A-35

28	44	30.8	263	4	US-09-551-656-27	Sequence 27, Appl
29	44	30.1	213	1	US-08-487-312-19	Sequence 19, Appl
30	44	30.1	213	3	US-08-778-728-18	Sequence 18, Appl
31	44	30.1	213	4	US-09-121-844-18	Sequence 18, Appl
32	44	30.1	380	4	US-08-153-840-40	Sequence 40, Appl
33	44	30.1	380	3	US-09-295-840-40	Sequence 40, Appl
34	44	30.1	380	4	US-09-068-370-40	Sequence 40, Appl
35	44	30.1	380	5	PCF-US93-1153-40	Sequence 40, Appl
36	44	28.4	322	4	US-09-359-161-7	Sequence 7, Appl
37	44	28.4	348	2	US-08-997-080-170	Sequence 170, App
38	44	28.4	348	2	US-08-997-362-170	Sequence 170, App
39	44	28.4	348	4	US-09-095-855-170	Sequence 170, App
40	44	28.4	348	4	US-09-324-542-170	Sequence 170, App
41	44	28.4	393	2	US-08-997-080-94	Sequence 94, Appl
42	44	28.4	393	2	US-08-997-362-94	Sequence 94, Appl
43	44	28.4	393	3	US-08-873-970-94	Sequence 94, Appl
44	44	28.4	393	4	US-09-095-855-94	Sequence 94, Appl
45	44	29.4	393	4	US-09-324-542-94	Sequence 94, Appl

ALIGNMENTS

RESULT 1
US-08-333-565-2
Sequence 2, Application US/08333565
Patent No. 5622852
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-X/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Knowrie and Crew
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,565
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURES:
NAME/KEY: protein
LOCATION: 1..204
OTHER INFORMATION: /note="Reduced amino acid sequence
OTHER INFORMATION: Of mouse BAD."

Query Match 96.5%; Score 138; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 7e-14; 0;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 NLMAAORYGRELRLMSDEFGSPKGL 27
 DB 140 NLMAAORYGRELRLMSDEFGSPKGL 165

RESULT 2

US-08-661-479-2

Sequence 2, Application US/08661479

Patent No. 5834209

GENERAL INFORMATION:

APPLICANT: KORSMEYER, Stanley J.

TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Kourile and Crew

STREET: 379 Lytton Avenue

CITY: Palo Alto

STATE: California

COUNTRY: US

ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

FILING DATE: 11-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/733,565

FILING DATE: 31-OCT-1994

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M

REGISTRATION NUMBER: 30,223

TELEPHONE/DOCKET NUMBER: 15726A-000700

TELEPHONE: (415) 326-2400

TELEFAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 204 amino acids

TYPE: amino acid

STRANDEDNESS: Single

MOLECULE TYPE: linear

FEATURE:

NAME/KEY: Protein

LOCATION: 1 204

OTHER INFORMATION: /note="Deduced amino acid sequence

US-08-661-479-2

Query Match

Best Local Similarity 100.0%; Score 138; DB 2; Length 204;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 NLMAAORYGRELRLMSDEFGSPKGL 27

DB 140 NLMAAORYGRELRLMSDEFGSPKGL 165

RESULT 3

US-08-733-505A-1

Sequence 1, Application US/08733505A

Patent No. 5856445

GENERAL INFORMATION:

APPLICANT: KORSMEYER, STANLEY J.

TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF

BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR

US-08-733-505A-1

Query Match

Best Local Similarity 100.0%; Score 138; DB 2; Length 204;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 NLMAAORYGRELRLMSDEFGSPKGL 27

DB 140 NLMAAORYGRELRLMSDEFGSPKGL 165

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: HOWELL & HAFERKAMP, L.C.

STREET: 7733 FORSYTH BLVD., SUITE 1400

CITY: ST. LOUIS

STATE: MISSOURI

COUNTRY: USA

ZIP: 63105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

FILING DATE:

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: HOLLAND, DONALD R.

REGISTRATION NUMBER: 35,197

TELEPHONE/DOCKET NUMBER: 965458

TELEPHONE: (314) 727-6092

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 204 amino acids

TYPE: amino acid

STRANDEDNESS:

MOLECULE TYPE: linear

US-08-733-505A-1

Query Match

Best Local Similarity 100.0%; Score 138; DB 2; Length 204;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 NLMAAORYGRELRLMSDEFGSPKGL 27

DB 140 NLMAAORYGRELRLMSDEFGSPKGL 165

RESULT 4

US-08-733-505A-12

Sequence 12, Application US/08733505A

Patent No. 5856445

GENERAL INFORMATION:

APPLICANT: KORSMEYER, STANLEY J.

TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF

BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: HOWELL & HAFERKAMP, L.C.

STREET: 7733 FORSYTH BLVD., SUITE 1400

CITY: ST. LOUIS

STATE: MISSOURI

COUNTRY: USA

ZIP: 63105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

FILING DATE:

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: HOLLAND, DONALD R.

REGISTRATION NUMBER: 35,197

TELEPHONE/DOCKET NUMBER: 965458

TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ. ID NO. 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-505A-12

Query Match 96.5%: Score 138; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 7e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 NMAAORYGRLRMSDEFGSFKGL 27
|||||
Db 140 NMAAORYGRLRMSDEFGSFKGL 165

RESULT 5
US-08-733-505A-13
Sequence 13, Application US/08733505A
Patent No. 5956445
GENERAL INFORMATION:
APPLICANT: KOSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HORNE, B. HAREKAMP, L.C.
STREET: 7733 FORNETH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-6092
TELEFAX: (314) 727-5188
INFORMATION FOR SEQ. ID NO. 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-505A-13

Query Match 96.5%: Score 138; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 7e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 NMAAORYGRLRMSDEFGSFKGL 27
|||||
Db 140 NMAAORYGRLRMSDEFGSFKGL 165

RESULT 6

US-08-733-505A-14
Sequence 14, Application US/08733505A
Patent No. 5956445
GENERAL INFORMATION:
APPLICANT: KOSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HORNE, B. HAREKAMP, L.C.
STREET: 7733 FORNETH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ. ID NO. 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-505A-14

Query Match 96.5%: Score 138; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 7e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 NMAAORYGRLRMSDEFGSFKGL 27
|||||
Db 140 NMAAORYGRLRMSDEFGSFKGL 165

RESULT 7
US-08-717-123-3
Sequence 3, Application US/08717123
Patent No. 5965703
GENERAL INFORMATION:
APPLICANT: Horne, William A.
TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/717,123
FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 1929
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
TOPOLOGY: Linear
US-08-717-123-3

Query Match 94.4%; Score 135; DB 2; Length 204;
Best Local Similarity 96.2%; Pred. No. 2e-13;
Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 NMAAORYGRLRMSDEFDSFGKL 27
DB 140 NMAAORYGRLRMTDDEFDSFGKL 165

RESULT 8
US-08-665-617-2
Sequence 2, Application US/08665617
Patent No. 5663316
GENERAL INFORMATION:
APPLICANT: Xudong, Yin
TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,617
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: CL-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-5800
TELEFAX: (352) 375-8100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-665-617-2

Query Match 79.7%; Score 114; DB 1; Length 166;
Best Local Similarity 91.7%; Pred. No. 2.8e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 NMAAORYGRLRMSDEFDSFGK 25

DB 101 NMAAORYGRLRMSDEFVDSFK 124

RESULT 9
US-08-717-123-2
Sequence 2, Application US/08717123
Patent No. 5965703
GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilmann
TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,123
FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 1929
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-717-123-2

Query Match 79.7%; Score 114; DB 2; Length 168;
Best Local Similarity 91.7%; Pred. No. 2.8e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 NMAAORYGRLRMSDEFDSFGK 25
DB 103 NMAAORYGRLRMSDEFVDSFK 126

RESULT 10
US-08-985-335-1
Sequence 1, Application US/08985335
Patent No. 6080847
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA

```

? COUNTRY: USA
? ZIP: 94304
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? OPERATING SYSTEM: IBM Compatible
? SOFTWARE: FASTSEQ DOS Windows Version 2.0
? CURRENT APPLICATION DATA:
? FILING DATE: Filed Herewith
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Billings, Lucy J.
? REGISTRATION NUMBER: 36,749
? REFERENCE/DOCKET NUMBER: PF-0421 US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 650-855-0555
? TELEFAX: 650-845-4166
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 168 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? IMMEDIATE SOURCE:
? LIBRARY: SYNORAB01
? CLONE: 358673
?
US-08-985-335-1

Query Match          79.7%; Score 114; DB 3; Length 168;
Best Local Similarity 91.7%; Pred. No. 2.8e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      2 NLMNAQRYGRELRRMSDFEGSRK 25
Db      103 NLMNAQRYGRELRRMSDFVDSRK 126

RESULT 11
US-08-985-335-7
? Sequence 7, Application US/08985335
? Patent No. 6080847
? GENERAL INFORMATION:
? APPLICANT: Hillman, Jennifer L.
? APPLICANT: Yue, Henry
? APPLICANT: Lal, Preeti
? APPLICANT: Shah, Purni
? APPLICANT: Corley, Neil C.
? TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
? NUMBER OF SEQUENCES: 9
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Incyte Pharmaceuticals, Inc.
? STREET: 3174 Porter Dr.
? CITY: Palo Alto
? STATE: CA
? COUNTRY: USA
? ZIP: 94304
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? OPERATING SYSTEM: DOS
? SOFTWARE: FASTSEQ for Windows Version 2.0
? CURRENT APPLICATION DATA:
? FILING DATE: Filed Herewith
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:

```

```

? NAME: Billings, Lucy J.
? REGISTRATION NUMBER: 36,749
? REFERENCE/DOCKET NUMBER: PF-0421 US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 650-855-0555
? TELEFAX: 650-845-4166
? INFORMATION FOR SEQ ID NO: 7:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 168 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? IMMEDIATE SOURCE:
? LIBRARY: Genbank
? CLONE: 1683637
?
US-08-985-335-7

Query Match          79.7%; Score 114; DB 3; Length 168;
Best Local Similarity 91.7%; Pred. No. 2.8e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      2 NLMNAQRYGRELRRMSDFEGSRK 25
Db      103 NLMNAQRYGRELRRMSDFVDSRK 126

RESULT 12
US-09-410-372-1
? Sequence 1, Application US/09410372
? Patent No. 6281334
? GENERAL INFORMATION:
? APPLICANT: Hillman, Jennifer L.
? APPLICANT: Yue, Henry
? APPLICANT: Lal, Preeti
? APPLICANT: Shah, Purni
? APPLICANT: Corley, Neil C.
? TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
? NUMBER OF SEQUENCES: 9
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Incyte Pharmaceuticals, Inc.
? STREET: 3174 Porter Dr.
? CITY: Palo Alto
? STATE: CA
? COUNTRY: USA
? ZIP: 94304
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? OPERATING SYSTEM: DOS
? SOFTWARE: FASTSEQ for Windows Version 2.0
? CURRENT APPLICATION DATA:
? FILING DATE:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/985,335
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Billings, Lucy J.
? REGISTRATION NUMBER: 36,749
? REFERENCE/DOCKET NUMBER: PF-0421 US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 650-855-0555
? TELEFAX: 650-845-4166
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 168 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? IMMEDIATE SOURCE:
? LIBRARY: SYNORAB01

```

CLONE: 358673
US-09-410-372-1

Query Match 79.7%: Score 114; DB 4; Length 168;
Best Local Similarity 91.7%: Pred. No. 2,8e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 2 N1MAA0RYGRELIRMSDEFECSFK 25
DB 103 N1MAA0RYGRELIRMSDEFEVDSFK 136

RESULT 13
US-09-410-372-7
Sequence 7, Application US/09410372
Patent No. 6281334
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yoe, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Parul C
APPLICANT: Sood, Neel C
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410,372
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,335
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PP-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMEDIATE SOURCE:
LIBRARY: Genbank
US-09-410-372-7

Query Match 79.7%: Score 114; DB 4; Length 168;
Best Local Similarity 91.7%: Pred. No. 2,8e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 N1MAA0RYGRELIRMSDEFECSFK 25
DB 103 N1MAA0RYGRELIRMSDEFEVDSFK 136

RESULT 14

US-08-333-565-10
Sequence 10, Application US/08333565
Patent No. 5622852
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,565
FILING DATE: 31-Oct-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-333-565-10

Query Match 79.0%: Score 113; DB 1; Length 23;
Best Local Similarity 100.0%: Pred. No. 4,5e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 N1MAA0RYGRELIRMSDEFECSFK 22
DB 3 N1MAA0RYGRELIRMSDEFECSFK 23

RESULT 15
US-08-661-479-10
Sequence 10, Application US/08661479
Patent No. 5834209
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,479

? FILING DATE: 11-JUN-1995
 ? CLASSIFICATION: 435
 ? PRIOR APPLICATION DATA: US 08/333,565
 ? APPLICATION NUMBER: 31-OCT-1994
 ? FILING DATE: 31-OCT-1994
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Smith, William M
 ? REGISTRATION NUMBER: 30, 223
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (415) 326-2400
 ? TELEFAX: (415) 326-2422
 ? INFORMATION FOR SEQ ID NO: 10:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 23 amino acids
 ? TYPE: amino acid
 ? STRANDEDNESS: single
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: peptide
 ? US-08-661-479-10

Query Match 79.0%; Score 113; DB 2; Length 23;
 Best Local Similarity 100.0%; Pred. No. 4.5e-11;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 NIMAAQRYGRELRRMSDFEG 22
 Db 3 NIMAAQRYGRELRRMSDFEG 23

Search completed: September 20, 2002, 10:37:21
 Job time: 409 sec

1. The first part of the document is a list of the names of the persons who have been appointed to the various offices of the city of New York.

GenDore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: September 20, 2002, 10:39:13 ; Search time 95.59 seconds
(Without alignments) 27.141 Million cell updates/sec

Title: US-09-544-664-56

Perfect score: 143

Sequence: 1 KNMAAGRYELRNMSDEFSGSKGL 27

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Minimum Match 100%

Listing first 45 summaries

Database :

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Precl. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	143	32.2	204	JC5575	inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster
2	143	32.2	204	JC5575	inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster
3	143	32.2	204	JC5575	inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster
4	143	32.2	204	JC5575	inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster
5	143	32.2	204	JC5575	inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster
6	143	32.2	204	JC5575	inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster
7	143	32.2	204	JC5575	inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster
8	143	32.2	204	JC5575	inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster
9	143	32.2	204	JC5575	inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster
10	143	32.2	204	JC5575	inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster
11	143	32.2	204	JC5575	inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster
12	143	32.2	204	JC5575	inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster
13	143	32.2	204	JC5575	inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster
14	143	32.2	204	JC5575	inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster
15	143	32.2	204	JC5575	inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster
16	143	32.2	204	JC5575	inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster
17	143	32.2	204	JC5575	inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster
18	143	32.2	204	JC5575	inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster
19	143	32.2	204	JC5575	inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster
20	143	32.2	204	JC5575	inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster
21	143	32.2	204	JC5575	inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster
22	143	32.2	204	JC5575	inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster
23	143	32.2	204	JC5575	inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster
24	143	32.2	204	JC5575	inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster
25	143	32.2	204	JC5575	inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster
26	143	32.2	204	JC5575	inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster
27	143	32.2	204	JC5575	inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster
28	143	32.2	204	JC5575	inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster
29	143	32.2	204	JC5575	inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster

30	45.5	31.8	327	2	AF2859	conserved hypochlorite
31	45.5	31.8	562	2	C71473	hypochlorite prote
32	45.5	31.8	905	2	G83314	NAOH dehydrogenase
33	45.5	31.8	273	2	S06735	photosystem II oxy
34	45.5	31.8	273	2	S06287	mangnase-stabilize
35	45.5	31.8	346	2	H95106	conserved hypochlorite
36	45.5	31.8	591	2	B44465	sodium ion pump ox
37	45.5	31.8	591	2	AB0509	oxalacetate decar
38	45.5	31.8	591	2	AB0509	oxalacetate decar
39	45.5	31.8	591	2	AB0509	oxalacetate decar
40	45.5	31.8	591	2	AB0509	oxalacetate decar
41	45.5	31.8	591	2	AB0509	oxalacetate decar
42	45.5	31.8	591	2	AB0509	oxalacetate decar
43	45.5	31.8	591	2	AB0509	oxalacetate decar
44	45.5	31.8	591	2	AB0509	oxalacetate decar
45	45.5	31.8	591	2	AB0509	oxalacetate decar

ALIGNMENTS

RESULT 1
A55671
Bad protein - mouse
C:Species: Mus musculus (house mouse)
C:Accession: A55671
R:Yang, E.; Zhu, J.; Jockel, J.; Boise, L.H.; Thompson, C.B.; Korsmeyer, S.J.
Cell 80, 285-293, 1995
A>Title: Bad, a heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and promotes apoptosis
A:Reference number: A55671; MID:95116361
A:Accession: A55671
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 220-220
A:Features: 200; CB:137296; MID:9639778; PIDN:AA64465.1; PID:9639779
C:Keywords: heterodimer

Query Match
Best local similarity 100.0%; Pred. No. 9,46-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 140 KNMAAGRYELRNMSDEFSGSKGL 165

RESULT 2
JC5575
inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text-change 20-Jun-2000
R:McKernan, T.; Suzuki, Y.; Yamamoto, T.; Sudojima, H.
J. Biochem. 122, 71-82, 1997
A>Title: Molecular cloning and sequencing of cDNAs encoding three heavy-chain precursors of inter-alpha-trypsin inhibitor heavy chain family.
A:Reference number: JC5575; MID:97420688
A:Accession: JC5575
A:Molecule type: mRNA
A:Residues: 1-946 <NA>
A:Cross-references: CDB:109286; NID:91594689; PIDN:BA11339.1; PID:91594690
A:Accession: PC4485; Liver
A:Molecule type: protein
A:Residues: 55-64;140-146;151-156;424-447;500-528;577-605 <NA>
C:Comment: In the plasma three inter-alpha-trypsin inhibitor heavy chains 1, 2 and 3 that the complexes play important role for pancreatic cancer.
C:Superfamily: inter-alpha-trypsin inhibitor complex component II
F:261-264,717-916/Dissulfide bonds: *status predicted

C.Species: Homo sapiens (man)
 C.Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C.Accession: S40376
 R.Klein, R.; JerniChon, R.; Zachay, H.G.
 Eur. J. Immunol. 23:3248-3271, 1993
 A.Title: Expressed human immunoglobulin cHt genes and their hypermutation.
 A.Reference number: S40312; MUID:94080891
 A.Accession: S40376
 A.Status: preliminary; translation not shown
 A.Molecule type: mRNA
 A.Residues: 1-114 <XREF>
 A.Cross-references: EMBL:X72486; NID:g441440; PIDD:CAA51154.1; PTD:g441441
 C.Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C.Keywords: heterocytene; Immunoglobulin
 F:34-113/Domain: Immunoglobulin homology <IMM>

Query Match 33.9%; Score 48.5; DB 2; Length 134;
 Best Local Similarity 38.2%; Pred. No. 8.7;
 Matches 13; Conservative 1; Mismatches 9; Indels 11; Gaps 1;
 QY 4 AAORRGELRRM-----SDEPGSFGK 26
 DB 58 WFRGKSPRLTVNKRSGVSDRSGSGSG 91

RESULT 11
 T02975
 A.Title: Zea mays - maize
 C.Species: Zea mays (maize)
 C.Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
 C.Accession: T02975
 R.Batley, N.H.; James, N.C.; Greenland, A.J.
 Plant Physiol. 112:1391-1396, 1996
 A.Title: CDNA isolation and gene expression of maize annexins P33 and P35.
 A.Reference number: Z14796; MUID:97092863
 A.Accession: T02975
 A.Status: preliminary; translated from GB/EMBL/DBJ
 A.Molecule type: mRNA
 A.Residues: 1-314 <BAT>
 A.Cross-references: EMBL:X98245; NID:g1370602; PIDD:CAA66901.1; PTD:g1370603
 A.Experimental source: cultivar clipper; root tip
 C.Superfamily: annexin I; annexin repeat homology
 F:14-85/Domain: annexin repeat homology <ANX>

Query Match 33.9%; Score 48.5; DB 2; Length 314;
 Best Local Similarity 47.6%; Pred. No. 21;
 Matches 10; Conservative 4; Mismatches 6; Indels 1; Gaps 1;
 QY 6 AORVGRELRMSDEFGSFGK 25
 DB 54 AEAYGKELRALDDEHGKPE 74

RESULT 12
 C6365
 A.Title: Rhizomucor racemosus
 C.Species: Rhizomucor racemosus
 C.Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 19-Jan-2001
 C.Accession: C6365
 R.Casale, W.L.; McConnelly, D.G.; Wang, S.Y.; Lee, Y.J.; Linz, J.E.
 Mol. Cell. Biol. 10:6654-6663, 1990
 A.Title: Expression of a gene family in the dimorphic fungus Mucor racemosus which exhibit
 A.Reference number: A36365; MUID:91061774
 A.Accession: C6365
 A.Status: preliminary
 A.Molecule type: DNA
 A.Residues: 1-206 <CAS>
 A.Cross-references: GB:M55177
 C.Superfamily: ras transforming protein; translation elongation factor Tu homology
 C.Keywords: GTP binding; nucleotide binding; P-loop
 F:11-126/Domain: translation elongation factor Tu homology <ETU>

F:17-24/Region: nucleotide-binding motif A (P-loop)
 F:123-126/Region: GTP-binding NKXD motif
 F:153-155/Region: GTP-binding SAK/L motif
 F:23,24,42,123,124,126,153/Binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser) #

Query Match 33.6%; Score 48; DB 2; Length 206;
 Best Local Similarity 62.5%; Pred. No. 16;
 Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 11 RLRRMSDEFGSFGK 26
 DB 169 RLRRMRNEQGRSGK 184

RESULT 13
 F72289
 A.Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
 C.Species: Thermococcus maritima
 C.Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
 C.Accession: F72289
 R.Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.R.; Hic
 Garrell, M.M.; Stewart, A.M.; Colton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
 C.M.
 Nature 399:323-329, 1999
 A.Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
 A.Reference number: A72200; MUID:99287316
 A.Accession: F72289
 A.Status: preliminary
 A.Molecule type: DNA
 A.Residues: 1-220 <ARN>
 A.Cross-references: GB:AE001772; GB:AE000512; NID:g4981693; PIDD:AA036230.1; PTD:g498
 A.Experimental source: strain MSB8
 C.Genetics:
 A.Gene: TM1154
 C.Superfamily: yeast SOL3 protein

Query Match 33.6%; Score 48; DB 2; Length 220;
 Best Local Similarity 34.8%; Pred. No. 17;
 Matches 8; Conservative 8; Mismatches 7; Indels 0; Gaps 0;
 QY 5 AAORVGRELRMSDEFGSFGK 27
 DB 111 ACEYERHRSATDFOALIGM 133

RESULT 14
 T08545
 A.Title: Arabidopsis thaliana
 C.Species: Arabidopsis thaliana (mouse-ear cress)
 C.Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 07-Dec-1999
 C.Accession: T08545; S71362; S74307
 R.Beyer, M.; Zimmermann, M.; Gruenewald, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.;
 submitted to the protein Sequence Database, May 1999
 A.Reference number: Z16442
 A.Accession: T08545
 A.Molecule type: DNA
 A.Residues: 1-526 <BEV>
 A.Cross-references: EMBL:A1050352; GSPDB:GM00062; ATSP:F27B13.80
 A.Experimental source: cultivar Columbia; BAC clone F27B13
 R.Curtis, G.; Dumas, R.; Ravanelli, S.; Douce, R.
 FEBS Lett. 390:85-90, 1996
 A.Title: Characterization of an Arabidopsis thaliana cDNA encoding an S-adenosylmethi
 A.Reference number: S71362; MUID:96314555
 A.Accession: T08545
 A.Molecule type: mRNA
 A.Residues: 1-526 <CUR>
 A.Cross-references: EMBL:LA1666; NID:g1448916; PIDD:AA04607.1; PTD:g1448917
 A.Accession: S74307
 A.Molecule type: protein
 A.Residues: 40-54 <CUR>

C:Genetics:

A:Gene: ATSP:F27H13.80
A:Map position: 4

A:Genome: nuclear

C:Keywords: carbon-oxygen lyase; chloroplast
F:1.39/Domain: transit peptide (chloroplast) #status predicted <TMP>

F:40-526/Product: threonine synthase #status experimental <MAT>

Query Match

33.6%; Score 48; DB 2; Length 526;

Best Local Similarity 35.3%; Pred. No. 42;
Matches 12; Conservative 6; Mismatches 8; Indels 8; Gaps 1;

OY 2 NLMMAORYGRELRRMSD-----EPEGSEFKGL 27

DB 172 NLFVAFERFGKPLGMDLVYKHGGSHTGSEFKDL 205

RESULT 15

A39172 Antho-RfamIde neuropetide 19 repeat precursor - sea anemone (Calliactis parasitica)

C:Species: Calliactis parasitica

C>Date: 07-Feb-1992 #sequence_revision 07-Feb-1992 #text_change 21-Jul-2000

C:Accession: A39172

R:Darmer, D.; Schmutzler, C.; Diekhoff, D.; Grimmelikhuijzen, C.J.P.
Proc. Natl. Acad. Sci. U.S.A. 88, 2555-2559, 1991

A:Title: Primary structure of the precursor for the sea anemone neuropetide Antho-RfamI

A:Reference number: A39172; MUID:91172845

A:Accession: A39172

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-334 <DAR>

A:Cross-references: GB:M59166; NID:g156133; PIDN:AAA27878.1; PID:g156134

C:Keywords: neuropetide

Query Match

33.2%; Score 47.5; DB 2; Length 334;

Best Local Similarity 44.0%; Pred. No. 31;
Matches 11; Conservative 3; Mismatches 10; Indels 1; Gaps 1;

OY 1 KNLMAAORTGRELRR-RMSDEFGSP 24

DB 89 KRRTVPGRTGREFGREFGREFGRT 113

Search completed: September 20, 2002, 10:39:13
Job time: 465 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2002, 11:04:35 : Search time 44.99 Seconds

(without alignments)
23.237 Million cell updates/sec

Title: us-09-544-664-56

Sequence: 1 KMLMAORIGRELRLNMSDEPESFKGL 27

Scoring table: BL0SDUM62
Gap0 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Database : SwissProt_40.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	138	96.5	204	1	BAD_MOUSE
2	138	96.5	204	1	BAD_MOUSE
3	114	79.7	168	1	BAD_MOUSE
4	94	37.1	946	1	ITR2_MOUSE
5	94	37.1	946	1	ITR2_MOUSE
6	94	37.1	946	1	ITR2_MOUSE
7	94	37.1	946	1	ITR2_MOUSE
8	94	37.1	946	1	ITR2_MOUSE
9	94	37.1	946	1	ITR2_MOUSE
10	94	37.1	946	1	ITR2_MOUSE
11	94	37.1	946	1	ITR2_MOUSE
12	94	37.1	946	1	ITR2_MOUSE
13	94	37.1	946	1	ITR2_MOUSE
14	94	37.1	946	1	ITR2_MOUSE
15	94	37.1	946	1	ITR2_MOUSE
16	94	37.1	946	1	ITR2_MOUSE
17	94	37.1	946	1	ITR2_MOUSE
18	94	37.1	946	1	ITR2_MOUSE
19	94	37.1	946	1	ITR2_MOUSE
20	94	37.1	946	1	ITR2_MOUSE
21	94	37.1	946	1	ITR2_MOUSE
22	94	37.1	946	1	ITR2_MOUSE
23	94	37.1	946	1	ITR2_MOUSE
24	94	37.1	946	1	ITR2_MOUSE
25	94	37.1	946	1	ITR2_MOUSE
26	94	37.1	946	1	ITR2_MOUSE
27	94	37.1	946	1	ITR2_MOUSE
28	94	37.1	946	1	ITR2_MOUSE
29	94	37.1	946	1	ITR2_MOUSE
30	94	37.1	946	1	ITR2_MOUSE
31	94	37.1	946	1	ITR2_MOUSE
32	94	37.1	946	1	ITR2_MOUSE
33	94	37.1	946	1	ITR2_MOUSE

RESULT	1	STANDARD:	PRT:	204 AA.
BAD_MOUSE				
AC	061337.			
AD	01-NOV-1997 (Bel. 35, Created)			
AE	01-NOV-1997 (Bel. 35, Last sequence update)			
AF	01-MAR-2002 (Bel. 41, Last annotation update)			
AG	Bcl2, Bcl2 antagonist of cell death (BMD) (Bcl-2 binding component			
AH	6) (Bcl2/Bcl-2 associated death promoter).			
AI	BAD OR BDC.			
AJ	MUS MUSCULUS (Mouse).			
AK	FUKUYOTA, Metazoa; Chordata; Vertebrata; Euteleostomi;			
AL	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
AM	NCBI_TaxID=10090;			
AN	1)			
AO	SEQUENCE FROM N.A.			
AP	THESOU-BALU, and Thymsus.			
AQ	MEDLINE=93116301; PubMed=7834748.			
AR	Tang E., Zhu J., Jockel J., Boise L.H., Thompson C.B., Korsmeyer S.J.;			
AS	Bcl-2, a heterodimeric partner for Bcl-XL and Bcl-2, displaces Bax and			
AT	Promotes cell death.			
AV	Cell 60:285-291(1995).			
AW	12)			
AX	PHOSPHORYLATION, AND MUTAGENESIS OF SER-112 AND SER-136.			
AY	MEDLINE=98022383; PubMed=9381178; Page C., Herrera R., Nunez G.;			
AZ	Del Peso L., Gonzalez-Garcia M., Page C., Herrera R., Nunez G.;			
BA	Interleukin-3-induced phosphorylation of BMD through the protein			
BB	kinase Akt.			
BC	Science 278:1687-689(1997).			
BD	13)			
BE	MUTAGENESIS OF SERINE RESIDUES.			
BF	MEDLINE=20403302; PubMed=10949026;			
BG	Datta S.R., Katsuy A., Ho L., Petros A., Fesik S.W., Yaffe M.B.;			
BH	Greenberg M.E.;			
BI	Bcl-2, B			

CC ser-136 is the major site of AKT/PKB phosphorylation, Ser-155 the
 CC major site of protein kinase A (CAPK) phosphorylation.
 CC -1- SIMILARITY: BELONGS TO BCL-2 HOMOLOGOUS DOMAIN 3 (BH3).
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.1sb-sib.ch/announce/>
 CC or send an email to license@1sb-sib.ch).
 CC -----
 CC EMBL: L37296; AAA64465.1; -
 CC DR MGD: MGI:1096330; Bcl-2.
 CC DR InterPro: IPR000712; Bcl-2.
 CC DR PROSITE: PS01259; BH3; FALSE_NEG.
 CC KW Apoptosis; Phosphorylation.
 CC FT DOMAIN 147 161 BH3.
 CC FT MOD_RES 112 112 PHOSPHORYLATION (BY CAPK AND PKB).
 CC FT MOD_RES 136 136 PHOSPHORYLATION (BY CAPK AND PKB).
 CC FT MOD_RES 155 155 PHOSPHORYLATION (BY CAPK AND PKB).
 CC FT MOD_RES 112 112 S->A: NO PHOSPHORYLATION.
 CC FT MUTAGEN 136 136 S->A: NO PHOSPHORYLATION.
 CC FT MUTAGEN 155 155 S->A: NO PHOSPHORYLATION; INTERACTS WITH
 CC BCL-X(L).
 CC SEQUENCE 204 AA; 22080 MW; 6C2BA91020503F7 CRC64;
 CC
 CC Query Match 96.5%; Score 138; DB 1; Length 204;
 CC Best Local Similarity 100.0%; Pred. No. 1,2e-13;
 CC Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC 2 NMAAQRGRLRMSDEFGFGL 27
 CC DB 140 NMAAQRGRLRMSDEFGFGL 165
 CC
 CC RESULT 2
 CC BAD_RAT STANDARD; PRT; 205 AA.
 CC ID O3147; O70256; G9JHX1;
 CC AC 16-OCT-2001 (Rel. 40; Created)
 CC DT 16-OCT-2001 (Rel. 40; Last sequence update)
 CC DT 01-MAR-2002 (Rel. 41; Last annotation update)
 CC DE Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component
 CC 6) (Bcl-xL/Bcl-2 associated death promoter).
 CC DE BAD.
 CC OS Rattus norvegicus (Rat).
 CC OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC OX NCBI_TaxID=10116;
 CC RN 1)
 CC RP SEQUENCE FROM N.A., AND MUTAGENESIS OF SER-113 AND SER-137.
 CC RC TISSUE=Ovary;
 CC RX MEDLINE=98034386; PubMed=9369453;
 CC RA Han S.Y., Kalpita A., Zhu L., Haugh A.J.W.;
 CC RT "Interference of BAD (Bcl-xL/Bcl-2-associated death promoter)-induced
 CC RT apoptosis in mammalian cells by 14-3-3 isoforms and p11.";
 CC RL MOL. Endocrinol. 11:1858-1867(1997).
 CC RN 2)
 CC RP SEQUENCE FROM N.A.
 CC RC TISSUE=Brain;
 CC RX MEDLINE=98194755; PubMed=9535132;
 CC RA D'Agata V., Magro G., Travali S., Musco S., Cavallaro S.;
 CC RT "Cloning and expression of the programmed cell death regulator BAD in
 CC RT the rat brain.";
 CC RL Neurosci. Lett. 243:137-140(1998).
 CC RN 3)
 CC RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
 CC RC TISSUE=Brain;
 CC RX MEDLINE=21109372; PubMed=1161472;
 CC RA Hamner S., Arumae U., Yu L.-Y., Sun Y.-F., Saarma M., Lindholm D.;

RT "Functional characterization of two splice variants of rat BAD and
 RT their interaction with Bcl-w in sympathetic neurons.";
 RL Mol. Cell. Neurosci. 17:97-106(2001).
 CC -1- FUNCTION: Promotes cell death. Successfully competes for the
 CC binding to Bcl-x(L). Bcl-2 and Bcl-w, thereby affecting the level
 CC of heterodimerization of these proteins with BAX. Can rescue the
 CC death repressor activity of Bcl-x(L) but not that of Bcl-2 (by
 CC similarity). Appears to act as a link between growth factor
 CC receptor signaling and the apoptotic pathway.
 CC -1- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-
 CC 113/Ser-137 phosphorylated form binds 14-3-3 proteins.
 CC -1- SUPRACELLULAR LOCATION: Outer mitochondrial membrane. Upon
 CC phosphorylation, locates to the cytoplasm (by similarity).
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms: alpha (shown here) and beta; are
 CC produced by alternative splicing. They differ only in their C-
 CC terminal regions.
 CC -1- TISSUE SPECIFICITY: Expressed in all tissues tested, including
 CC brain, liver, spleen and heart. In the brain, restricted to
 CC epithelial cells of the choroid plexus. Isoform alpha is the more
 CC abundant form.
 CC -1- DOMAIN: Interact BH3 domain is required by BAX, BID, BAK, BAD AND
 CC BAX for their pro-apoptotic activity and for their interaction
 CC with anti-apoptotic members of the Bcl-2 family.
 CC -1- PTM: Phosphorylated on Ser-113 in response to survival stimuli.
 CC Subsequent phosphorylation on Ser-137 promotes heterodimerization
 CC with 14-3-3 proteins. This interaction then facilitates the
 CC phosphorylation at Ser-156, a site with the BH3 domain, leading
 CC to the release of Bcl-x(L) and the promotion of cell survival.
 CC Ser-137 is the major site of AKT/PKB phosphorylation, Ser-136 the
 CC major site of protein kinase A (CAPK) phosphorylation (by
 CC similarity).
 CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLOGOUS DOMAIN 3 (BH3).
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.1sb-sib.ch/announce/>
 CC or send an email to license@1sb-sib.ch).
 CC -----
 CC EMBL: AF003523; AAC33374.1; -
 CC DR EMBL: AF031227; AAC5100.1; -
 CC DR EMBL: AF279911; AAP1428.1; -
 CC DR EMBL: AF279911; AAP1428.1; -
 CC DR InterPro: IPR000712; Bcl-2.
 CC DR PROSITE: PS01259; BH3; FALSE_NEG.
 CC KW Apoptosis; Phosphorylation; Alternative splicing.
 CC FT DOMAIN 148 162
 CC FT MOD_RES 113 113
 CC FT MOD_RES 137 137
 CC FT MOD_RES 156 156
 CC FT MOD_RES 166 205
 CC FT VARSPPLIC 166 205
 CC FT MUTAGEN 113 113
 CC FT MUTAGEN 137 137
 CC FT MUTAGEN 156 156
 CC FT MUTAGEN 166 205
 CC FT CONFLICT 29 34
 CC SEQUENCE 205 AA; 22228 MW; 7AFA71DAE9C64A81 CRC64;
 CC
 CC Query Match 96.5%; Score 138; DB 1; Length 205;
 CC Best Local Similarity 100.0%; Pred. No. 1,2e-13;
 CC Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC

OY 2 NLMAORYGRELRLMSDFEGSGFGL 27
 DB 141 NLMAORYGRELRLMSDFEGSGFGL 166
 RESULT 3
 BAD_HUMAN STANDARD: PRT; 168 AA.
 AC 092934; 014803;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component
 6) (Bcl-xL/Bcl-2 associated death promoter).
 GN BAD OR BIRC6 OR BCL2L8.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN 11
 RA YIN D.X., LI Z., Huang B., Chen S., Zhou H.;
 RT A human protein that interacts with Bcl-2 and have homology to mouse
 RT BAD.";
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN 12
 RA SEQUENCE FROM N.A., AND PHOSPHORYLATION BY RAF-1.
 RX MEDLINE=97083574; PubMed=6929532;
 RA Wang J., G., Rapp U.R., Reed J.C.;
 RT Bcl-2 targets the protein kinase Raf-1 to mitochondria.";
 RL Cell 87:629-638(1996).
 RN 13
 RA SEQUENCE FROM N.A.
 RA Takayama S., Reed J.C.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RN 14
 RA SEQUENCE FROM N.A., AND DIMERIZATION.
 RX MEDLINE=98049514; PubMed=9388232;
 RA Ohtsuka S., Diaz J.-L., Horne W., Chang J., Wang Y., Wilson G.,
 RA Chang S., Weeks S., Fritz L.C., Oltersdorf T.;
 RL Dimerization properties of human BAD.";
 RL J. Biol. Chem. 272:30866-30872(1997).
 RN 15
 RA SEQUENCE FROM N.A.
 RA Tissue-Lung;
 RC TISSUE: Lung;
 RA Strausberg R.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN 16
 RA STRUCTURE BY NMR OF 103-127.
 RX MEDLINE=21073561; PubMed=11206074;
 RA Petros A.M., Nettekheim D.G., Wang Y., Olejniczak E.T., Meadows R.P.,
 RA Mack J., Swift K., Matayoshi E.D., Zhang H., Thompson C.B.,
 RA Fesk S.W.;
 RT *Rationale for Bcl-xL/Bad peptide complex formation from structure,
 RT mutagenesis, and biophysical studies.";
 RL Protein Sci. 9:2528-2534(2000).
 CC -1- FUNCTION: Promotes cell death. Successfully competes for the
 CC binding to Bcl-x(L). Bcl-2 and Bcl-w, thereby affecting the level
 CC of heterodimerization of these proteins with BAX. Can reverse the
 CC death repressor activity of Bcl-x(L), but not that of Bcl-2 (By
 CC similarity). Appears to act as a link between growth factor
 CC receptor signaling and the apoptotic pathways.
 CC -1- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-
 CC x(L), Bcl-2 and Bcl-w. Also binds protein S100A10 (by similarity).
 CC The Ser-75/Ser-99 phosphorylated form binds 14-3-3 proteins (by
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon
 CC phosphorylation, localizes to the cytoplasm.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
 CC -1- DOMAIN: Interact Bcl-2 domain is required by BIR, BID, BAK, BAD AND
 CC BAX for their pro-apoptotic activity and for their interaction
 CC with anti-apoptotic members of the Bcl-2 family.

CC -1- PTM: Phosphorylated on Ser-75 in response to survival stimuli.
 CC Subsequent phosphorylation on Ser-99 promotes heterodimerization
 CC with 14-3-3 proteins. This interaction then facilitates the
 CC phosphorylation at Ser-118, a site within the BH3 domain, leading
 CC to the release of Bcl-x(L) and the promotion of cell survival.
 CC Ser-99 is the major site of ATR/PKA phosphorylation. Ser-118 the
 CC major site of protein kinase A (CAK) phosphorylation (by
 CC similarity).
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 BCL-3 HOMOLOG DOMAIN 3 (BH3).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL: U66879; AAB36516.1; -;
 DR EMBL: AF021792; BAB72092.1; -;
 DR EMBL: AF031523; AAB88124.1; -;
 DR EMBL: BC001901; AAB01901.1; -;
 DR FDB: 16557; 07-FEB-01.
 DR PMID: 603167; -;
 DR InterPro: IPR000712; Bcl-2.
 DR PROSITE: PS01259; BH3; FALSE_NEG.
 DR Apoptosis; Phosphorylation; 3D-structure.
 KW DOMAIN
 FT 110 124 BH3.
 FT MOD_RES 75 75 PHOSPHORYLATION (BY CAK AND PKB) (BY
 FT SIMILARITY).
 FT MOD_RES 99 99 PHOSPHORYLATION (BY CAK AND PKB) (BY
 FT SIMILARITY).
 FT MOD_RES 118 118 PHOSPHORYLATION (BY CAK AND PKB) (BY
 FT SIMILARITY).
 FT CONFLICT 64 91 STANLEY-SER-99 AND SER-118 ARE NOT
 FT POLYMERIZED IN THE SAME PROTEIN (IN REF. 1).
 FT
 SQ SEQUENCE 168 AA; 18392 MW; 695DD027DDEE2241 CRC64;
 Query Match 79.7%; Score 114; DB 1; Length 168;
 Best Local Similarity 91.7%; Pred. No. 4e-10; Z; Indels 0; Gaps 0;
 Matches 22; conservative 0; Mismatches 2;
 OY 2 NLMAORYGRELRLMSDFEGSGFGL 25
 DB 103 NLMAORYGRELRLMSDFEGSGFGL 126
 RESULT 4
 ITH2_MESAU STANDARD: PRT; 946 AA.
 AC P97279;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITH2 heavy
 DE chain H2) (HC2).
 GN ITH2.
 OS Mesocricetus auratus (Golden hamster).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 CC Mesocricetus.
 CC NCBI_TaxID=10036;
 RN 11
 RA SEQUENCE FROM N.A.
 RC TISSUE: Liver;
 RX MEDLINE=97420688; PubMed=9276673;
 RA Nakatani T., Suzuki Y., Yamamoto T.;
 RT *Molecular cloning and sequencing of cDNAs encoding three heavy-chain
 RT precursors of the inter-alpha-trypsin inhibitor in Syrian hamster:
 RT implications for the evolution of the inter-alpha-trypsin inhibitor
 RT heavy chain family.";

RL J. Blochem. 122:71-82(1997).
 RN (2)
 RP SEQUENCE OF 55-64; 140-146; 151-156; 424-447; 500-528 AND 577-605.
 RC AND SUBUNIT.
 RE TISSUE-Plasma.
 RX MEDLINE-97018241; PubMed-8864857;
 RA Yamamoto T., Yamamoto K., Sinocheta R.;
 RT Inter-alpha-trypsin inhibitor and its related proteases in Syrian
 hamster urine and plasma.
 RL Blochem. 120:145-152(1996).
 J. FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
 BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
 INCLUDING THOSE SURFACES THAT TEND TO REGULATE THE
 LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
 ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (B)
 SIMILARITY)
 CC -1- SUBUNIT: 1-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
 ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN.
 CC BIKUNIN, INTER-ALPHA-INHIBITOR (I-ALPHA-1) IS COMPOSED OF H1, H2
 AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-L1) OF H2 AND
 CC BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-1) OF H3 AND BIKUNIN.
 CC -1- PM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY
 SIMILARITY)
 CC -1- SIMILARITY: BELONGS TO THE ITIH FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 WMFA DOMAIN.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-slb.ch/announce/>
 CC or send an email to license@isb-slb.ch).
 CC -----
 CC EMBL: D89286; BAA1393.1;
 DR InterPro: IPR02035; WMFA.
 DR Pfam: PF00092; vwa; 1.
 DR SMART: SM00327; VMA; 1.
 DR PROSITE: PS50234; WMFA; 1.
 KW Serine protease inhibitor; Repeat; Signal; Multigene family;
 KM Glycoprotein.
 FT SIGNAL 1 18
 FT PROPEP 19 54
 FT CHAIN 55 702
 FT PROPEP 703 946
 FT DOMAIN 308 468
 FT CARBOHYD 118 118
 FT CARBOHYD 263 263
 FT CARBOHYD 445 445
 FT CARBOHYD 578 578
 FT BINDING 702 702
 FT CONFLICT 510 510
 FT CONFLICT 595 595
 FT SEQUENCE 946 AA; 106580 MW; CABP56545BE7B2E CRC64;
 QY 2 N1MAA0RYGRELIRMSDEFGSKGL 27
 Db 212 NWMIIEPGMKRFLHVPDFEGHGV 237
 RESULT 5
 ITIH_MOUSE STANDARD: PPT; 946 AA.
 ID ITIH_MOUSE
 AC 061703; 13-JUL-1998 (rel. 36, Created)

DT 15-JUL-1998 (rel. 36, last sequence update)
 DT 15-JUL-1999 (rel. 38, last annotation update)
 DE Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy
 DE chain H2).
 GN ITIH2.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI-Taxid=10090;
 RP SEQUENCE FROM N.A.
 RN STRAIN=C57BL/6N; TISSUE=LIVER;
 RC MEDLINE-95194326; PubMed-7534067;
 RA Chan P., Ralster J., Raguene G., Saller J.-P.;
 RT The three heavy-chain precursors for the inter-alpha-inhibitor
 family of mouse: new members of the multicopper oxidase protein group
 family.
 RL Blochem. 125:505-512(1995).
 J. FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
 BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
 INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
 LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
 ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (B)
 SIMILARITY)
 CC -1- SUBUNIT: 1-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
 ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN.
 CC BIKUNIN, INTER-ALPHA-INHIBITOR (I-ALPHA-1) IS COMPOSED OF H1, H2
 AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-L1) OF H2 AND
 CC BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-1) OF H3 AND BIKUNIN.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN BOTH LIVER AND BRAIN.
 CC -1- PM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY
 SIMILARITY)
 CC -1- SIMILARITY: BELONGS TO THE ITIH FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 WMFA DOMAIN.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-slb.ch/announce/>
 CC or send an email to license@isb-slb.ch).
 CC -----
 CC EMBL: X70392; CAA49842.1;
 DR MGD: MGI:96619; Itih2.
 DR InterPro: IPR02035; WMFA.
 DR Pfam: PF00092; vwa; 1.
 DR SMART: SM00327; VMA; 1.
 DR PROSITE: PS50234; WMFA; 1.
 KW Serine protease inhibitor; Repeat; Signal; Multigene family;
 KM Glycoprotein.
 FT SIGNAL 1 18
 FT PROPEP 19 54
 FT CHAIN 55 702
 FT PROPEP 703 946
 FT DOMAIN 308 468
 FT CARBOHYD 118 118
 FT CARBOHYD 263 263
 FT CARBOHYD 445 445
 FT BINDING 702 702
 FT CONFLICT 510 510
 FT CONFLICT 595 595
 FT SEQUENCE 946 AA; 105927 MW; 40DB5716433ED9DC CRC64;
 QY 2 N1MAA0RYGRELIRMSDEFGSKGL 27
 Db 212 NWMIIEPGMKRFLHVPDFEGHGV 237
 Query Match 37.1%; Score 53; DB 1; Length 946;
 Best Local Similarity 34.6%; Pred. No. 4.2;
 Matches 9; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

[illegible]

```

DT      01-MAR-2002 (Rel. 41, Created)
DT      01-MAR-2002 (Rel. 41, Last sequence update)
DE      01-MAR-2002 (Rel. 41, Last annotation update)
DB      DNA recombination protein rmcuc homolog.
GN      RMCUC OR PAI031.
OS      Pseudomonas aeruginosa.
OC      Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae.
OX      Mesodermata;687;
OY      (1)-TaxId=287;
RN      SEQUENCE FROM N.A.
RP      STRAIN=ATCC 15692 / PAOI;
RX      MEDLINE=2043737; PubMed=10984043;
RA      Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA      Hickey M.J., Brinkman F.S.L., Huffnagle W.O., Kowalik D.J., Lagrimo M.,
RA      Gader R.L., Gotley L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA      Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA      Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.V.;
RA      Reiter J., Salter M.H., Hancock R.E.W., Lory S., Olson M.T.;
RT      Complete genome sequence of Pseudomonas aeruginosa PAOI, an
RF      opportunistic pathogen.;
RZ      NC_005726(4280); DNA recombination (by similarity).
FT      -1 SIMILARITY BELONGS TO THE RMCUC FAMILY.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL Outstation at
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
DR      EMBL: AE004535..AE004420.1.
DR      Y12991:YP003798..YP003798.1.
DR      RefSeq: RP02545; DXP155;11935.
KM      DNA recombination; coiled coil; Complete proteome.
FT      DOMAIN 16 COILED COIL (POTENTIAL).
SQ      SEQUENCE 453 AA: 51539 MW: 1ETEA97B2CE5E4B CRC64;

Query Match          34.3%; Score 49; DB 1: Length 453;
Best Local Similarity 55.6%; Pred. No. 7.3;
Matches 10; Conservative 4; Mismatches 2; Indels 2; Gaps 1.

CY      4 WAAGRYGR-ELRRMSDE 19
DB      65 WASERGGREELRLASE 82

RESULT 9
RAS3 RHTRA STANDARD: PROT: 205 AA.
ID RAS3_RHTRA AC P22280;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ras-like protein 3.
OS RAS3.
GN Rhizomucor racemosus (Mucor cliticellatoides f. instansicus).
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
OC Mucor.
OY      (1)-TaxId=4841;
RN      SEQUENCE FROM N.A.
RP      STRAIN=ATCC 1216B;
RX      MEDLINE=91061724; PubMed=17010211;
RA      Casale W.L., McConnell D.G., Wang S.-Y., Lee Y.-J., Lin J.E.;
RA      "Expression of a gene family in the dimorphic fungus Mucor racemosus
RA      which encodes striking similarity to human ras genes.";
ML      Mol. Cell. Biol. 10:6554-6563(1990).
CC      -1- ENZYME REGULATION: ALTERNATE BETWEEN AN INACTIVE FORM BOUND TO GDP
CC      AND AN ACTIVE FORM BOUND TO GTP. ACTIVATED BY A GUANINE

```

CC NUCLEOTIDE-EXCHANGE FACTOR (GEF) AND INACTIVATED BY A GTPASE-
 CC ACTIVATING PROTEIN (GAP)
 CC -1- SUBCELLULAR LOCATION: PLASMA MEMBRANE
 CC -1- DEVELOPMENTAL STAGE: IN SPORULATING MYCELIUM AND MUCH LESS IN
 CC GERMING AND YEAST
 CC -1- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RAS FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M55177; AAA83379.1; -
 CC FTR: C36365; C36365.
 CC HSRP: P01112; 1pL.
 CC InterPro: IPR003577; Ras.
 CC InterPro: IPR001806; Ras_unsfrmg.
 CC Pfam: PF00071; ras_1
 CC PRINTS: SM00173; RAS_1
 CC SMART: SM00173; RAS_1
 CC CTP-binding; Prenylation; Lipoprotein.
 CC KW: NR_BIND 16 23 GTP (BY SIMILARITY).
 CC FT: NR_BIND 63 67 GTP (BY SIMILARITY).
 CC FT: NP_BIND 122 125 GTP (BY SIMILARITY).
 CC FT: DOMAIN 38 46 EFECTOR REGION (PROBABLE).
 CC FT: LIPID 202 202 FARNESYL (BY SIMILARITY).
 CC SEQUENCE 205 AA; 23408 MW; D5F086466F090F50 CRC64;
 CC
 CC Query Match 33.6%; Score 48; DB 1; Length 205;
 CC Best Local Similarity 62.5%; Pred No. 4.3;
 CC Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 CC
 CC Oy 11 RELRMSDPEFGSKG 26
 CC Db 168 RELRMSDPEFGSKG 183
 CC
 CC RESULT 10
 CC 6PGL_THEMA STANDARD; PRT; 220 AA.
 CC ID 6PGL_THEMA
 CC AC 09-XONB;
 CC DT 30-MAY-2000 (Rel. 39, Created)
 CC DT 30-MAY-2000 (Rel. 39, Last sequence update)
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
 CC DE 6-phosphogluconolactonase (EC 3.1.1.31) (6PGL).
 CC CN PGL OR PPGA OR TM1154.
 CC OS Thermotoga maritima.
 CC CC Bacteria; Thermotogales; Thermotoga.
 CC NCBI_TaxID=2336;
 CC RX
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=MSB8 / DSM 3109;
 CC RX MEDLINE=99287316; PubMed=10360571;
 CC RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
 CC Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
 CC McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
 CC Stewart A.W., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
 CC Heidelberg J., Sutton G.G., Fleischmann R.D., Eison J.A., White O.,
 CC Salzberg S.L., Sutton H.O., Venter J.C., Fraser C.M.;
 CC FT genome sequence of *Thermotoga maritima*.
 CC RL Nature 399:323-329 (1999).
 CC -1- FUNCTION: HYDROLYSIS OF 6-PHOSPHOGLUCONOLACTONE TO 6-
 CC PHOSPHOGLUCONATE.
 CC -1- CATALYTIC ACTIVITY: 6-phospho-D-glucono-1,5-lactone + H(2)O = 6-
 CC phospho-D-gluconate.
 CC -1- PATHWAY: SECOND STEP IN PENTOSE PHOSPHATE PATHWAY.
 CC -1- SIMILARITY: BELONGS TO THE GLUCOSAMINE/GLACTOSAMINE-6- PHOSPHATE
 CC ISOMERASE FAMILY. 6-PHOSPHOGLUCONOLACTONASE SUBFAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF001772; AAB36230.1; -
 CC FTR: TM1154;
 CC InterPro: IPR000457; Glucosamine Iso.
 CC Pfam: PF01182; Glucosamine Iso. 1.
 CC KW Hydrolase; Complete proteome.
 CC SEQUENCE 220 AA; 25325 MW; 9B0FD07DE01E60C3 CRC64;
 CC
 CC Query Match 33.6%; Score 48; DB 1; Length 220;
 CC Best Local Similarity 34.8%; Pred. No. 4.6;
 CC Matches 8; Conservative 8; Mismatches 7; Indels 0; Gaps 0;
 CC
 CC Oy 5 AADPYGRELARMSDPEFGSKL 27
 CC Db 111 AADPYGRELARMSDPEFGSKL 133
 CC
 CC RESULT 11
 CC THRC_SOL7U STANDARD; PRT; 519 AA.
 CC ID THRC_SOL7U
 CC AC G8MT28;
 CC DT 01-MAR-2002 (Rel. 41, Created)
 CC DT 01-MAR-2002 (Rel. 41, Last sequence update)
 CC DE Threonine synthase, chloroplast precursor (EC 4.2.99.2) (TSS).
 CC OS Solanum tuberosum (potato)
 CC CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC CC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 CC NCBI_TaxID=4113;
 CC RX
 CC RP SEQUENCE FROM N.A.
 CC RA Casazza P., Kaiser S., Willmitzer L., Hoefgen R., Hesse H.;
 CC FT isolation and characterization of a cDNA encoding threonine synthase
 CC from Solanum tuberosum.
 CC RL Submitted (AUG-1998) to the EMBL/Genbank/DBJ databases.
 CC CC -1- CATALYTIC ACTIVITY: O-phospho L-homoserine + H(2)O = L-threonine +
 CC phosphate
 CC -1- COFACTOR: pyridoxal phosphate (by similarity).
 CC -1- ENZYME REGULATION: Allosterically activated by S-adenosyl-
 CC methionine (SAM) (by similarity).
 CC -1- PATHWAY: Threonine biosynthesis; last step.
 CC -1- SUBUNIT: Homodimer (by similarity).
 CC -1- SUBCELLULAR LOCATION: Chloroplast (by similarity).
 CC -1- SIMILARITY: BELONGS TO THE SPRINE/THREONINE DEHYDRATASE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF08284; AAF74984.1; -
 CC InterPro: IPR001926; B6_enzyme_beta.
 CC Pfam: PF00291; PALP; 1.
 CC DR PROSITE: PS00165; DEHYDRATASE, SEX_YMR, 1.
 CC KW Threonine biosynthesis; Lyase; Pyridoxal phosphate; Allosteric enzyme;
 CC KW Chloroplast; Transit peptide.
 CC FT TRANSIT 1 40 CHLOROPLAST (BY SIMILARITY).
 CC FT CHAIN 41 519 THREONINE SYNTHASE.
 CC FT BINDING 196 196 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 CC SEQUENCE 519 AA; 57412 MW; 114C0979CD231464 CRC64;

DT 01-NOV-1998 (TREMBLrel. 08, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE HYPOTHETICAL 24.1 KDA PROTEIN CY39.03C.
 GN RV2014 OR MFCY39.03C.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglemaner K., Gas S., Barry C.E. III, Tekala P.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies K., Devlin K., Feltham T., Galloway S., Hamlin N., Holtroyd S.,
 RA Hornsby T., Jagels K., Kiroh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers R.,
 RA Rutter S., Taylor K., Whitehead S., Barrett B.C.;
 RA Sulston J.B., Taylor K., Whitehead S., Barrett B.C.;
 RA Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.
 RI Nature 393:537-544(1998).
 RI -1- SIMILARITY: TO M PARATUBERCULOSIS IS900.
 CC EMBL: Z74025; CAA98415.1; -;
 DR TubercuList: RZ2014; -;
 DR InterPro: IPR003346; Transposase_20.
 DR Pfam: PF02371; Transposase_20; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 223 AA: 24132 MW: 70456750017FEF37 CRC64:

Query Match 37.1%; Score 53; DB 16; Length 223;
 Best Local Similarity 58.1%; Pred. No. 6.8;
 Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 QY 2 NLMAAQRGRELRRMSD 18
 DB 165 NLMAADRYNAIRGHD 181
 ID 047148 PRELIMINARY; PRT; 505 AA.
 AC 047148;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-MAY-2001 (TREMBLrel. 19, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE RIBOSOMAL MATURASE (FRAGMENT).
 GN MARK.
 OS Menziesia ciliolata.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Ericales; Ericaceae; Menziesia.
 OX NCBI_TaxID=49154;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Kron K.A.;
 RX *Phylogenetics of Rhododendroideae (Ericaceae).";
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 DE EMBL: U61311; AAC15245.2; -;
 DR InterPro: IPR000442; Intron_maturase2.
 DR InterPro: IPR002866; MatK_N.
 DR Pfam: PF01348; Intron_maturase2; 1.
 DR Pfam: PF01824; MatK_N; 1.
 KW Chloroplast.
 RN NON_TER 1
 FT SEQUENCE 505 AA: 60233 MW: E55F927AD2E37DE5 CRC64:

Query Match 36.7%; Score 52.5; DB 8; Length 505;
 Best Local Similarity 37.5%; Pred. No. 20;

Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;
 QY 1 KNLMAA-----QRYGRELRRMSDFEGSGSK 25
 DB 390 KPYMAALSDSDITERRGRITRNLSHYSGSLK 421

RESULT 4
 ID 063960 PRELIMINARY; PRT; 506 AA.
 AC 063960;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE RIBOSOMAL MATURASE.
 GN YCP14 OR MATK.
 OS Rhododendron laschroli, and
 OS Rhododendron faurerae.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Ericales; Ericaceae; Rhododendron.
 OX NCBI_TaxID=75582; 75580;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Kuraishi Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
 RA Kuraishi Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
 RA Yukawa T.;
 RL J. Jpn. Bot. 0:0-0(1998).
 DR EMBL: AB012749; BAA25870.1; -;
 DR EMBL: AB012745; BAA25866.1; -;
 DR InterPro: IPR000442; Intron_maturase2.
 DR InterPro: IPR002866; MatK_N.
 DR Pfam: PF01348; Intron_maturase2; 1.
 DR Pfam: PF01824; MatK_N; 1.
 KW Chloroplast.
 SQ SEQUENCE 506 AA: 60389 MW: DE0C07AE608B787 CRC64:

Query Match 36.7%; Score 52.5; DB 8; Length 506;
 Best Local Similarity 37.5%; Pred. No. 20;
 Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;
 QY 1 KNLMAA-----QRYGRELRRMSDFEGSGSK 25
 DB 391 KPYMAALSDSDITERRGRITRNLSHYSGSLK 422
 ID 063972 PRELIMINARY; PRT; 506 AA.
 AC 063972;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE RIBOSOMAL MATURASE.
 GN MARK.
 OS Rhododendron ovatum.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; Ericales; Ericaceae; Rhododendron.
 OX NCBI_TaxID=49169;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Kuraishi Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
 RA Kuraishi Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
 RA Yukawa T.;
 RL *Investigation of sectional relationships in the genus
 RT Rhododendron (Ericaceae) based on matK sequences.";
 RL J. Jpn. Bot. 0:0-0(1998).
 DR EMBL: AB012749; BAA25870.1; -;
 DR InterPro: IPR000442; Intron_maturase2.
 DR InterPro: IPR002866; MatK_N.
 DR Pfam: PF01348; Intron_maturase2; 1.

DR Pfam: PF01824; Matk_N.1.

KW Chloroplast.

SO SEQUENCE 506 AA; 60493 MW; D230E54B8C20FEF0 CRC64;

Query Match

Best Local Similarity 36.7%; Score 52.5; DB 8; Length 506;

Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

OY 1 KN1MAA-----ORYGRELRLMSDEFEGSRK 25

DB 391 KPVMALSDSDITERFGRTYRLNLSHYSGSLK 422

RESULT 6

062973 PRELIMINARY; PRT: 506 AA.

AC 062973:

DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE RIBOSOMAL MATURASE.

GN MATK.

OS Rhododendron stamineum.

OC Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; Ericales; Ericaceae; Rhododendron.

OX NCBI_TaxID=75575;

RN [1]

RP SEQUENCE FROM N.A.

RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,

Yukawa T.;

RT Investigation of Sectional Relationships in the Genus

RT Rhododendron(Ericaceae) based on matk Sequences."

RL J. Jpn. Bot. 0:0-0(1998).

RL EMBL: AB012731; BAA25852.1;

RL InterPro: IPR000442; Intron_maturase2.

DR InterPro: IPR002866; Matk_N.

DR Pfam: PF01348; Intron_maturase2; 1.

DR Pfam: PF01824; Matk_N.1.

KW Chloroplast.

SO SEQUENCE 506 AA; 60611 MW; 53FA36E7CD99483C CRC64;

Query Match

Best Local Similarity 36.7%; Score 52.5; DB 8; Length 506;

Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

OY 1 KN1MAA-----ORYGRELRLMSDEFEGSRK 25

DB 391 KPVMALSDSDITERFGRTYRLNLSHYSGSLK 422

RESULT 7

062974 PRELIMINARY; PRT: 506 AA.

AC 062974:

DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE RIBOSOMAL MATURASE.

GN MATK.

OS Rhododendron alabiflorum.

OC Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; Ericales; Ericaceae; Rhododendron.

OX NCBI_TaxID=49161;

RN [1]

RP SEQUENCE FROM N.A.

RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,

Yukawa T.;

RT Investigation of Sectional Relationships in the Genus

RT Rhododendron(Ericaceae) based on matk Sequences."

RL J. Jpn. Bot. 0:0-0(1998).

RL EMBL: AB012731; BAA25852.1;

RL InterPro: IPR000442; Intron_maturase2.

DR InterPro: IPR002866; Matk_N.

DR Pfam: PF01348; Intron_maturase2; 1.

DR Pfam: PF01824; Matk_N.1.

KW Chloroplast.

SO SEQUENCE 506 AA; 60491 MW; 3CCG9303B5B12B8C CRC64;

Query Match

Best Local Similarity 36.7%; Score 52.5; DB 8; Length 506;

Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

OY 1 KN1MAA-----ORYGRELRLMSDEFEGSRK 25

DB 391 KPVMALSDSDITERFGRTYRLNLSHYSGSLK 422

RESULT 8

062975 PRELIMINARY; PRT: 506 AA.

AC 062975:

DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE RIBOSOMAL MATURASE.

GN MATK.

OS Rhododendron ponticum.

OC Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; Ericales; Ericaceae; Rhododendron.

OX NCBI_TaxID=49628;

RN [1]

RP SEQUENCE FROM N.A.

RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,

Yukawa T.;

RT Investigation of Sectional Relationships in the Genus

RT Rhododendron(Ericaceae) based on matk Sequences."

RL J. Jpn. Bot. 0:0-0(1998).

RL EMBL: AB012732; BAA25853.1;

RL InterPro: IPR000442; Intron_maturase2.

DR InterPro: IPR002866; Matk_N.

DR Pfam: PF01348; Intron_maturase2; 1.

DR Pfam: PF01824; Matk_N.1.

KW Chloroplast.

SO SEQUENCE 506 AA; 60449 MW; 21DFE700B071B5B8 CRC64;

Query Match

Best Local Similarity 36.7%; Score 52.5; DB 8; Length 506;

Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

OY 1 KN1MAA-----ORYGRELRLMSDEFEGSRK 25

DB 391 KPVMALSDSDITERFGRTYRLNLSHYSGSLK 422

RESULT 9

062977 PRELIMINARY; PRT: 506 AA.

AC 062977:

DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE RIBOSOMAL MATURASE.

GN MATK.

OS Rhododendron luteum.

OC Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae: Ericales; Ericaceae; Rhododendron.
 NC NCB1_TaxID=49467;
 RN (1)
 RS SEQUENCE FROM N.A.
 RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
 RA Yukawa T.;
 RT *Investigation of Sectional Relationships in the Genus
 Rhododendron(Ericaceae) based on mark Sequences.*;
 RL J. Jpn. Bot. 0:0-0(1998).
 DR EMBL: AB012734; BAA25855.1; -;
 DR InterPro: IPR000442; Intron_mature2.
 DR InterPro: IPR002866; Mark_N.
 DR Pfam: PF01348; Intron_mature2; 1.
 DR Pfam: PF01824; Mark_N; 1.
 KW Chloroplast.
 SQ SEQUENCE 506 AA: 60359 MW: F2BDAC4BF91A609 CRC64;

Query Match 36.7%; Score 52.5; DB 8; Length 506;
 Best Local Similarity 37.5%; Pred. No. 20;
 Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;
 QY 1 KNLMAA-----ORYGRLRMSDEFGSPK 25
 Db 391 KPWAALSDSDIERGRIYRNLSHYSGSLK 422

RESULT 10
 ID 062978 PRELIMINARY; PRT; 506 AA.
 AC 062978;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE RIBOSOMAL MATURASE.
 GN MARK.
 OS Rhododendron canadense.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae: Ericales; Ericaceae; Rhododendron.
 NC NCB1_TaxID=49465;
 RN (1)
 RS SEQUENCE FROM N.A.
 RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
 RA Yukawa T.;
 RT *Investigation of Sectional Relationships in the Genus
 Rhododendron(Ericaceae) based on mark Sequences.*;
 RL J. Jpn. Bot. 0:0-0(1998).
 DR EMBL: AB012735; BAA25856.1; -;
 DR InterPro: IPR000442; Intron_mature2.
 DR InterPro: IPR002866; Mark_N.
 DR Pfam: PF01348; Intron_mature2; 1.
 DR Pfam: PF01824; Mark_N; 1.
 KW Chloroplast.
 SQ SEQUENCE 506 AA: 60350 MW: 5E83259ED64EA25 CRC64;

Query Match 36.7%; Score 52.5; DB 8; Length 506;
 Best Local Similarity 37.5%; Pred. No. 20;
 Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;
 QY 1 KNLMAA-----ORYGRLRMSDEFGSPK 25
 Db 391 KPWAALSDSDIERGRIYRNLSHYSGSLK 422

RESULT 11
 ID 062980 PRELIMINARY; PRT; 506 AA.
 AC 062980;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)

DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE RIBOSOMAL MATURASE.
 GN MARK.
 OS Rhododendron albrechtii.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae: Ericales; Ericaceae; Rhododendron.
 NC NCB1_TaxID=49463;
 RN (1)
 RS SEQUENCE FROM N.A.
 RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
 RA Yukawa T.;
 RT *Investigation of Sectional Relationships in the Genus
 Rhododendron(Ericaceae) based on mark Sequences.*;
 RL J. Jpn. Bot. 0:0-0(1998).
 DR EMBL: AB012737; BAA25858.1; -;
 DR InterPro: IPR000442; Intron_mature2.
 DR InterPro: IPR002866; Mark_N.
 DR Pfam: PF01348; Intron_mature2; 1.
 DR Pfam: PF01824; Mark_N; 1.
 KW Chloroplast.
 SQ SEQUENCE 506 AA: 60301 MW: 9D5877E063B56CB CRC64;

Query Match 36.7%; Score 52.5; DB 8; Length 506;
 Best Local Similarity 37.5%; Pred. No. 20;
 Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;
 QY 1 KNLMAA-----ORYGRLRMSDEFGSPK 25
 Db 391 KPWAALSDSDIERGRIYRNLSHYSGSLK 422

RESULT 12
 ID 062981 PRELIMINARY; PRT; 506 AA.
 AC 062981;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE RIBOSOMAL MATURASE.
 GN MARK.
 OS Rhododendron pentaphyllum.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae: Ericales; Ericaceae; Rhododendron.
 NC NCB1_TaxID=75376;
 RN (1)
 RS SEQUENCE FROM N.A.
 RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
 RA Yukawa T.;
 RT *Investigation of Sectional Relationships in the Genus
 Rhododendron(Ericaceae) based on mark Sequences.*;
 RL J. Jpn. Bot. 0:0-0(1998).
 DR EMBL: AB012738; BAA25859.1; -;
 DR InterPro: IPR000442; Intron_mature2.
 DR InterPro: IPR002866; Mark_N.
 DR Pfam: PF01348; Intron_mature2; 1.
 DR Pfam: PF01824; Mark_N; 1.
 KW Chloroplast.
 SQ SEQUENCE 506 AA: 60449 MW: B138208746D99258 CRC64;

Query Match 36.7%; Score 52.5; DB 8; Length 506;
 Best Local Similarity 37.5%; Pred. No. 20;
 Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;
 QY 1 KNLMAA-----ORYGRLRMSDEFGSPK 25
 Db 391 KPWAALSDSDIERGRIYRNLSHYSGSLK 422

```

RESULT 13
ID 062982 PRELIMINARY; PRT; 506 AA.
AC 062982;
DT 01-AUG-1998 (TRENBLER, 07, Created)
DT 01-AUG-1998 (TRENBLER, 07, Last sequence update)
DE RHODODENDRON MATURESE.
OS RHODODENDRON nipponicum.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Ericales; Ericaceae; Rhododendron.
NCBI_TaxID=35577;
GN NCBI
LN (1)
RP SEQUENCE FROM N.A.
RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
RA Yukawa T.;
RT "Investigation of Sectional Relationships in the Genus
RT Rhododendron(Ericaceae) based on matk Sequences."
RL J. Jpn. Bot. 0:0-0(1998).
DR EMBL; AB012739; BAA25860.1; -
DR InterPro; IPR000442; Intron_maturese2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01348; Intron_maturese2; 1.
DR Pfam; PF01824; MatK_N; 1.
KW Chloroplast.
SQ SEQUENCE 506 AA; 60419 MW; 1P95132CCFAFB40 CRC64;

Query Match 36.7%; Score 52.5; DB 8; Length 506;
Best Local Similarity 37.5%; Pred. No. 20;
Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

QY 1 KNLMAA-----ORIGRELIRMSDEPESFK 25
DB 391 KPWWALSDSDIIEFGRIRNLSHYSGSLK 422

RESULT 14
ID 062983 PRELIMINARY; PRT; 506 AA.
AC 062983;
DT 01-AUG-1998 (TRENBLER, 07, Created)
DT 01-AUG-1998 (TRENBLER, 07, Last sequence update)
DE RHODODENDRON MATURESE.
OS RHODODENDRON nipponicum.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Ericales; Ericaceae; Rhododendron.
NCBI_TaxID=35578;
GN NCBI
LN (1)
RP SEQUENCE FROM N.A.
RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
RA Yukawa T.;
RT "Investigation of Sectional Relationships in the Genus
RT Rhododendron(Ericaceae) based on matk Sequences."
RL J. Jpn. Bot. 0:0-0(1998).
DR EMBL; AB012740; BAA25861.1; -
DR InterPro; IPR000442; Intron_maturese2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01348; Intron_maturese2; 1.
DR Pfam; PF01824; MatK_N; 1.
KW Chloroplast.
SQ SEQUENCE 506 AA; 60393 MW; DAA47A759CFPC46 CRC64;

Query Match 36.7%; Score 52.5; DB 8; Length 506;
Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

```

```

Best Local Similarity 37.5%; Pred. No. 20;
Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

QY 1 KNLMAA-----ORIGRELIRMSDEPESFK 25
DB 391 KPWWALSDSDIIEFGRIRNLSHYSGSLK 422

RESULT 15
ID 062984 PRELIMINARY; PRT; 506 AA.
AC 062984;
DT 01-AUG-1998 (TRENBLER, 07, Created)
DT 01-AUG-1998 (TRENBLER, 07, Last sequence update)
DE RHODODENDRON MATURESE.
OS RHODODENDRON ferrugineum (Alpenrose).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Ericales; Ericaceae; Rhododendron.
NCBI_TaxID=49622;
GN NCBI
LN (1)
RP SEQUENCE FROM N.A.
RA Kurashige Y., Mine M., Kobayashi N., Handa T., Takayanagi K.,
RA Yukawa T.;
RT "Investigation of Sectional Relationships in the Genus
RT Rhododendron(Ericaceae) based on matk Sequences."
RL J. Jpn. Bot. 0:0-0(1998).
DR EMBL; AB012741; BAA25862.1; -
DR InterPro; IPR000442; Intron_maturese2.
DR InterPro; IPR002866; MatK_N.
DR Pfam; PF01348; Intron_maturese2; 1.
DR Pfam; PF01824; MatK_N; 1.
KW Chloroplast.
SQ SEQUENCE 506 AA; 60534 MW; ADA44B25E92436E8 CRC64;

```

```

Query Match 36.7%; Score 52.5; DB 8; Length 506;
Best Local Similarity 37.5%; Pred. No. 20;
Matches 12; Conservative 5; Mismatches 8; Indels 7; Gaps 1;

QY 1 KNLMAA-----ORIGRELIRMSDEPESFK 25
DB 391 KPWWALSDSDIIEFGRIRNLSHYSGSLK 422

Search completed: September 20, 2002, 11:03:48
Job time: 1665 sec

```

```

Query Match 36.7%; Score 52.5; DB 8; Length 506;

```


GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd

OM protein - protein search, using sw model

Run on: September 20, 2002, 10:28:52 ; Search time 228.86 Seconds
(without alignments)
12.619 Million cell updates/sec

Title:	US-09-544-664-1
Perfect score:	138
Sequence:	1 NLMAQRYGRELRLRMSDFEGSPKGL 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

```

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

```

```
post-processing: Minimum Match 0%
Maximum Match 100%
```

Listing first 45 summaries

```
Database :
A.GeneSeq.032802.*
1: /SDSI1/gcgdata/hold-genseq/genseqp-emb1/AA1980.DAT.*
2: /SDSI1/gcgdata/hold-genseq/genseqp-emb1/AA1981.DAT.*
3: /SDSI1/gcgdata/hold-genseq/genseqp-emb1/AA1982.DAT.*
4: /SDSI1/gcgdata/hold-genseq/genseqp-emb1/AA1983.DAT.*
5: /SDSI1/gcgdata/hold-genseq/genseqp-emb1/AA1984.DAT.*
6: /SDSI1/gcgdata/hold-genseq/genseqp-emb1/AA1985.DAT.*
7: /SDSI1/gcgdata/hold-genseq/genseqp-emb1/AA1987.DAT.*
8: /SDSI1/gcgdata/hold-genseq/genseqp-emb1/AA1989.DAT.*
9: /SDSI1/gcgdata/hold-genseq/genseqp-emb1/AA1988.DAT.*
10: /SDSI1/gcgdata/hold-genseq/genseqp-emb1/AA1988.DAT.*
11: /SDSI1/gcgdata/hold-genseq/genseqp-emb1/AA1990.DAT.*
12: /SDSI1/gcgdata/hold-genseq/genseqp-emb1/AA1991.DAT.*
13: /SDSI1/gcgdata/hold-genseq/genseqp-emb1/AA1992.DAT.*
14: /SDSI1/gcgdata/hold-genseq/genseqp-emb1/AA1993.DAT.*
15: /SDSI1/gcgdata/hold-genseq/genseqp-emb1/AA1994.DAT.*
16: /SDSI1/gcgdata/hold-genseq/genseqp-emb1/AA1995.DAT.*
17: /SDSI1/gcgdata/hold-genseq/genseqp-emb1/AA1996.DAT.*
18: /SDSI1/gcgdata/hold-genseq/genseqp-emb1/AA1997.DAT.*
19: /SDSI1/gcgdata/hold-genseq/genseqp-emb1/AA1998.DAT.*
20: /SDSI1/gcgdata/hold-genseq/genseqp-emb1/AA1999.DAT.*
21: /SDSI1/gcgdata/hold-genseq/genseqp-emb1/AA2001.DAT.*
22: /SDSI1/gcgdata/hold-genseq/genseqp-emb1/AA2001.DAT.*
```

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	138	100.0	26	21	AA837001	Bol12 polypeptide
2	138	100.0	26	21	AA837002	Bol12 polypeptide
3	138	100.0	27	21	AA837003	Bol12 polypeptide
4	138	100.0	27	21	AA837055	Bol12 polypeptide
5	138	100.0	28	21	AA837056	Bol12 polypeptide
6	138	100.0	162	22	AA8370370	Shorter murine Bcl-2
7	136	100.0	204	19	AA851568	Bcl-2 (X1)/Bcl-2
8	136	100.0	204	19	AA851515	Murine Bcl-XL/BCL
9	136	100.0	204	19	AA851316	Murine Bcl-XL/BCL
10	136	100.0	204	19	AA851317	Mutant Bcl-XL/BCL
11	138	100.0	204	19	AA851318	Mutant Bcl-XL/BCL

[illegible]

ALIGNMENTS

RESULT	1
AAAB37001	
ID	AAAB37001 standard; peptide: 26 AA.
AC	AAAB37001;
DT	28-FEB-2001 (first entry)
DE	Bcl2 polypeptide B33 domain peptide #1.
XX	Cytostatic; neuroprotective; anti-HIV; vlrucide; cerebroprotective;
XX	KR carianst; Bcl-2 superfamily; B33 domain; cell death agonist; Bad;
XX	KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;
XX	KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
XX	KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
XX	stroke; myocardial infarction.
OS	Homo sapiens.
PN	WO200059526-A1.
PD	12-OCT-2000.
XX	06-APR-2000; 2000WO-US09352.
XX	07-APR-1999; 99US-0128202.
XX	(UVE-1) UNIT JEFFERSON THOMAS.
XX	
PI	Huang Z, Wang J, Zhang Z, Shan S, Lu Z;
DR	WPI; 2000-679325/66.
XX	
XX	New peptide conjugates for modulating apoptosis or for inhibiting B

XX (UJJE-) UNIV JEFFERSON THOMAS.
 PA Huang Z, Wang J, Zhang Z, Shan S, Lu Z;
 XX WPI: 2000-679325/66.
 XX
 PT New peptide conjugates for modulating apoptosis or for inhibiting B
 PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
 PT treating neurodegenerative disorders, stroke, or cancer
 XX
 XX Claim 18; Page 17; 74pp; English.
 XX
 XX The invention relates to a peptide conjugate having the formula:
 CC (R-X)-peptide where n = 1-10; X = C=O when the R-X group is attached
 CC to the N-terminus of the peptide, or a side chain of the peptide where
 CC the functional group of the side chain is NH₂ or OH; or X = O or NH,
 CC when the R-X group is attached to the C-terminus of the peptide, or a
 CC side chain of the peptide, where the side chain functional group is COOH
 CC or CONH₂; and R = 2-18C alkyl or alkoxy, 2-14C alkenyl containing one
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain
 CC alkyl group, or benzyl. The peptides AAB37055 and AAB37056 represent examples
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
 CC the Bcl-2 domain of the cell death agonist Bad. The peptide conjugate is
 CC useful for modulating apoptosis in the cells of a subject, or for
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
 CC function. In particular, the peptide conjugate is useful for treating a
 CC subject afflicted with a cancer characterized by cancer cells that
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
 CC conjugate is also useful for treating disorders characterized by
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
 XX
 XX Sequence 27 AA:
 SQ
 Query Match 100.0%; Score 138; DB 21; Length 27;
 Best Local Similarity 100.0%; Pred. No. 1,4e-14;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CY 1 NLMAAORYGRELRLMSDFEGSFKGL 26
 DB 1 nlwaadrygrelrlmsdfegsfkyl 26
 RESULT 4
 AAB37056
 XX AAB37056 standard; peptide: 27 AA.
 XX AAB37056;
 DT 28-FEB-2001 (first entry)
 XX
 DE Bcl2 polypeptide Bcl2 domain peptide #56.
 XX
 XX Cytostatic; neuroprotective; anti-HIV; virocidic; cerebroprotective;
 KW cardiant; Bcl-2 superfamily; Bcl2 domain; cell death agonist; Bad;
 KW apoptosis; modulation; B cell lymphoma/leukemia 2; cancer; prostate;
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
 KW stroke; myocardial infarction.
 XX
 OS Homo sapiens.
 XX WO200059526-A1.
 PN 12-OCT-2000.

XX 06-APR-2000; 2000WO-US03352.
 XX
 XX 07-APR-1999; 98US-0128202.
 XX
 PA (UJJE-) UNIV JEFFERSON THOMAS.
 XX
 XX Huang Z, Wang J, Zhang Z, Shan S, Lu Z;
 XX WPI: 2000-679325/66.
 XX
 PT New peptide conjugates for modulating apoptosis or for inhibiting B
 PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
 PT treating neurodegenerative disorders, stroke, or cancer
 XX
 XX Claim 18; Page 19; 74pp; English.
 XX
 XX The invention relates to a peptide conjugate having the formula:
 CC (R-X)-peptide where n = 1-10; X = C=O, when the R-X group is attached
 CC to the N-terminus of the peptide, or a side chain of the peptide where
 CC the functional group of the side chain is NH₂ or OH; or X = O or NH,
 CC when the R-X group is attached to the C-terminus of the peptide, or a
 CC side chain of the peptide, where the side chain functional group is COOH
 CC or CONH₂; and R = 2-18C alkyl or alkoxy, 2-14C alkenyl containing one
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain
 CC alkyl group, or benzyl. The peptides AAB37001-A37058 represent examples
 CC of the peptide portion of the conjugate. The peptides represent analogues
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
 CC the Bcl-2 domain of the cell death agonist Bad. The peptide conjugate is
 CC useful for modulating apoptosis in the cells of a subject, or for
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
 CC function. In particular, the peptide conjugate is useful for treating a
 CC subject afflicted with a cancer characterized by cancer cells that
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
 CC conjugate is also useful for treating disorders characterized by
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
 XX
 XX Sequence 27 AA:
 SQ
 Query Match 100.0%; Score 138; DB 21; Length 27;
 Best Local Similarity 100.0%; Pred. No. 1,4e-14;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CY 1 NLMAAORYGRELRLMSDFEGSFKGL 26
 DB 2 nlwaadrygrelrlmsdfegsfkyl 27
 RESULT 5
 AAB37055
 XX AAB37055 standard; peptide: 28 AA.
 XX AAB37055;
 DT 28-FEB-2001 (first entry)
 XX
 DE Bcl2 polypeptide Bcl2 domain peptide #55.
 XX
 XX Cytostatic; neuroprotective; anti-HIV; virocidic; cerebroprotective;
 KW cardiant; Bcl-2 superfamily; Bcl2 domain; cell death agonist; Bad;
 KW apoptosis; modulation; B cell lymphoma/leukemia 2; cancer; prostate;
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
 KW stroke; myocardial infarction.
 XX
 OS Homo sapiens.
 XX

KM neurodegenerative disease; senescence; ischaemia; neoplasia.
 OS Mus musculus.
 FI Key Location/Qualifiers
 FI Region 147..149
 FI /note="BHL conserved amino acids"
 FI Region 191..192
 FI /note="BHL conserved amino acids"
 FI Domain 38..61
 FI /note="PEST sequence"
 FI Domain 111..130
 FI /note="PEST sequence"
 KM M09613614-A1.
 XX 09-MAY-1996.
 XX 31-OCT-1995; 95WO-US14246.
 XX 31-OCT-1994; 94US-033565.
 XX (UNIV) UNIV WASHINGTON.
 XX Korsmeyer SJ;
 XX WPI: 1996-251465/25.
 XX N-PSDB: AAV29479.
 XX Polyomaoncoic encoding bcl-x(l)/bcl-2 associated death promoter -
 XX useful to create neoplasia and apoptosis and to identify agents
 XX inhibiting its binding to bcl-2 or bcl-x(l) to form heterodimers
 XX Claim 3; Fig 1; 130pp; English.
 CC This sequence represents the murine bcl-x(l)/bcl-2 associated death
 CC promoter (Bad) gene. Bad is a 22.1 kb protein which interacts with
 CC bcl-2 and bcl-x proteins and regulates cell death. It has homology
 CC to the bcl-2-related family clustered in the BHL and BH2 domain. Bad
 CC has been found to hybridise to bcl-x(l) and bcl-2 in yeast two-hybrid
 CC assays and in vivo in mammalian cells. Overexpressed Bad counters the
 CC death inhibitory activity of bcl-x(l). Overexpression of bcl-2 in
 CC cells results in increased cell survival. Bad expression can
 CC accelerate apoptotic cell death induced by cytokine deprivation in an
 CC IL-3 dependent cell line expressing bcl-x(l), and its also counters the
 CC death repressor activity of bcl-x(l). Bad competes with Bax for binding
 CC to bcl-x(l). Bad may be used to identify agents which inhibit its
 CC binding to bcl-2 or bcl-x(l) to form heterodimers. Such agents may be
 CC used to treat neurodegenerative diseases, immunodeficiency diseases,
 CC e.g. AIDS, senescence or ischaemia.
 XX Sequence 204 AA.
 SQ
 Query Match 100.0%; Score 138; DB 17; Length 204;
 Best Local Similarity 100.0%; Pred. No. 1,46-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NMAAORGRRLRMNSDFRSCFGL 26
 DB 140 nlwaagrygellrmnsdfsgfkl 165
 RESULT 8
 AAM61315
 ID AAM61315 standard; Protein: 204 AA.
 XX AAM61315:
 XX 07-OCT-1998 (first entry)
 XX Murine BCL-XL/BCL-2 associated cell death regulator.

KM Murine; mouse: BCL-XL/BCL-2 associated cell death regulator; BAD protein;
 KM serine substituted mutant; apoptosis; cancer; viral infection.
 OS Mus sp.
 FI Key Location/Qualifiers
 FI Region 147..149
 FI /note="BHL conserved amino acids"
 FI Region 191..192
 FI /note="BHL conserved amino acids"
 FI Domain 38..61
 FI /note="PEST sequence"
 FI Domain 111..130
 FI /note="PEST sequence"
 KM M09617682-A1.
 XX 30-APR-1998.
 XX 17-OCT-1997; 97WO-US19175.
 XX 18-OCT-1996; 96US-0733505.
 XX (UNIV) UNIV WASHINGTON.
 XX Korsmeyer SJ;
 XX WPI: 1998-261422/23.
 XX N-PSDB: AAV27833.
 XX New mutant BAD polypeptide with phosphorylatable serine replaced -
 XX useful for, e.g. treating reduced apoptosis such as in cancer or
 XX viral infection
 XX Claim 1; Fig 10; 95pp; English.
 CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
 CC death regulator) proteins, having an amino acid other than Ser at
 CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
 CC present sequence is the murine BAD protein. Also described are: (1)
 CC fragments of mutant BAD protein able to decrease cell viability; (2)
 CC fusion proteins of mutant BAD with a heterologous polypeptide that
 CC increases intracellular signalling activity; (3) antibodies that bind to and
 CC neutralize the activity of BAD protein; (4) methods of using BAD protein to treat
 CC viral infection, lymphoproliferation, arthritis, infertility,
 CC inflammation and autoimmune disease. Polyomaoncoic sequences encoding
 CC mutant BAD proteins can be used similarly by gene therapy or to produce
 CC transgenic animals for use as disease models or in drug screening. BAD
 CC proteins phosphorylated at specified Ser are used to screen for enhancers
 CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful
 CC in treatment of cancer. Apoptosis is determined by measuring relative
 CC amounts of phosphotyrosylated and non-phosphorylated BAD, by usual
 CC immunosays. Mutant BAD proteins have greater death-promoting activity
 CC than wild-type BAD which can become phosphorylated on the specified Ser,
 CC forming a product that does not heterodimerise with BCL-2 or BCL-XL
 CC but instead binds to 14-3-3 family proteins in the cytosol, thus promoting cell survival. The mutants with
 CC Ser substituted cannot bind 14-3-3.
 XX Sequence 204 AA.
 SQ
 Query Match 100.0%; Score 138; DB 19; Length 204;
 Best Local Similarity 100.0%; Pred. No. 1,46-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NMAAORGRRLRMNSDFRSCFGL 26
 DB 140 nlwaagrygellrmnsdfsgfkl 165
 RESULT 9
 AAM61316
 ID AAM61316 standard; Protein: 204 AA.
 XX AAM61316:
 XX 07-OCT-1998 (first entry)
 XX Mutant BCL-XL/BCL-2 associated cell death regulator #1.
 XX Murine; mouse: BCL-XL/BCL-2 associated cell death regulator; BAD protein;

KM serine substituted mutant; apoptosis; cancer; viral infection.
 XX Mus sp.
 OS Synthetic.
 PN W09817682-A1.
 XX 30-APR-1998.
 PD 17-OCT-1997: 97MO-US19175.
 XX 18-OCT-1996: 96US-0733505.
 PR (UNIW) UNIV WASHINGTON.
 PA Korsmeyer SJ.
 PI WPI: 1998-26142/23.
 DR N-PSDB: AMV27834.
 XX New mutant BAD polypeptide with phosphorylatable serine replaced -
 PT useful for, e.g. treating reduced apoptosis such as in cancer or
 PT viral infection
 XX
 PS Claim 7: Page 59: 95pp: English.
 CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
 CC death regulator) proteins, having an amino acid other than Ser at
 CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
 CC present sequence represents a mutant BAD protein. Also described are: (1)
 CC fragments of mutant BAD protein able to decrease cell viability; (2)
 CC fusion proteins of mutant BAD with a heterologous polypeptide that
 CC increases intracellular delivery. Mutant BAD proteins are used to treat
 CC or prevent diseases associated with reduced apoptosis, e.g., cancer,
 CC inflammation and autoimmune disease. Polynucleotide sequences encoding
 CC mutant BAD proteins can be used similarly by gene therapy or to produce
 CC transgenic animals for use as disease models or in drug screening. BAD
 CC proteins phosphorylated at specified Ser are used to screen for enhancers
 CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful
 CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,
 CC aging or ischemic cell death. The apoptotic status of cells is non-
 CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
 CC greater death-promoting activity than wild-type BAD which can become
 CC phosphorylated on the specified Ser, forming a product that does not
 CC heterodimerize with BCL-2 or BCL-XL but instead binds to 14-3-3 family
 CC proteins in the cytosol, thus promoting cell survival. The mutants with
 CC Ser substituted cannot bind 14-3-3.
 XX
 SQ Sequence 204 AA:
 DB 140 ntwaagdygrelrmdelegskgl 165
 QY 1 NMAAAGYRELRMSDEPESFKGL 26
 ID AAM61317 standard; Protein: 204 AA.
 AC AAM61317:
 XX 07-OCT-1998 (first entry)
 XX Mutant BCL-XL/BCL-2 associated cell death regulator #2.
 DE Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;
 KM

KM serine substituted mutant; apoptosis; cancer; viral infection.
 XX Mus sp.
 OS Synthetic.
 PN W09817682-A1.
 XX 30-APR-1998.
 PD 17-OCT-1997: 97MO-US19175.
 XX 18-OCT-1996: 96US-0733505.
 PR (UNIW) UNIV WASHINGTON.
 PA Korsmeyer SJ.
 PI WPI: 1998-26142/23.
 DR N-PSDB: AMV27834.
 XX New mutant BAD polypeptide with phosphorylatable serine replaced -
 PT useful for, e.g. treating reduced apoptosis such as in cancer or
 PT viral infection
 XX
 PS Claim 7: Page 60: 95pp: English.
 CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
 CC death regulator) proteins, having an amino acid other than Ser at
 CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
 CC present sequence represents a mutant BAD protein. Also described are: (1)
 CC fragments of mutant BAD protein able to decrease cell viability; (2)
 CC fusion proteins of mutant BAD with a heterologous polypeptide that
 CC increases intracellular delivery. Mutant BAD proteins are used to treat
 CC or prevent diseases associated with reduced apoptosis, e.g., cancer,
 CC inflammation and autoimmune disease. Polynucleotide sequences encoding
 CC mutant BAD proteins can be used similarly by gene therapy or to produce
 CC transgenic animals for use as disease models or in drug screening. BAD
 CC proteins phosphorylated at specified Ser are used to screen for enhancers
 CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful
 CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,
 CC aging or ischemic cell death. The apoptotic status of cells is non-
 CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
 CC greater death-promoting activity than wild-type BAD which can become
 CC phosphorylated on the specified Ser, forming a product that does not
 CC heterodimerize with BCL-2 or BCL-XL but instead binds to 14-3-3 family
 CC proteins in the cytosol, thus promoting cell survival. The mutants with
 CC Ser substituted cannot bind 14-3-3.
 XX
 SQ Sequence 204 AA:
 DB 140 ntwaagdygrelrmdelegskgl 165
 QY 1 NMAAAGYRELRMSDEPESFKGL 26
 ID AAM61318 standard; Protein: 204 AA.
 AC AAM61318:
 XX 07-OCT-1998 (first entry)
 XX Mutant BCL-XL/BCL-2 associated cell death regulator #3.
 DE Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein
 KM

```

XX  serine substituted mutant; apoptosis; cancer; viral infection.
XX  Mus sp.
XX  synthetic.
XX  NC09817682-A1.
XX  30-APR-1998.
XX  17-OCT-1997: 97MO-US191975.
XX  18-OCT-1996: 9605-073505.
XX  (UNIV) ONLY WASHINGTON.
XX  Kormeyer SJ:
XX  WPI: 1998-201422/23.
XX  N-RSDB: AAV27836.
XX  New mutant BAD polypeptide with phosphorylatable serine replaced -
XX  useful for e.g. testing reduced apoptosis such as in cancer or
XX  viral infection
XX  Claim 7: Page 60-61: 95pp: English.
XX  The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
XX  death regulator) proteins having an amino acid residue that Ser at
XX  position 143 is replaced by a different amino acid. The mutant BAD
XX  present sequence represents a mutant BAD protein. Also described are: (1)
XX  fragments of mutant BAD protein able to decrease cell viability; (2)
XX  fusion proteins of mutant BAD with a heterologous polypeptide that
XX  increases intracellular delivery. Mutant BAD proteins are used to treat
XX  or prevent diseases associated with reduced apoptosis, e.g. cancer,
XX  inflammation, lymphoma, osteoporosis, arthritis, osteoarthritis,
XX  immunodeficiency, diabetes, atherosclerosis, osteoporosis, or producing
XX  mutant BAD proteins can be used similarly by gene therapy or to produce
XX  transgenic animals for use as disease models or in drug screening. BAD
XX  proteins phosphorylated at specified Ser are used to screen for enhancers
XX  and inhibitors of serine-phosphatase. Inhibitors are potentially useful
XX  in treatment of excessive apoptosis such as AIDS, neurodegeneration,
XX  aging or ischemic cell death. The apoptotic status of cells is
XX  determined by measuring the amount of BAD protein in cells and non-
XX  phosphorylated BAD, by using immunoassays. Mutant BAD proteins have
XX  greater death-promoting activity than wild-type BAD which can become
XX  phosphorylated on the specified Ser, forming a product that does not
XX  heterodimerize with BCL-2 or BCL-XL but instead binds to 14-3-3 family
XX  proteins in the cytosol, thus promoting cell survival. The mutants with
XX  Ser substituted cannot bind 14-3-3.
XX  Sequence 204 AA:
XX  1
XX  2
XX  3
XX  4
XX  5
XX  6
XX  7
XX  8
XX  9
XX  10
XX  11
XX  12
XX  13
XX  14
XX  15
XX  16
XX  17
XX  18
XX  19
XX  20
XX  21
XX  22
XX  23
XX  24
XX  25
XX  26
XX  27
XX  28
XX  29
XX  30
XX  31
XX  32
XX  33
XX  34
XX  35
XX  36
XX  37
XX  38
XX  39
XX  40
XX  41
XX  42
XX  43
XX  44
XX  45
XX  46
XX  47
XX  48
XX  49
XX  50
XX  51
XX  52
XX  53
XX  54
XX  55
XX  56
XX  57
XX  58
XX  59
XX  60
XX  61
XX  62
XX  63
XX  64
XX  65
XX  66
XX  67
XX  68
XX  69
XX  70
XX  71
XX  72
XX  73
XX  74
XX  75
XX  76
XX  77
XX  78
XX  79
XX  80
XX  81
XX  82
XX  83
XX  84
XX  85
XX  86
XX  87
XX  88
XX  89
XX  90
XX  91
XX  92
XX  93
XX  94
XX  95
XX  96
XX  97
XX  98
XX  99
XX  100
XX  101
XX  102
XX  103
XX  104
XX  105
XX  106
XX  107
XX  108
XX  109
XX  110
XX  111
XX  112
XX  113
XX  114
XX  115
XX  116
XX  117
XX  118
XX  119
XX  120
XX  121
XX  122
XX  123
XX  124
XX  125
XX  126
XX  127
XX  128
XX  129
XX  130
XX  131
XX  132
XX  133
XX  134
XX  135
XX  136
XX  137
XX  138
XX  139
XX  140
XX  141
XX  142
XX  143
XX  144
XX  145
XX  146
XX  147
XX  148
XX  149
XX  150
XX  151
XX  152
XX  153
XX  154
XX  155
XX  156
XX  157
XX  158
XX  159
XX  160
XX  161
XX  162
XX  163
XX  164
XX  165
XX  166
XX  167
XX  168
XX  169
XX  170
XX  171
XX  172
XX  173
XX  174
XX  175
XX  176
XX  177
XX  178
XX  179
XX  180
XX  181
XX  182
XX  183
XX  184
XX  185
XX  186
XX  187
XX  188
XX  189
XX  190
XX  191
XX  192
XX  193
XX  194
XX  195
XX  196
XX  197
XX  198
XX  199
XX  200
XX  201
XX  202
XX  203
XX  204
XX  205
XX  206
XX  207
XX  208
XX  209
XX  210
XX  211
XX  212
XX  213
XX  214
XX  215
XX  216
XX  217
XX  218
XX  219
XX  220
XX  221
XX  222
XX  223
XX  224
XX  225
XX  226
XX  227
XX  228
XX  229
XX  230
XX  231
XX  232
XX  233
XX  234
XX  235
XX  236
XX  237
XX  238
XX  239
XX  240
XX  241
XX  242
XX  243
XX  244
XX  245
XX  246
XX  247
XX  248
XX  249
XX  250
XX  251
XX  252
XX  253
XX  254
XX  255
XX  256
XX  257
XX  258
XX  259
XX  260
XX  261
XX  262
XX  263
XX  264
XX  265
XX  266
XX  267
XX  268
XX  269
XX  270
XX  271
XX  272
XX  273
XX  274
XX  275
XX  276
XX  277
XX  278
XX  279
XX  280
XX  281
XX  282
XX  283
XX  284
XX  285
XX  286
XX  287
XX  288
XX  289
XX  290
XX  291
XX  292
XX  293
XX  294
XX  295
XX  296
XX  297
XX  298
XX  299
XX  300
XX  301
XX  302
XX  303
XX  304
XX  305
XX  306
XX  307
XX  308
XX  309
XX  310
XX  311
XX  312
XX  313
XX  314
XX  315
XX  316
XX  317
XX  318
XX  319
XX  320
XX  321
XX  322
XX  323
XX  324
XX  325
XX  326
XX  327
XX  328
XX  329
XX  330
XX  331
XX  332
XX  333
XX  334
XX  335
XX  336
XX  337
XX  338
XX  339
XX  340
XX  341
XX  342
XX  343
XX  344
XX  345
XX  346
XX  347
XX  348
XX  349
XX  350
XX  351
XX  352
XX  353
XX  354
XX  355
XX  356
XX  357
XX  358
XX  359
XX  360
XX  361
XX  362
XX  363
XX  364
XX  365
XX  366
XX  367
XX  368
XX  369
XX  370
XX  371
XX  372
XX  373
XX  374
XX  375
XX  376
XX  377
XX  378
XX  379
XX  380
XX  381
XX  382
XX  383
XX  384
XX  385
XX  386
XX  387
XX  388
XX  389
XX  390
XX  391
XX  392
XX  393
XX  394
XX  395
XX  396
XX  397
XX  398
XX  399
XX  400
XX  401
XX  402
XX  403
XX  404
XX  405
XX  406
XX  407
XX  408
XX  409
XX  410
XX  411
XX  412
XX  413
XX  414
XX  415
XX  416
XX  417
XX  418
XX  419
XX  420
XX  421
XX  422
XX  423
XX  424
XX  425
XX  426
XX  427
XX  428
XX  429
XX  430
XX  431
XX  432
XX  433
XX  434
XX  435
XX  436
XX  437
XX  438
XX  439
XX  440
XX  441
XX  442
XX  443
XX  444
XX  445
XX  446
XX  447
XX  448
XX  449
XX  450
XX  451
XX  452
XX  453
XX  454
XX  455
XX  456
XX  457
XX  458
XX  459
XX  460
XX  461
XX  462
XX  463
XX  464
XX  465
XX  466
XX  467
XX  468
XX  469
XX  470
XX  471
XX  472
XX  473
XX  474
XX  475
XX  476
XX  477
XX  478
XX  479
XX  480
XX  481
XX  482
XX  483
XX  484
XX  485
XX  486
XX  487
XX  488
XX  489
XX  490
XX  491
XX  492
XX  493
XX  494
XX  495
XX  496
XX  497
XX  498
XX  499
XX  500
XX  501
XX  502
XX  503
XX  504
XX  505
XX  506
XX  507
XX  508
XX  509
```

KM	setine phosphotyrosine; post-translational modification; apoptosis;
KM	signal transduction regulator; phosphoserine phosphatase; senescence;
KM	immunodeficiency disease; neurodegenerative disease; interliffy;
KM	cancer, viral infection; lymphoproliferative condition; arthritis;
KM	inflammation; autoimmune diseases.
OS	Mus sp.
PN	W09080643-A1.
PD	12-MAR-1998.
XX	09-SEP-1997; 97MO-0515871.
XX	09-SEP-1996; 96US-0707868.
PR	(UNIV) UNIV WASHINGTON.
PA	Korsmeyer SJ.
P1	WPI: 1998-207049/18.
XX	Setine-phosphorylated Bcl-X-L/Bcl-2 Associated cell Death regulator
PT	polypeptide - useful for modulation of apoptosis associated with.
PT	e.g. cancer and immunodeficiency diseases
PS	Claim 3, Fig 8; 61pp: English.
CC	This sequence represents a novel setine-phosphorylated protein, PAP
CC	(Bcl-XL/Bcl-2 associated cell death regulator). The serine residue is
CC	phosphorylated in a post-translational modification and allows binding
CC	to the 14-3-3 protein which is a signal transduction regulator.
CC	Modulators of phosphoserine BMD, which act through inhibition/activation
CC	of a phosphoserine phosphatase, are useful for preventing/treating
CC	increased/decreased apoptosis in the cell sense cancer caused by
CC	disease, ischemic cell death, reperfusion cell death, interliffy and
CC	wound-healing. Decreased apoptosis may result from cancer, viral
CC	infection, lymphoproliferative conditions, arthritis, interliffy,
CC	inflammation and autoimmune diseases. Measuring the amount of
CC	phosphorylated computed to upphosphorylated BMD polypeptide and/or total
CC	BMD in a cell is useful for determining the apoptotic state of a cell.
SD	Sequence 204 AA:
QY	1 NITAAQRCHELRNRSSESGEFCFL 26
DB	140 nlwvqyrgfelmstdegtstgl 165
XX	Query Match 100.0%; Score 138; DB 19; Length 204;
XX	Best Local Similarity 100.0%; Pred. No. 1,4e-13;
XX	Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	RESULT 13
XX	AAB70369
ID	AAB70369 standard; protein: 204 AA.
XX	AAB70369;
XX	02-MAY-2001 (first entry)
XX	Longer murine BMD mutant amino acid sequence SEQ ID NO-2.
XX	Bcl-XL/Bcl-2 associated cell death regulator; BMD; mutant; apoptosis;
XX	immunostimulant; neuroprotective; neurotrophic; antischismic; interliffy;
XX	immunopressive; apoptosis induced; apoptosis inhibitor; cancer; 199;
XX	immunodeficiency disease; neurodegenerative disease; viral infection;
XX	ischemic cell death; reperfusion cell death; arthritis; interliffy;
XX	lymphoproliferative condition; inflammation; autoimmune disease.

OS Mus musculus.
 XX Synthetic.
 XX WO200110888-A1.
 XX 15-FEB-2001.
 XX 30-MAY-2000: 2000MO-US11864.
 XX 28-MAY-1999: 99US-0136783.
 XX (APOF-) APOPTOSIS TECHNOLOGY INC.
 XX Zhou X:
 XX WPI: 2001-138734/14.
 XX New mutant Bcl-XL/Bcl-2 associated Cell Death Regulator polypeptide useful for screening for candidate compounds which induce or inhibit apoptosis, comprises amino acid substitutions at Ser118, Ser155 or Ser113.
 XX Claim 4: Page 148: 157pp: English.
 XX The present invention describes an isolated or synthetic polypeptide (1) comprising a less than full length amino acid sequence of Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its fragment, which contains amino acid substitutions at Ser155 of a human BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine BAD (shorter murine BAD). (1) has immunostimulant, neuroprotective, antiapoptotic, antischismatic, vulnerary, cytoskeletal, antiviral, antileukemic, antitumorigenic and immunosuppressive activities, and is useful for the treatment of cancer, AIDS, HIV, Bcl polypeptides and for the induction of apoptosis in a cell. Candidate compounds for activity that promote cell survival of apoptosis. Other uses include inducing or inhibiting apoptosis in a cell. Candidate compounds identified and (mutant) BAD polypeptides are useful in treating CC immunodeficiency diseases, neurodegenerative diseases, ischemic cell death, reperfusion cell death, wound healing, cancer, viral infections, lymphoproliferative conditions, arthritis, infertility, inflammation and CC claimed longer murine BAD mutant amino acid sequence from the present invention.
 XX Sequence 204 AA:
 SO Query Match 100.0%; Score 138; DB 22; Length 204;
 Best Local Similarity 100.0%; Pred. No. 1,4e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NIMMAQRYGRLRMASDEPGSPKGL 26
 DB 140 nlwaagrygrlrmadefegstkgj 165
 RESULT 14
 ID AAM00220 standard; Protein: 567 AA.
 XX AAM00220:
 DT 31-MAY-2001 (first entry)
 DE Bad-DTRR apoptosis-modifying fusion protein.
 XX Mouse: Bad-DTRR: apoptosis: cancer: spinal muscular atrophy;
 XX diptheria toxin: apoptosis: cancer: neoplasm: tumour;
 XX hyperproliferation: Alzheimer's disease: neurodegenerative disorders;
 XX transient ischemic neuronal injury: stroke: spinal cord injury;
 XX Huntington's disease.
 OS Chimeric - Mus sp.

OS Chimeric - Corynebacterium diptheriae.
 XX Chimeric - Synthetic.
 XX Key Location/Qualifiers
 XX Region 3..12
 XX /note="10x histidine tag"
 XX WO200112661-A2.
 XX 22-FEB-2001.
 XX 15-AUG-2000: 2000MO-US22293.
 XX 16-AUG-1999: 99US-0149220.
 XX (HARD) HARVARD COLLEGE.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Youle RJ, Liu X, Collier RJ:
 XX WPI: 2001-218343/22.
 XX N-PSDB: NAS00248.
 XX Novel fusion protein for modifying apoptosis in target cell and reducing apoptosis after transient ischemic neuronal injury, has two of cell which targets protein to a cell and modifies apoptotic response
 XX Claim 4: Page 59-61: 69pp: English.
 XX The sequence represents the amino acid sequence of Bad-DTRR apoptosis-modifying fusion protein comprising Bad gene sequence fused via a short linker to diptheria toxin translocation domain (DTRR). The functional apoptosis-modifying fusion protein is capable of binding a target cell. The apoptosis-modifying fusion protein comprises at least two domains: the DTR domain, which targets the fusion protein to the target cell and the Bcl-XL domain, which modifies an apoptotic response (inhibiting or enhancing) apoptosis in a target cell, such as neuron, hyperproliferative cell or an adipocyte. It is also useful for reducing CC immunodeficiency diseases, neurodegenerative diseases, ischemic cell death, reperfusion cell death, wound healing, cancer, viral infections, lymphoproliferative conditions, arthritis, infertility, inflammation and CC claimed longer murine BAD mutant amino acid sequence from the present invention.
 XX Sequence 567 AA:
 SO Query Match 100.0%; Score 138; DB 22; Length 567;
 Best Local Similarity 100.0%; Pred. No. 4.3e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NIMMAQRYGRLRMASDEPGSPKGL 26
 DB 161 nlwaagrygrlrmadefegstkgj 186
 RESULT 15
 ID AAM32476 standard; Protein: 166 AA.
 XX AAM32476:
 DT 15-JUN-1998 (first entry)
 DE BAC6 protein for regulating cell death.



Fri Sep 20 11:03:02 2002

us-09-544-664-1.ra1

Page 1

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2002, 10:30:32 : Search time 75.64 seconds
(without alignments)
8,336 Million cell updates/sec

Title: US-09-544-664-1
Perfect score: 138
Sequence: 1 NIMAAQRCRELRKMSDEFGSKCL 26

Scoring table:
BLAST64
Gap 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents, AA:*

- 1: /cgn2.6/prodate/2/1aa/5A.COMB.pep:*
- 2: /cgn2.6/prodate/2/1aa/5B.COMB.pep:*
- 3: /cgn2.6/prodate/2/1aa/5C.COMB.pep:*
- 4: /cgn2.6/prodate/2/1aa/5D.COMB.pep:*
- 5: /cgn2.6/prodate/2/1aa/PCRTS.COMB.pep:*
- 6: /cgn2.6/prodate/2/1aa/backfiles1.pep:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	138	100.0	204	1	US-08-333-565-2
2	138	100.0	204	2	US-08-661-479-2
3	138	100.0	204	2	US-08-733-505A-12
4	138	100.0	204	2	US-08-733-505A-13
5	138	100.0	204	2	US-08-733-505A-14
6	138	100.0	204	2	US-08-711-123-3
7	135	97.8	204	2	US-08-665-617-2
8	114	82.6	166	1	US-08-665-617-2
9	114	82.6	166	1	US-08-711-123-2
10	114	82.6	166	3	US-08-983-315-1
11	114	82.6	166	3	US-08-983-315-1
12	114	82.6	166	3	US-08-983-315-1
13	114	82.6	166	3	US-08-983-315-1
14	113	81.9	223	1	US-08-410-372-7
15	113	81.9	223	1	US-08-333-565-10
16	113	81.9	223	1	US-08-661-479-10
17	102	73.9	59	2	US-08-733-505A-55
18	102	73.9	59	2	US-08-733-505A-56
19	102	73.9	59	2	US-08-733-505A-57
20	102	73.9	59	2	US-08-733-505A-58
21	86	62.3	16	1	US-08-333-565-26
22	86	62.3	16	1	US-08-661-479-26
23	61	44.2	11	2	US-08-733-505A-34
24	61	44.2	11	2	US-08-706-741B-69
25	51	37.0	66	3	US-08-661-479B-40
26	46	33.3	946	3	US-09-074-379-3
27	46	33.3	946	4	US-09-568-774-3

28	44	31.9	263	4	US-09-651-656-27	Sequence 27, Appl
29	43	31.2	61	1	US-08-497-312-19	Sequence 19, Appl
30	43	31.2	213	3	US-08-718-736-18	Sequence 18, Appl
31	43	31.2	213	4	US-09-221-844-18	Sequence 18, Appl
32	43	31.2	380	1	US-08-153-848-40	Sequence 40, Appl
33	43	31.2	380	3	US-09-299-643A-40	Sequence 40, Appl
34	43	31.2	380	4	US-09-088-335B-40	Sequence 40, Appl
35	43	31.2	380	2	US-09-324-542-170	Sequence 170, Appl
36	43	31.2	380	2	US-09-324-542-170	Sequence 170, Appl
37	42	30.4	348	2	US-08-997-080-170	Sequence 170, Appl
38	42	30.4	348	2	US-08-997-080-170	Sequence 170, Appl
39	42	30.4	348	4	US-09-095-855-170	Sequence 170, Appl
40	42	30.4	348	4	US-09-324-542-170	Sequence 170, Appl
41	42	30.4	393	2	US-08-997-080-94	Sequence 94, Appl
42	42	30.4	393	2	US-08-997-080-94	Sequence 94, Appl
43	42	30.4	393	4	US-08-872-870-94	Sequence 94, Appl
44	42	30.4	393	4	US-08-872-870-94	Sequence 94, Appl
45	42	30.4	393	4	US-09-324-542-94	Sequence 94, Appl

ALIGNMENTS

RESULT 1
US-08-333-565-2
Sequence 2, Appl
Patent No. 5622652
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: bc1-x/bc1-2 ASSOCIATED CELL DEATH
REGULATOR
NUMBER OF SEQUENCES: 9
CO-INVENTORS: KORSMEYER, Stanley J.
ADDRESS: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,565
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
INVENTOR INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2420
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE INFORMATION:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE: Protein
LOCATION: 1-204
OTHER INFORMATION: /note: "Deduced amino acid sequence
of mouse BAP."

US-08-333-565-2

Query Match 100.0% Score 138, DB 1: Length 204:
Match Locality 100.0% First Match 14, 0:
Matches 26, Conservative 0, Mismatches 0:
Indels 0:
Gaps 0:

```

OY      1 NLMAAORGYRELRMSDEFGSGFKL 26
        |||
Db      140 NLMAAORGYRELRMSDEFGSGFKL 165

RESULT 2
US-08-661-479-2
Sequence No. 5834209
Patent No. 5834209
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: BCL-X/BCL-2 ASSOCIATED CELL DEATH
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Townsend and Townsend Knorle and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM: disk
MEDIUM TYPE: FLOPPY
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,479
FILING DATE: 11-JUN-1995
CLASSIFICATION: B35
PRIORITY DATE: 08/33/95
APPLICATION NUMBER: A: US 08/333,565
FILING DATE: 31-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30, 223
REFERENCE/POCKET NUMBER: 15726A-000700
TELEPHONE: (415) 326-2420
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLGIDY: Linear
MOTIF/DIGEST TYPE: Protein
FEATURES:
NAME/KEY: Protein
LOCATION: 1..204
OTHER INFORMATION: /note= "Deduced amino acid sequence
of mouse BAD."
US-08-661-479-2

Query Match          100.0%   Score 138; DB 2; Length 204;
Best Local Similarity 100.0%   Positives 14; Negatives 14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 NLMAAORGYRELRMSDEFGSGFKL 26
        |||
Db      140 NLMAAORGYRELRMSDEFGSGFKL 165

RESULT 3
US-08-733-505A-1
Sequence No. 5856445
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
```

```

1 NUMBER OF SEQUENCES: 60
2 CORRESPONDENCE ADDRESS:
3 ADDRESSEE: HOWELL & HAFERKAMP, L.C.
4 STREET: 7733 FORSYTH BLVD., SUITE 1400
5 CITY: ST. LOUIS
6 STATE: MISSOURI
7 COUNTRY: USA
8 ZIP: 63105
9
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: floppy disk
12 COMPUTER: IBM PC compatible
13 OPERATING SYSTEM: PC-DOS/MS-DOS
14 SOFTWARE: PatentIn Release #1.0, Version #1.30
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER: US/08/733,505A
17 FILING DATE:
18 CLASSIFICATION:
19 ATTORNEY/AGENT INFORMATION:
20 NAME: DONALD R.
21 REGISTRATION NUMBER: 137
22 TELECOMMUNICATION INFORMATION:
23 TELEPHONE: (314) 727-5188
24 TELEFAX: (314) 727-6092
25 INFORMATION FOR SEQ ID NO: 1:
26 SEQUENCE CHARACTERISTICS:
27 LENGTH: 204 amino acids
28 TYPE: amino acid
29 STRANDEDNESS:
30 TOPOLOGY: linear
31 MOLECULE TYPE: protein
32 US-08-733-505A-1
33
34 Query Match
35 Best Local Similarity 100.0% Score 138; DB 2; Length 204;
36 Matches 26; Conservative 0; Mismatches 14; 0; Indels 0; Gaps 0;
37
38 Db 140 NLMANORGYRELRRMSDEFGSFGCL 26
39 |((((((((((((((((((((((((((((((((
40
41 RESULT 4
42 US-08-733-505A-12
43 Sequence 12, Application US/08733505A
44 Patent No. 5856445
45 GENERAL INFORMATION:
46 APPLICANT: KOSMEYER, STANLEY J.
47 TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
48 NUMBER OF SEQUENCES: 60
49 CORRESPONDENCE ADDRESS:
50 ADDRESSEE: HOWELL & HAFERKAMP, L.C.
51 STREET: 7733 FORSYTH BLVD., SUITE 1400
52 CITY: ST. LOUIS
53 STATE: MISSOURI
54 COUNTRY: USA
55 ZIP: 63105
56 COMPUTER READABLE FORM:
57 MEDIUM TYPE: floppy disk
58 COMPUTER: IBM PC compatible
59 OPERATING SYSTEM: PC-DOS/MS-DOS
60 SOFTWARE: PatentIn Release #1.0, Version #1.30
61 CURRENT APPLICATION DATA:
62 APPLICATION NUMBER: US/08/733,505A
63 FILING DATE:
64 CLASSIFICATION:
65 ATTORNEY/AGENT INFORMATION:
66 NAME: DONALD R.
67 REGISTRATION NUMBER: 35,197
68 REFERENCE/DOCKET INFORMATION:
69 TELECOMMUNICATION INFORMATION:

```

TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-505A-12

Query Match 100.0%; Score 138; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 4e-14;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 N1MAAQRGRRLRMSDEFGSPKGL 26
DB 140 N1MAAQRGRRLRMSDEFGSPKGL 165

RESULT 5
US-08-733-505A-13
Sequence 13, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS: HAFERKAMP, L.C.
ADDRESS FOR SEQ ID NO: 13:
STREET: 7733 FORSTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-505A-13

Query Match 100.0%; Score 138; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 4e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 N1MAAQRGRRLRMSDEFGSPKGL 26
DB 140 N1MAAQRGRRLRMSDEFGSPKGL 165
RESULT 6

US-08-733-505A-14
Sequence 14, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESS: HOFELT & HAFERKAMP, L.C.
STREET: 7733 FORSTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-505A-14

Query Match 100.0%; Score 138; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 4e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 N1MAAQRGRRLRMSDEFGSPKGL 26
DB 140 N1MAAQRGRRLRMSDEFGSPKGL 165
RESULT 7
US-08-717-123-3
Sequence 3, Application US/08717123
Patent No. 5965703
GENERAL INFORMATION:
APPLICANT: William A. Oltersdorf
TITLE OF INVENTION: Human BAD Polypeptides, Encoding Nucleic
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/717,123
 FILING DATE: 20-SEP-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-ID 1929
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-8949
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 204 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-717-123-3

Query Match 97.8%; Score 135; DB 2; Length 204;
 Best Local Similarity 96.2%; Pred. No. 1,2e-13;
 Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLMANQYRGELRMSDEFGSFKL 26
 DB 140 NLMANQYRGELRMTDEFGSFKGL 165

RESULT 8
 US-08-665-617-2
 Sequence 2, Application US/0865617
 Patent No. 5663160
 GENERAL INFORMATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Saliwanchik, David R.
 REGISTRATION NUMBER: 31,794
 REFERENCE/DOCKET NUMBER: CT-8
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (352) 375-8100
 TELEFAX: (352) 372-5800
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 166 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-665-617-2

Query Match 82.6%; Score 114; DB 1; Length 166;
 Best Local Similarity 91.7%; Pred. No. 1,8e-10;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 NLMANQYRGELRMSDEFGSFK 24

DB 101 NLMANQYRGELRMSDEFGSFK 124

RESULT 9
 US-08-717-123-2
 Sequence 2, Application US/08717123
 Patent No. 5663160
 GENERAL INFORMATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-ID 1929
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-8949
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 168 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-717-123-2

Query Match 82.6%; Score 114; DB 2; Length 168;
 Best Local Similarity 91.7%; Pred. No. 1,8e-10;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 NLMANQYRGELRMSDEFGSFK 24
 DB 103 NLMANQYRGELRMSDEFGSFK 126

RESULT 10
 US-08-985-335-1
 Sequence 1, Application US/08985335
 Patent No. 6080847
 GENERAL INFORMATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Hillman, Jennifer L.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: CT-8
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (352) 375-8100
 TELEFAX: (352) 372-5800
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 166 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-985-335-1

OY 1 NLMANQYRGELRMSDEFGSFK 24

```

? COUNTRY: USA
? ZIP: 94304
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FASTSEQ for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/985,335
? FILING DATE: Filed Herewith
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Billings, Lucy J.
? REGISTRATION NUMBER: 36,749
? REFERENCE/DOCKET NUMBER: PF-0421 US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 650-845-4166
? TELEFAX: 650-845-4166
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 168 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? IMMEDIATE SOURCE:
? LIBRARY: SYNORAB01
? CLONE: 358673
? US-08-985-335-1

Query Match      82.6%; Score 114; DB 3; Length 168;
Best Local Similarity 91.7%; Pred. NO. 1.8e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NLMAORYGRELRRMSDEFFSFK 24
Db 103 NLMAORYGRELRRMSDEFFSFK 126

RESULT 11
US-08-985-335-7
? Sequence 7, Application US/08985335
? Patent No. 6080847
? GENERAL INFORMATION:
? APPLICANT: Hillman, Jennifer L.
? APPLICANT: Yee, Henry
? APPLICANT: Lal, Preeti
? APPLICANT: Shah, Purvi
? APPLICANT: Corley, Neil C.
? TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
? TITLE OF INVENTION: PROLIFERATION
? NUMBER OF SEQUENCES: 9
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Incyte Pharmaceuticals, Inc.
? STREET: 3174 Porter Dr.
? CITY: Palo Alto
? STATE: CA
? COUNTRY: USA
? ZIP: 94304
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FASTSEQ for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/985,335
? FILING DATE: Filed Herewith
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:

```

```

? NAME: Billings, Lucy J.
? REGISTRATION NUMBER: 36,749
? REFERENCE/DOCKET NUMBER: PF-0421 US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 650-845-0555
? TELEFAX: 650-845-4166
? INFORMATION FOR SEQ ID NO: 7:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 168 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? IMMEDIATE SOURCE:
? LIBRARY: GenBank
? CLONE: 1683637
? US-08-985-335-7

Query Match      82.6%; Score 114; DB 3; Length 168;
Best Local Similarity 91.7%; Pred. NO. 1.8e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 NLMAORYGRELRRMSDEFFSFK 24
Db 103 NLMAORYGRELRRMSDEFFSFK 126

RESULT 12
US-09-410-372-1
? Sequence 1, Application US/09410372
? Patent No. 6281334
? GENERAL INFORMATION:
? APPLICANT: Hillman, Jennifer L.
? APPLICANT: Yee, Henry
? APPLICANT: Lal, Preeti
? APPLICANT: Shah, Purvi
? APPLICANT: Corley, Neil C.
? TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
? TITLE OF INVENTION: PROLIFERATION
? NUMBER OF SEQUENCES: 9
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Incyte Pharmaceuticals, Inc.
? STREET: 3174 Porter Dr.
? CITY: Palo Alto
? STATE: CA
? COUNTRY: USA
? ZIP: 94304
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FASTSEQ for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/410,372
? FILING DATE:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/985,335
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Billings, Lucy J.
? REGISTRATION NUMBER: 36,749
? REFERENCE/DOCKET NUMBER: PF-0421 US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 650-845-0555
? TELEFAX: 650-845-4166
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 168 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? IMMEDIATE SOURCE:
? LIBRARY: SYNORAB01

```

CLONE: 358673
US-09-410-372-1

Query Match 82.6%; Score 114; DB 4; Length 168;
Best Local Similarity 91.7%; Pred. No. 1,8e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 N1MAA0RYGRELRRMSDEFECSFK 24
DB 103 N1MAA0RYGRELRRMSDEFECSFK 136

RESULT 13
US-09-410-372-7
Sequence 7, Application US/09410372
Patent No. 6281334
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410,372
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,335
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-845-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1683637
US-09-410-372-7

Query Match 82.6%; Score 114; DB 4; Length 168;
Best Local Similarity 91.7%; Pred. No. 1,8e-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 N1MAA0RYGRELRRMSDEFECSFK 24
DB 103 N1MAA0RYGRELRRMSDEFECSFK 126

RESULT 14

US-08-333-565-10
Sequence 10, Application US/08333565
Patent No. 5622852

GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Knourle and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US

ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,565
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-333-565-10

Query Match 81.9%; Score 113; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2,8e-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 N1MAA0RYGRELRRMSDEFC 21
DB 3 N1MAA0RYGRELRRMSDEFC 23

RESULT 15
US-08-661-479-10
Sequence 10, Application US/08661479
Patent No. 5834209
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Knourle and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,479

FILING DATE: 11-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/333,565
 FILING DATE: 31-OCT-1994
 ATTORNEY/AGENCY INFORMATION:
 NAME: SMITH, WILLIAM W.
 REGISTRATION NUMBER: 30,223
 REFERENCE/DOCKET NUMBER: 15726A-000700
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 TELEFAX: (415) 326-2422
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 23 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-661-479-10

Query Match 81.9%; Score 113; DB 2; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.8e-11;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	NLMAAORYGRELRRMSDEFEFG	21
DB	3	NLMAAORYGRELRRMSDEFEFG	23

Search completed: September 20, 2002, 10:37:18
 Job time: 406 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: September 20, 2002, 10:31:08 ; Search time 95.59 Seconds
(without alignments)
26.136 Million cell updates/sec.

Title: US-09-544-664-1

Sequence: 1 NLMAAQRGRELRLMSDFEGSFKGL 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	138	100.0	204	2	A55671
2	54	39.1	946	2	JC5575
3	53	38.4	223	2	D70760
4	52	38.4	946	2	S54354
5	52	37.7	370	2	S38185
6	51	37.0	232	2	A42095
7	50	36.2	374	2	C84338
8	49	35.5	516	2	A96753
9	48	35.5	453	2	E83517
10	48.5	35.1	134	2	S40376
11	48.5	35.1	314	2	T02975
12	48	34.8	206	2	C36365
13	48	34.8	220	2	F72289
14	48	34.8	526	2	T08545
15	47	34.1	597	2	G82308
16	47	34.1	5138	2	F82668
17	47	34.1	5138	2	B96695
18	46.5	33.7	435	2	T02961
19	46.5	33.7	435	2	A44308
20	46.5	33.7	1140	2	T09486
21	46	33.3	399	2	T35440
22	46	33.3	946	1	TYH02
23	46	33.3	1164	2	T24806
24	46	33.3	1378	2	A81393
25	45.5	33.0	261	2	G69510
26	45.5	33.0	287	2	S43852
27	45.5	33.0	334	2	A39172
28	45.5	33.0	562	2	C71473
29	45.5	33.0	905	2	G83314

30	45	32.6	165	2	S59899	chlorocornurin chat
31	45	32.6	295	2	F83201	conserved hypotet
32	45	32.6	346	2	H95406	conserved hypotet
33	45	32.6	591	2	B44465	sodium ion pump ox
34	45	32.6	591	2	A80509	oxalacetate decar
35	45	32.6	591	2	AB0903	oxalacetate decar
36	45	32.6	596	2	A28088	oxalacetate decar
37	45	32.6	715	2	S52675	probable membrane
38	45	32.6	864	1	VCLJ72	env polyprotein
39	45	32.6	1263	2	T19472	hypothetical prote
40	45	32.6	1557	2	T28811	hypothetical prote
41	45	32.6	2125	2	T15566	hypothetical prote
42	44.5	32.2	75	2	T01993	hypothetical prote
43	44.5	32.2	455	2	D83264	hypothetical prote
44	44.5	32.2	536	2	AG1482	hypothetical prote
45	44.5	32.2	910	2	G91024	NADH dehydrogenase

ALIGNMENTS

RESULT 1
A55671
bad protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 05-Nov-1999
C:Accession: A55671
R:Yang, E.; Zha, J.; Jockel, J.; Bolse, L.H.; Thompson, C.B.; Korsmeyer, S.J.
Cell 80, 285-291, 1995
A:Title: Bad, a heterodimeric partner for Bcl-X-L and Bcl-2, displaces Bax and promot
A:Reference number: A55671; MUID:95136361
A:Accession: A55671
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-204 <YAN>
A:Cross-references: GB:L37296; NID:9639778; PIDN:AAA64465.1; PID:9639779
C:Keywords: heterodimer

Query Match 100.0% Score 138; DB 2; Length 204;
Best local Similarity 100.0%; Pred. No. 7.1e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLMAAQRGRELRLMSDFEGSFKGL 26
DB 140 NLMAAQRGRELRLMSDFEGSFKGL 165

RESULT 2
JC5575
inter-alpha-trypsin inhibitor heavy chain 2 - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
C:Accession: JC5575; PC4485
R:Nakatani, T.; Suzuki, Y.; Yamamoto, T.; Sinohtara, H.
J. Biochem. 122, 71-82, 1997
A:Title: Molecular cloning and sequencing of cDNAs encoding three heavy-chain precurs
sin inhibitor heavy chain family.
A:Reference number: JC5574; MUID:97420668
A:Accession: JC5575
A:Molecule type: mRNA
A:Residues: 1-946 <NAN>
A:Cross-references: DDB:DB9286; NID:91694689; PIDN:BAA13939.1; PID:91694690
A:Experimental source: liver
A:Accession: PC4485
A:Molecule type: protein
A:Residues: 55-64;140-146;151-156;424-447;500-528;577-605 <NAN>
C:Comment: In the plasma three inter-alpha-trypsin inhibitor heavy chains 1, 2 and 3
that the complexes play important role for pancreatic cancer.
C:Superfamily: Inter-alpha-trypsin inhibitor complex component II
F:261-264, 717-916/Disulfide bonds: #status predicted

C:Species: Homo sapiens (man)
 C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C:Accession: S40376
 R:Kleio, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A>Title: Expressed human immunoglobulin chain genes and their hypermutation.
 A:Reference number: S40312; MUID:94080891
 A:Accession: S40376
 A>Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-134
 A:Cross-references: EMBL:X72486; NID:g441440; PIDN:CA51154.1; PID:g441441
 C:Superfamily: Immunoglobulin Y region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:34-113/Domain: immunoglobulin homology <IM>

Query Match 35.1%; Score 48.5; DB 2; Length 134;
 Best Local Similarity 38.2%; Pred. No. 7.8;
 Matches 13; Conservative 1; Mismatches 9; Indels 11; Gaps 1;
 Oy 3 AAORGRGRLRRM-----SDEFGSGFK 25
 DB 58 WFRGRGRSPRLIYVNSKSGVSDPSGSG 91

RESULT 11
 T02975
 C:Species: Zea mays (maize)
 C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
 C:Accession: T02975
 R:Bailey, N.H.; James, N.C.; Greenland, A.J.
 Plant Physiol. 112, 1391-1396, 1996
 A>Title: cDNA isolation and gene expression of maize annexins P33 and P35.
 A:Reference number: 214796; MUID:97092863
 A:Accession: T02975
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-314
 A:Cross-references: EMBL:X98245; NID:g1370602; PIDN:CA66901.1; PID:g1370603
 A:Experimental source: cultivar clipper; root tip
 C:Superfamily: annexin I; annexin repeat homology
 F:1485/Domain: annexin repeat homology <AN>

Query Match 35.1%; Score 48.5; DB 2; Length 314;
 Best Local Similarity 47.6%; Pred. No. 19;
 Matches 10; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

Oy 5 AAGRGRE-RRMSDEFGSGFK 24
 DB 54 KEAYGKELRALDEHCKFE 74

RESULT 12
 C36365
 C:Species: Rhizomucor racemosus
 C>Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 19-Jan-2001
 C:Accession: C36365
 R:Connelly, D.G.; Wang, S.Y.; Lee, Y.J.; Linz, J.E.
 Mol. Cell Biol. 10, 6554-6563, 1990
 A>Title: Expression of a gene family in the dimorphic fungus Mucor racemosus which exhibit
 A:Reference number: A36365; MUID:91061774
 A:Accession: C36365
 A:Molecule type: DNA
 A>Status: preliminary
 A:Residues: 1-206 <C>
 C:Cross-references: GB:M55177
 C:Superfamily: ras transforming protein; translation elongation factor Tu homology
 C:Keywords: GTP binding; nucleotide binding; P-loop
 F:11-126/Domain: translation elongation factor Tu homology <ETU>

F:17-24/Region: nucleotide-binding motif A (P-loop)
 F:123-126/Region: GTP-binding NKXD motif
 F:153-155/Region: GTP-binding SAK/L motif
 F:23,24,42,123,124,126,153/Binding site: Mg-GNP (Gys, Ser, Thr, Asn, Lys, Asp, Ser) *

Query Match 34.8%; Score 48; DB 2; Length 206;
 Best Local Similarity 62.5%; Pred. No. 14;
 Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Oy 10 RELRMDSEFGSGFK 25
 DB 169 KEIRKMDKDESRSG 184

RESULT 13
 F72289
 C:Species: Thermotoga maritima (strain MSB)
 C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
 C:Accession: F72289
 R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
 C.M.
 Nature 399, 323-329, 1999
 A>Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
 A:Reference number: A72200; MUID:99287316
 A:Accession: F72289
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-220 <AN>
 A:Cross-references: GB:AE001772; GB:AE000512; NID:g4981693; PIDN:AMD36230.1; PID:g498
 A:Experimental source: strain MSB
 C:Genetics:
 A:Gene: TM1154
 C:Superfamily: yeast SDC3 protein

Query Match 34.8%; Score 48; DB 2; Length 220;
 Best Local Similarity 34.8%; Pred. No. 15;
 Matches 8; Conservative 8; Mismatches 7; Indels 0; Gaps 0;
 Oy 4 AAORGRGRLRRMSDEFGSGFK 26
 DB 111 ACGEREHRKSRDPDLALGM 133

RESULT 14
 T08545
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 07-Dec-1999
 C:Accession: T08545; S71362; S74307
 R:Bevan, M.; Zimmermann, W.; Gruenewald, A.; Wandl, R.; Bancroft, I.; Mewes, H.W.;
 submitted to the Protein Sequence Database, May 1999
 A:Reference number: 216442
 A:Accession: T08545
 A:Molecule type: DNA
 A:Residues: 1-526
 A:Cross-references: EMBL:AL050352; GSFDB:GM00062; ATSP:F27B13.80
 A:Experimental source: cultivar Columbia; BAC clone F27B13
 R:Wang, G.; Wang, R.; Havens, S.; Douce, R.
 Plant Cell 10, 1989-1990
 A>Title: Characterization of an Arabidopsis thaliana cDNA encoding an S-adenosylmeth
 A:Reference number: S71362; MUID:96314555
 A:Accession: S71362
 A:Molecule type: mRNA
 A:Residues: 1-17, 3-526 <C>
 A:Cross-references: EMBL:L41666; NID:g4448916; PIDN:AB04607.1; PID:g4448917
 A:Accession: S74307
 A:Molecule type: protein
 A:Residues: 40-54 <CUT>

Fri-Sep 20 11:03:03 2002

us-09-544-664-1.rpt

C:Genetics:

A:Gene: ATSP:227B3.80

A:Map position: 4

C:Keywords: carbon-oxygen lyase; chloroplast
F:1-35/Domain: transil peptides (chloroplast) #status predicted <TNP>

F:40-526/Product: threonine synthase #status experimental <MT>

Query Match

Best Local Similarity 34.8%; Score 48; DB 2; Length 526;

Matches 12; Conservative 6; Mismatches 8; Indels 8; Gaps 1;

OY 1 NLMAQRVGRGLRMSD-----EPEGSPKGI, 26

DB 172 NLMAERGRKQFLGNDLWYKHCISITGSPKDL 205

RESULT 15

G82308 oxaloacetate decarboxylase, alpha chain VC0550 [similarity] - Vibrio cholerae (strain NL

C:Species: Vibrio cholerae

C:Accession: G82308

R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.J.; Dodson, R.J.;

1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: AB2035; M01D:20406833

A:Accession: G82308

A:Status: preliminary

A:Molecule type: DNA

A:Restriction sites: 135; <MT>

A:Experimental source: serogroup O1; strain M1661; biotype El Tor

C:Genetics:

A:Gene: VC0550

A:Map position: 1

C:Superfamily: Klebsiella pneumoniae oxaloacetate decarboxylase alpha chain; lipoyl/biot

OY 8 YGRLRRMSDFEGSKGL 26

DB 272 YFBNYKRYAFBQULKGV 290

Search completed: September 20, 2002, 10:39:02

Job time: 474 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2002, 10:37:23 (Search time 44.99 Seconds)

(without alignments)
22,376 Million cell updates/sec

Title: US-09-544-664-1

Sequence: 138
1 NIMAAQRGRLRMSDEPFGSPKGL 26

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than the observed score. The observed score
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	138	100.0	204	1 BAD_MOUSE	O61337 mus musculus
2	136	100.0	205	1 BAD_MOUSE	O61337 mus musculus
3	136	100.0	205	1 BAD_MOUSE	O61337 mus musculus
4	136	100.0	205	1 BAD_MOUSE	O61337 mus musculus
5	136	100.0	205	1 BAD_MOUSE	O61337 mus musculus
6	136	100.0	205	1 BAD_MOUSE	O61337 mus musculus
7	136	100.0	205	1 BAD_MOUSE	O61337 mus musculus
8	136	100.0	205	1 BAD_MOUSE	O61337 mus musculus
9	136	100.0	205	1 BAD_MOUSE	O61337 mus musculus
10	136	100.0	205	1 BAD_MOUSE	O61337 mus musculus
11	136	100.0	205	1 BAD_MOUSE	O61337 mus musculus
12	136	100.0	205	1 BAD_MOUSE	O61337 mus musculus
13	136	100.0	205	1 BAD_MOUSE	O61337 mus musculus
14	136	100.0	205	1 BAD_MOUSE	O61337 mus musculus
15	136	100.0	205	1 BAD_MOUSE	O61337 mus musculus
16	136	100.0	205	1 BAD_MOUSE	O61337 mus musculus
17	136	100.0	205	1 BAD_MOUSE	O61337 mus musculus
18	136	100.0	205	1 BAD_MOUSE	O61337 mus musculus
19	136	100.0	205	1 BAD_MOUSE	O61337 mus musculus
20	136	100.0	205	1 BAD_MOUSE	O61337 mus musculus
21	136	100.0	205	1 BAD_MOUSE	O61337 mus musculus
22	136	100.0	205	1 BAD_MOUSE	O61337 mus musculus
23	136	100.0	205	1 BAD_MOUSE	O61337 mus musculus
24	136	100.0	205	1 BAD_MOUSE	O61337 mus musculus
25	136	100.0	205	1 BAD_MOUSE	O61337 mus musculus
26	136	100.0	205	1 BAD_MOUSE	O61337 mus musculus
27	136	100.0	205	1 BAD_MOUSE	O61337 mus musculus
28	136	100.0	205	1 BAD_MOUSE	O61337 mus musculus
29	136	100.0	205	1 BAD_MOUSE	O61337 mus musculus
30	136	100.0	205	1 BAD_MOUSE	O61337 mus musculus
31	136	100.0	205	1 BAD_MOUSE	O61337 mus musculus
32	136	100.0	205	1 BAD_MOUSE	O61337 mus musculus
33	136	100.0	205	1 BAD_MOUSE	O61337 mus musculus

34	43.5	31.5	1014	1	UTRA_STRCO	O92507 streptomyc
35	43	31.2	377	1	APL_MOUSE	O04008 mus musculu
36	43	31.2	380	1	APL_HUMAN	P35414 mus musculu
37	43	31.2	380	1	APL_MOUSE	O97666 macaca mula
38	43	31.2	578	1	ACER_ECOLI	P11071 escherichia
39	43	31.2	583	1	ACER_SALTY	P51067 salmonelella
40	43	31.2	695	1	MDL1_YEAS	P33310 saccharomyc
41	43	31.2	905	1	ZOS_MOUSE	O96xy1 mus musculu
42	42	30.4	207	1	THE_PIRAB	O96xy2 pyrococcus
43	42	30.4	359	1	REPA_YEAS	O96xy3 pyrococcus
44	42	30.4	359	1	REPA_YEAS	O96xy3 pyrococcus
45	42	30.4	463	1	Y030_MPVAC	P41434 autographa

ALIGNMENTS

RESULT 1	BAD_MOUSE	STANDARD:	PRT:	204 AA.
ID	BAD_MOUSE			
AC	O61337			
DT	01-NOV-1997 (Ref. 35, Created)			
DT	01-MAR-2002 (Ref. 41, Last annotation update)			
DE	Bcl-2 antagonist of cell death (BAD) (Bcl-2 binding component			
DE	6) (Bcl-xL/Bcl-2 associated death promoter).			
GN	BAD OR BAC6.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI-Taxid-10090.			
LN	SEQUENCE FROM N.A.			
RC	TISSUE=Brain, and Thymus;			
RX	MEDLINE=9516361; PubMed=7834748;			
RT	Yang E., Zhu J., Jockel J., Boise L.H., Thompson C.B., Korsmeyer S.J.;			
RT	"Bad, a heterodimeric partner for Bcl-xL and Bcl-2, displaces Bax and			
RT	promotes cell death."			
RL	Cell 80:285-291(1995).			
RP	PHOSPHORYLATION, AND MUTAGENESIS OF SER-112 AND SER-136.			
RX	MEDLINE=9602283; PubMed=2381718; Page C., Herrera R., Nunez G.;			
RT	"Interleukin-3-induced phosphorylation of BAD through the protein			
RT	kinase Akt."			
RL	Science 278:687-689(1997).			
RP	MUTAGENESIS OF SERINE RESIDUES.			
RX	MEDLINE=20403302; PubMed=10949026;			
RA	Datta S.R., Katslov A., Hu L., Petros A., Fesik S.W., Yaffe M.B.,			
RT	"14-3-3 proteins and survival kinases cooperate to inactivate BAD by			
RT	BH3 domain phosphorylation."			
RL	Mol. Cell 6:41-51(2000).			
RT	"Binding of BAD to 14-3-3 promotes cell death. Successively competes for the			
CC	binding of Bcl-xL. Bcl-2 and Bcl-w, thereby affecting the level			
CC	of heterodimerization of these proteins with BAX. Can reverse the			
CC	death repressor activity of Bcl-xL, but not that of Bcl-2.			
CC	Appears to act as a link between growth factor receptor signaling			
CC	and the apoptotic pathways.			
CC	-1- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-			
CC	x(L), Bcl-2 and Bcl-w. Also binds protein S100A10 (by similarity).			
CC	The Ser-112/Ser-136 phosphorylated form binds 14-3-3 proteins.			
CC	-1- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon			
CC	phosphorylation, locates to the cytoplasm.			
CC	-1- DOMAIN: Interact BH3 domain is regulated by BIK, BID, BAX, BAD AND			
CC	BAX for their pro-apoptotic activity and their interaction			
CC	with phosphatidylserine. Ser-112 fails to interact			
CC	with phosphatidylserine. Ser-112 in response to survival stimuli.			
CC	Subsequent phosphorylation on Ser-136 promotes heterodimerization			
CC	with 14-3-3 proteins. This interaction then facilitates the			
CC	phosphorylation at Ser-15, a site within the BH3 domain, leading			
CC	to the release of Bcl-x(L) and the promotion of cell survival.			

CC Ser-136 is the major site of AKT/PKB phosphorylation. Ser-155 the
CC majo site of protein kinase A (CAK) phosphorylation.
CC -1- SIMILARITY: CONTAINS A BCL-2 HOMOLGY DOMAIN 3 (BH3).
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC This SWISS-PROT entry is a copy-right. It is produced through a collaboration
CC between the Swiss Institute for Experimental Medicine and the EMBL Outstation
CC at the European Bioinformatics Institute. There are no restrictions on ways
CC use by non-profit institutions as long as its content is left unchanged and no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement>,
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L37296; AA064465.1; -
CC MGI: MGI:096630; Bcl-2.
CC PDB: 1D9D; PDB: 1D9D; Bcl-2.
CC PROSITE: PS01259; BH3; PHO-NEC.
CC KEGG: K04491; Bcl-2.
CC APOPTOSIS: Phosphorylation.
CC PT DOVAIN 147 151
CC PT MOD_RES 112 112
CC PT MOD_RES 136 136
CC PT MOD_RES 155 155
CC PT MUTAGEN 112 112
CC PT MUTAGEN 136 136
CC PT MUTAGEN 155 155
CC SEQUENCE 204 AA; 22080 MW; 6C2BA910205035F7 CRC64;
SO
Query Match 100.00; Score 136; Db 1; Length 204;
Best Local Similarity 100.00; Pctd. No. 8, Ee: 14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 NCMAAQRGRLRRNSDEFGSGKL 26
Db 140 NCMAAQRGRLRRNSDEFGSGKL 165
RESULT 2
BAD_RAT
BAD_RAT BAD_RAT STANDARD; PRT; 205 AA.
ID BAD_RAT
AC Q35147; Q70356; Q9JHX1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 01-DEC-2001 (Rel. 40, Last sequence update)
DT 01-DEC-2001 (Rel. 40, Last annotation update)
DE Bcl-2 antagonist of cell apoptosis (induced)
DE 6) (bcl-xl/bcl-2 associated death promoter).
DE BAD.
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eultheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus;
NCBI_Taxid=10116;
OX 117
RN 117
RS 117
TS TSSEQ-DNA: 98034386; Pubmed-9365453;
RX MEDLINE-98034386; Pubmed-9365453;
RX Han S.-Y., Kalpa A., Zhu L., Hauch A.J.W.;
RT "Interference of Bcl (bcl-xl/bcl-2-associated death promoter). Induced
RT Apoptosis in mammalian cells by 14-3-3 isoforms and p11".
RT Mo. Endocrinol. 11:1858-1867(1997).
LN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain.
RC MEDLINE-9353132; Pubmed-9535132;
RC D'Amico G., Traversi S., Musco S., Cavallaro S.;
RT "Cloning and expression of the programmed cell death regulator Bcl in
RT the rat brain".
LN [3]
RN Neurosci. Lett. 243:137-140(1998).
RP SEQUENCE FROM N.A. (ISOPROMS ALPHA AND BETA).
RC TISSUE=Brain;
RC MEDLINE-2109372; Pubmed-11161472;
RC Hammer U., Arumae U., Yu L.-Y., Sun Y.-F., Saarma M., Lindholm D.;

[illegible]

QY	1	NLMAAORYGRELIRMSDEFGSFKCL 26
Db	141	NLMAAORYGRELIRMSDEFGSFKCL 166
RESULT	3	
BAD_HUMAN	STANDARD;	PRT; 168 AA.
ID	BAD_HUMAN	092934; 014803;
AC	01-NOV-1997	(Rel. 35, Created)
DT	16-OCT-2001	(Rel. 40, Last sequence update)
DE	01-MAR-2002	(Rel. 41, Last annotation update)
DE	Bcl-2 antagonist of cell death (BAD) (Bcl-2 binding component	
DE	6) (Bcl-xL/Bcl-2 associated death promoter).	
GN	BAD OR BBC6 OR BCL2L8.	
OS	Homo sapiens (human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eumetaria; Primates; Catarrhini; Hominoidea; Homo.	
RN	NC_017432;taxid=9606;	
RN	1)	
RP	SEQUENCE FROM N.A.	
RA	Lin D.X., Li Z., Huang B., Chen S., Zhou H.;	
RA	"A human protein that interacts with Bcl-2 and have homology to mouse	
RT	Bcl-2	
RT	Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.	
RN	12)	
RP	SEQUENCE FROM N.A., AND PHOSPHORYLATION BY Raf-1.	
RA	MEDLINE-87083574; PubMed-8825523;	
RA	Wang H.-G., Rapp U.R., Reed J.C.	
RT	"Bcl-2 targets the protein kinase Raf-1 to mitochondria."	
RT	Cell 87:623-638(1996).	
RN	13)	
RP	SEQUENCE FROM N.A.	
RA	Takayama S., Reed J.C.;	
RA	Submitted (OCT-1997) to the EMBL/Genbank/DBJ databases.	
RN	14)	
RP	SEQUENCE FROM N.A., AND DIMERIZATION.	
RA	TISSUE-Bone marrow;	
RA	MEDLINE-98049554; PubMed-9388232;	
RA	Medilla S., Diaz J.-L., Horne W., Chang J., Wilson G.,	
RA	Chang S., Weeks S., Filiz L.C., Oltersdorf T.;	
RT	"Dimerization properties of human BAD."	
RT	J. Biol. Chem. 272:30866-30872(1997).	
RN	15)	
RP	SEQUENCE FROM N.A.	
RA	TISSUE-Lung;	
RA	Strausberg R.;	
RT	Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.	
RN	16)	
RP	STRUCTURE BY NMR OF 103-127.	
RA	MEDLINE-21073561; PubMed-11206074;	
RA	Petros A.M., Nettesheim D.G., Wang Y., Olejniczak E.T., Meadows R.P.,	
RA	MacK J., Swift K., Matsuyoshi E.D., Zhang H., Thompson C.B.,	
RA	Fesik S.W.;	
RT	"Rationale for Bcl-xL/Bad peptide complex formation from structure,	
RT	mutagenesis, and biophysical studies."	
RT	Protein Sci. 9:2528-2534(2000).	
CC	-1- BINDING: Promotes cell death. Successfully competes for the	
CC	binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level	
CC	of heterodimerization of these proteins with BAX. Can reverse the	
CC	death repressor activity of Bcl-x(L), but not that of Bcl-2 (by	
CC	similarity). Appears to act as a link between growth factor	
CC	receptor signaling and the apoptotic pathways.	
CC	-1- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-x	
CC	(L), Bcl-2 and Bcl-w. Also binds protein S100A10 (by similarity)	
CC	(by Ser-75/Ser-99 phosphorylated form binds 14-3-3 proteins (by	
CC	similarity).	
CC	-1- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon	
CC	phosphorylation, locates to the cytoplasm.	
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.	
CC	-1- DOMAIN: Intact BH3 domain is required by BIK, BID, BAK, BAD AND	
CC	BAX for their pro-apoptotic activity and for their interaction	
CC	with anti-apoptotic members of the Bcl-2 family.	

CC	-1- PPM Phosphorylation on Ser-75 in response to survival stimuli.	CC	-1- PPM Phosphorylation on Ser-99 promotes heterodimerization
CC	Subsequent phosphorylation on Ser-99 promotes heterodimerization	CC	with 14-3-3 proteins. This interaction then facilitates the
CC	phosphorylation at Ser-118, a site within the BH3 domain, leading	CC	to the release of Bcl-x(L) and the promotion of cell survival.
CC	Ser-99 is the major site of AKT/PKB phosphorylation. Ser-118 the	CC	major site of protein kinase A (CAK) phosphorylation (by
CC	similarity).	CC	similarity).
CC	-1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.	CC	-1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC	-1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.	CC	-1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its	CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial	CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).	CC	or send an email to license@isb-sib.ch).
CC	EMBL: U06879; AAB36516.1; -	CC	EMBL: U06879; AAB36516.1; -
DR	EMBL: AF021522; AAB72092.1; -	DR	EMBL: AF021522; AAB72092.1; -
DR	EMBL: AF031523; AAB8124.1; -	DR	EMBL: AF031523; AAB8124.1; -
DR	FBI: BC001901; AAH01901.1; -	DR	FBI: BC001901; AAH01901.1; -
DR	PIR: IGS5; 07-FEB-01.	DR	PIR: IGS5; 07-FEB-01.
DR	MIM: 603167; -	DR	MIM: 603167; -
DR	InterPro: IPR000712; BCL_2	DR	InterPro: IPR000712; BCL_2
DR	PROSITE: PS01259; BH3; FALSIS_NSG.	DR	PROSITE: PS01259; BH3; FALSIS_NSG.
DR	AP000001; Phosphorylation; 3D-structure.	DR	AP000001; Phosphorylation; 3D-structure.
FT	DOMAIN 110 124	FT	DOMAIN 110 124
FT	MOD_RES 75 75	FT	MOD_RES 75 75
FT	MOD_RES 99 99	FT	MOD_RES 99 99
FT	MOD_RES 118 118	FT	MOD_RES 118 118
FT	CONFLICT 64 91	FT	CONFLICT 64 91
FT	SEQUENCE 168 AA; 16392 MW; 69PBD027DDEE241 CRG64.	FT	SEQUENCE 168 AA; 16392 MW; 69PBD027DDEE241 CRG64.
QY	1 NLMAAGRGRLRMSDFEESFC 24	QY	1 NLMAAGRGRLRMSDFEESFC 24
Db	103 NLMAAGRGRLRMSDFEESFC 126	Db	103 NLMAAGRGRLRMSDFEESFC 126
RESULT 4		RESULT 4	
ID	ITR2_MESAU	ID	ITR2_MESAU
DT	15-JUL-1998 (Rel. 36, Created)	DT	15-JUL-1998 (Rel. 36, Created)
DE	01-MAR-2002 (Rel. 41, Last annotation update)	DE	01-MAR-2002 (Rel. 41, Last annotation update)
DE	Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITR1 heavy	DE	Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITR1 heavy
GN	chain H2) (HC2).	GN	chain H2) (HC2).
OS	Mesocricetus auratus (Golden hamster).	OS	Mesocricetus auratus (Golden hamster).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC	Mesocricetus.	OC	Mesocricetus.
OX	NCBI_TaxID=10036;	OX	NCBI_TaxID=10036;
RN	1	RN	1
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RC	TISSUE=Liver;	RC	TISSUE=Liver;
RA	MEDLINE=97420688; PubMed=9276673;	RA	MEDLINE=97420688; PubMed=9276673;
RT	Nakatani T., Suzuki Y., Yamamoto T., Shinohara H.;	RT	Nakatani T., Suzuki Y., Yamamoto T., Shinohara H.;
RT	"Molecular cloning and sequencing of cDNAs encoding three heavy-chain	RT	"Molecular cloning and sequencing of cDNAs encoding three heavy-chain
RT	precursors of the inter-alpha-trypsin inhibitor in Syrian hamster:	RT	precursors of the inter-alpha-trypsin inhibitor in Syrian hamster:
RT	Implications for the evolution of the inter-alpha-trypsin inhibitor	RT	Implications for the evolution of the inter-alpha-trypsin inhibitor
RT	heavy chain family";	RT	heavy chain family";

RL J. Biochem. 122:71-82(1997).
 RP SEQUENCE OF 55-64; 140-146; 151-156; 424-447; 500-528 AND 577-605,
 AND SUBUNIT 1.
 RC TISSUE-Plasma;
 RA MEDLINE-97018241; PubMed-8864857;
 RX Yamamoto T., Yamamoto K., Shimohara H.;
 RT Inter-alpha-trypsin inhibitor and its related proteins in Syrian
 hamster urine and plasma.
 RL J. Biochem. 120:145-152(1996).
 CC -1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A
 BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN.
 CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
 CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
 CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
 CC SIMILARITY).
 CC -1- SUBUNIT 1-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
 CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,
 CC BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-1) IS COMPOSED OF H1, H2
 CC AND BIKUNIN. INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND
 CC BIKUNIN. AND PRE-ALPHA-LIKE INHIBITOR (P-ALPHA-LI) OF H3 AND BIKUNIN.
 CC -1- FTH: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
 CC 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY
 CC SIMILARITY). BELONGS TO THE ITIH FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch)

 DR EMBL: D89286; BAA13939.1;
 DR InterPro: IPR002035; VWFA.
 DR Pfam: PF00092; vwa; 1.
 DR SMART: SM00327; VWFA; 1.
 DR PROSITE: PS50234; VWFA; 1.
 KW Serine protease inhibitor; Repeat; Signal; Multigene family;
 KM Glycoprotein.
 FT SIGNAL 1 18
 FT PROPEP 19 54
 FT CHAIN 55 702
 FT BY SIMILARITY.
 FT INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN
 FT H2.
 FT BY SIMILARITY.
 FT PROPEP 703 946
 FT DOMAIN 308 468
 FT CARBOHYD 118 118
 FT CARBOHYD 263 263
 FT CARBOHYD 445 445
 FT CARBOHYD 578 578
 FT BINDING 702 702
 FT N-LINKED (GLCNAc...) (POTENTIAL).
 FT N-LINKED (GLCNAc...) (POTENTIAL).
 FT N-LINKED (GLCNAc...) (POTENTIAL).
 FT CHONDROITIN 4-SULFATE, CROSS-LINK SITE
 FT (BY SIMILARITY).
 FT V->Y (IN REF. 2).
 FT E->I (IN REF. 2).
 FT PROPEP 510 510
 FT CONFLICT 595 595
 FT SEQUENCE 946 AA; 106580 MW; CABBF65458B7B2E CRC64;
 SO
 Query Match 39.1%; Score 54; DB 1; Length 946;
 Best Local Similarity 34.6%; Pred. No. 2.6;
 Matches 9; Conservative 5; Mismatches 12; Indels 0; Gaps 0;
 Oy 1 NLMAORYGRELRRMSDEFGSKGL 26
 Db 212 NWIVELQGWRLHVPDFEGHGOV 237
 RESULT 5
 ITIH2_MOUSE STANDARD; PRT; 946 AA.
 ID ITIH2_MOUSE
 AC 061703;
 DT 15-JUL-1998 (Rel. 36, Created)

DR 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1999 (Rel. 36, Last annotation update)
 DE Inter-alpha-trypsin inhibitor heavy chain H2 precursor (IT heavy
 DE chain H2).
 GN ITIH2.
 OS Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId:10090;
 CC SEQUENCE FROM N.A.
 CC STRAIN-C57BL/6N; PubMed-7534067;
 CC MEDLINE-95194326;
 CC Chan P., Ristler J.-L., Ragueneau G., Sallier J.-P.;
 RA The three heavy-chain precursors for the inter-alpha-inhibitor
 RT family in mouse: new members of the multicopper oxidase protein group
 RT with differential expression in liver and brain.
 RL Biochem. J. 306:503-512(1995).
 CC -1- FUNCTION: THIS PROTEIN IS A CARRIER OF HYALURONAN IN SERUM OR AS A
 CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN.
 CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE
 CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE
 CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY
 CC SIMILARITY).
 CC -1- SUBUNIT: I-ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM
 CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,
 CC BIKUNIN. INTER-ALPHA-INHIBITOR (I-ALPHA-1) IS COMPOSED OF H1, H2
 CC AND BIKUNIN. INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LI) OF H2 AND
 CC BIKUNIN. AND PRE-ALPHA-LIKE INHIBITOR (P-ALPHA-LI) OF H3 AND BIKUNIN.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN BOTH LIVER AND BRAIN.
 CC -1- FTH: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN
 CC 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY
 CC SIMILARITY). BELONGS TO THE ITIH FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch)

 DR EMBL: X70392; CAA49842.1;
 DR MGI: 96619; Itih2.
 DR InterPro: IPR002035; VWFA.
 DR Pfam: PF00092; vwa; 1.
 DR SMART: SM00327; VWFA; 1.
 DR PROSITE: PS50234; VWFA; 1.
 KW Serine protease inhibitor; Repeat; Signal; Multigene family;
 KM Glycoprotein.
 FT SIGNAL 1 18
 FT PROPEP 19 54
 FT CHAIN 55 702
 FT BY SIMILARITY.
 FT INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN
 FT H2.
 FT BY SIMILARITY.
 FT PROPEP 703 946
 FT DOMAIN 308 468
 FT CARBOHYD 118 118
 FT CARBOHYD 263 263
 FT CARBOHYD 445 445
 FT BINDING 702 702
 FT N-LINKED (GLCNAc...) (POTENTIAL).
 FT N-LINKED (GLCNAc...) (POTENTIAL).
 FT CHONDROITIN 4-SULFATE, CROSS-LINK SITE
 FT (BY SIMILARITY).
 FT SEQUENCE 946 AA; 105927 MW; 40DB6716433EB9DC CRC64;
 SO
 Query Match 38.4%; Score 53; DB 1; Length 946;
 Best Local Similarity 34.6%; Pred. No. 3.7;
 Matches 9; Conservative 5; Mismatches 12; Indels 0; Gaps 0;
 Oy 1 NLMAORYGRELRRMSDEFGSKGL 26
 Db 212 NWIVELQGWRLHVPDFEGHGOV 237

RESULT 6
 AROC_YEAST STANDARD: PRT: 370 AA.
 AC P32449;
 DT 01-OCT-1993 (rel. 27, Created)
 DT 01-FEB-1994 (rel. 28, Last sequence update)
 DT 30-MAY-2000 (rel. 39, Last annotation update)
 DE Phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited
 (EC 4.1.2.15) (Phospho-2-keeto-3-deoxyheptonate aldolase) (DHP
 synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase).
 GN ARO4 OR YBR249C OR YBR1701.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 CX NCBI_TaxID=4932;
 RN 111
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92225349; PubMed=1348717;
 RA Kuenzler M., Paravicini G., Egli C., Imjager S., Braus G.H.;
 RT Cloning, primary structure and regulation of the ARO4 gene, encoding
 the tyrosine-inhibited 3-deoxy-D-arabino-heptulosonate 7-phosphate
 synthase from *Saccharomyces cerevisiae*.
 RL Gene 113:67-74(1992).
 RN 121
 RP REVISIONS TO 205-207.
 RA Kuenzler M.;
 RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
 RN 31
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94078675; PubMed=8256522;
 RA Boignon F., Bateau N., Aigle A., Crouzet M.;
 RT "The complete sequence of a 6794 bp segment located on the right arm
 of chromosome 11 of *Saccharomyces cerevisiae*. Finding of a putative
 dimerase in yeast."
 RL Yeast 9:1121-1137(1993).
 RN 141
 RP SEQUENCE FROM N.A.
 RA STRAIN=5288C; Pohl F.M., Pohl T.M.;
 RL Submitted (Nov-1994) to the EMBL/GenBank/DBJ databases.
 CC -1 FUNCTION: SPERMATOPHYTIC CONDENSATION OF PHOSPHOENOLPYRUVATE (PEP)
 AND D-BRIVHOSE-7-PHOSPHATE (E4P) GIVING RISE TO 3-DEOXY-D-
 ARABINO-HEPTULOSONATE-7-PHOSPHATE (DAMP)
 CC -1 CATALYTIC ACTIVITY: 2-dehydro-3-deoxy-D-arabino-heptone 4-
 phosphate + H(2)O
 CC -1 ENZYME REGULATION: INHIBITED BY TYROSINE
 CC -1 PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN
 THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY);
 CC -1 INDUCTION: BY AMINO ACID STARVATION
 CC -1 SIMILARITY: BELONGS TO CLASS-I DAMP SYNTHETASE FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed, usage by and for commercial
 CC entities requires a license agreement (See <http://www.isp-sib.ch/annouce/>
 CC or send an email to license@sib-sib.ch)
 CC
 CC EMBL: X61107; CAA43419.1;
 CC EMBL: L20296; AAA65607.1;
 CC EMBL: L26118; CAA85212.1;
 CC FIR: S38185; S38185;
 CC HSR: P00886; 1087;
 CC SGD: S0000453; ARO4;
 CC InterPro: IPR001785; DAMP synth.1;
 CC Pfam: PF00793; DAMP synth.1;
 CC ProDom: PD00560; DAMP synth.1;
 CC Aromatic amino acid biosynthesis; Lyase; Multigene family.

SC SEQUENCE 370 AA: 39749 MW: 594ED08F24175979 CRC64;
 Query Match 37.7%; Score 52; DB 1; Length 370;
 Best Local Similarity 47.6%;
 Matches 10; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 QY 1 NMAACHYGRRLRMSPDEEC 21
 :|||||:|:|||||:
 DB 80 DLEACHYRLRLKLSDELNG 100
 RESULT 7
 AF3_ARATH STANDARD: PRT: 232 AA.
 ID AF3_ARATH
 AC P35632; 039003;
 DT 01-JUN-1994 (rel. 29, Created)
 DT 01-JUN-1994 (rel. 29, Last sequence update)
 DT 16-OCT-2001 (rel. 40, Last annotation update)
 DE Floral homeotic protein APETALA3.
 GN AP3 OR A19G54340 OR T12E18_30.
 OS Arabidopsis thaliana (mouse-ear cress).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 CX NCBI_TaxID=3702;
 RN 111
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9214682; PubMed=1346756;
 RA Jack T., Brockman L.L., Heywood E.M.;
 RT "The homeotic gene APETALA3 of *Arabidopsis thaliana* encodes a MADS
 box and is expressed in petals and stamens."
 RL Cell 68:685-697(1992).
 RN 121
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95036018; PubMed=75248893;
 RA Okamoto H., Yano A., Shirasahi H., Okada K., Shimura Y.;
 RT "Genetic complementation of a floral homeotic mutation, *apetala3*,
 with an *Arabidopsis thaliana* gene homologous to DEFICIENS of
Antirrhinum majus."
 RL Plant Mol. Biol. 26:465-472(1994).
 RN 131
 RP SEQUENCE FROM N.A.
 RX STRAIN-VARIOUS STRAINS;
 CC MEDLINE=99126449; PubMed=9927474;
 CC Purugganan M.D., Sudhith J.I.;
 CC "Molecular population genetics of floral homeotic loci, *DEPAREPES*
 CC *RT* genes of *Arabidopsis thaliana*."
 CC Genetics 151:835-848(1999).
 CC
 CC SEQUENCE FROM N.A.
 CC STRAIN=CV, COLUMBIA;
 CC MEDLINE=21016720; PubMed=11130713;
 CC Salomonst B., Lemcke K., Rieger M., Ansoorge W., Unsel G.,
 CC Fritmann B., Valle G., Bloeker H., Perez-Alonso M., Obermayer B.,
 CC Delany M., Boutry M., Griwell L.A., Macho R., Puigdomenech P.,
 CC de Simone V., Choisy N., Arfkenave F., Robert C., Brottier P.,
 CC Winkler P., Cattolico L., Weissbach J., Saurin W., Queller F.,
 CC Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
 CC Wundbach E., Drzonek H., Erle H., Jordan R., Bangert S.,
 CC Weinmann R., Kranz H., Voss H., Holland R., Brandt P., Nykatura G.,
 CC Vezzi A., D'Angelo M., Pallavicini A., Toppi S., Simionati B.,
 CC Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordstiek G.,
 CC Reichelt J., Schirfe M., Schoen O., Barques M., Terol J., Clement J.,
 CC Navarro P., Collado C., Perez-Perez A., Ottenwelder B., Duchemin D.,
 CC Cooke R., Landie M., Berger-Laurio C., Purrelle B., Masny D.,
 CC de Haan M., Maarse A.C., Alcaraz J.-P., Corbelli A., Casacubeta E.,
 CC Monfort A., Argilov A., Flores M., Liguori R., Vitale D.,
 CC Monhapt G., Haase D., Schoof H., Radd S., Zaccaria P.,
 CC Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,


```

CC NUCLEOTIDE-EXCHANGE FACTOR (GEF) AND INACTIVATED BY A GTPASE-
CC ACTIVATING PROTEIN (GAP).
CC -1- SUBCELLULAR LOCATION: PLASMA MEMBRANE.
CC -1- DEVELOPMENTAL STAGE: IN SPORULATING MYCELIUM AND MUCH LESS IN
CC GERMINATING AND YEAST.
CC -1- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RAS FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M55177; AAA8379.1; -.
CC PIR: C36365; C36365.
CC HSSP: P01112; P1EL.
CC InterPro: IPR003577; Ras.
CC InterPro: IPR001806; Ras_Grnfamng.
CC Pfam: PF00071; Ras; 1.
CC PRINTS: PR00449; RASTRNSFRNG.
CC SMART: SM00173; RAS; 1.
CC GTP-binding; Phenylation; Lipoprotein.
CC NP_BIND 16 23 GTP (BY SIMILARITY).
CC NP_BIND 53 53 GTP (BY SIMILARITY).
CC NP_BIND 122 125 GTP (BY SIMILARITY).
CC DOMAIN 38 44 EFFECTOR REGION (PROBABLE).
CC LIPID 202 202 FRANKSTL (BY SIMILARITY).
CC SEQUENCE 205 AA; 23408 MW; D8F086406F090F50 CRC64;

Query Match 34.8%; Score 48; DB 1; Length 205;
Best Local Similarity 62.5%; Pred. No. 3; 8;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 10 RELRMSDEFGSKG 25
DB 168 RELRMSDEFGSKG 183

RESULT 10
6PGL.THEMA STANDARD: PRT: 220 AA.
AC 09YXN8;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 6-phosphogluconolactonase (EC 3.1.1.31) (6PGL).
GN PGL OR DBVA OR TML154.
OS Thermotoga maritima.
OC Bacteria; Thermotogales; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109;
RA MEDLINE=99287316; PubMed=10360571;
RA Haft D.H., Hickey R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA McDonald L., Utechtack T.R., Malek J.A., Nelson W.C., Ketchum K.A.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RA "Evidence for lateral gene transfer between Archaea and Bacteria from
RA genome sequence of Thermotoga maritima."
RL Nature 399:323-329(1999).
RT
CC -1- FUNCTION: HYDROLASIS OF 6-PHOSPHOGLUCONOLACTONE TO 6-
CC PHOSPHOGLUCONATE.
CC -1- CATALYTIC ACTIVITY: 6-phospho-D-glucono-1,5-lactone + H(2)O -> 6-
CC phospho-D-gluconate.
CC -1- PATHWAY: SECOND STEP IN PENTOSE PHOSPHATE PATHWAY.
CC -1- SIMILARITY: BELONGS TO THE GLUCOSAMINE/GALACTOSAMINE-6-PHOSPHATE
CC ISOMERASE FAMILY. 6-PHOSPHOGLUCONOLACTONASE SUBFAMILY.

```

```

CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AE001772; AAD36230.1; -.
CC TIGR: TML154; -.
CC InterPro: IPR000457; Glucosamine_Iso.
CC Pfam: PF01182; Glucosamine_Iso; 1.
CC Hydrolase; Complete proteome.
CC SEQUENCE 220 AA; 25325 MW; 9BDFD07E01E60C3 CRC64;

Query Match 34.8%; Score 48; DB 1; Length 220;
Best Local Similarity 34.8%; Pred. No. 4; 1;
Matches 8; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 4 AAGRGRELRMSDEFGSKGL 26
DB 111 ACETRELRMSADFDLALDM 133

RESULT 11
THRC.SOLITU STANDARD: PRT: 519 AA.
AC 09MT28;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Threonine synthase, chloroplast precursor (EC 4.2.99.2) (TS).
OS Solanum tuberosum (potato)
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
CC Asteridae; eusterids I; Solanales; Solanaceae; Solanum.
CC NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RA Casazza P., Kaiser S., Willmitzer L., Hoefgen R., Hesse H.;
RA "Isolation and characterization of a cDNA encoding threonine synthase
RA from Solanum tuberosum."
RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: O-phospho-L-homoserine + H(2)O -> L-threonine +
CC phosphate.
CC -1- COFACTOR: pyridoxal phosphate (by similarity).
CC -1- ENZYME REGULATION: Allosterically activated by S-adenosyl-
CC methionine (SAM) (by similarity).
CC -1- PATHWAY: Threonine biosynthesis; last step.
CC -1- SUBUNIT: Homodimer (by similarity).
CC -1- SUBCELLULAR LOCATION: Chloroplast (by similarity).
CC -1- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF082694; AAF74984.1; -.
CC InterPro: IPR001926; B6_enzyme_Delta.
CC Pfam: PF00291; PALP; 1.
CC PROSITE: PS00165; DEHYDRATASE_SER_THR; 1.
CC Threonine biosynthesis; lysase; pyridoxal phosphate; Allosteric enzyme;
CC chloroplast; Transil peptide.
CC TRANSIT 1 40 CHLOROPLAST (BY SIMILARITY).
CC CHAIN 41 519 THREONINE SYNTHASE.
CC FT BINDING 136 196 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC SEQUENCE 519 AA; 57412 MW; 114C0979CD231464 CRC64;

```



```

DB 172 NLFMAERKOFIGNMDLWKHOGISHTSPFDL 205
RESULT 13
BLM_HUMAN
ID BLM_HUMAN STANDARD: PRT; 198 AA.
AC 043522: 043522:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Bcl2-like protein 11 (Bcl2 interacting mediator of cell death).
GN Bcl2l1 OR BIM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606.
RA MEDLINE-98094360: PubMed-9430630:
RX "Connor L., Strasser A., O'Reilly L.A., Hausmann G., Adams J.M.,
RX Cory S., Huang D.C.S.:
RX "Bim: a novel member of the Bcl-2 family that promotes apoptosis";
RX FMOB J. 17:384-395(1998).
RL -1- FUNCTION: INDUCES APOPTOSIS. ISOFORM BIML IS MORE POTENT THAN
CC ISOFORM BIMEL.
CC -1- SUBUNIT: FORMS HETERODIMERS WITH A NUMBER OF ANTIAPOPTOTIC BCL-2
CC PROTEINS INCLUDING MCL-1, BCL-2, BCL-XL, BFL-1, AND BHRF-1. DOES
CC NOT HETERODIMERIZE WITH PROAPOPTOTIC PROTEINS SUCH AS BAD, BOK,
CC BAX OR BAK (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: ASSOCIATED WITH INTRACYTOSOLIC MEMBRANES
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS, BIMEL (SHOWN HERE) AND
CC BIML; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- DOMAIN: THE BHL3 DOMAIN IS REQUIRED FOR BCL-2 BINDING AND
CC CYTOTOXICITY.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 3 (BH3).
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: AF032457; AAC39593.1; -
CC EMBL: AF032456; AAC39594.1; -
CC EMBL: AF032455; AAC39595.1; -
CC EMBL: AF032454; AAC39596.1; -
CC EMBL: AF032453; AAC39597.1; -
CC EMBL: AF032452; AAC39598.1; -
CC EMBL: AF032451; AAC39599.1; -
CC EMBL: AF032450; AAC39600.1; -
CC EMBL: AF032449; AAC39601.1; -
CC EMBL: AF032448; AAC39602.1; -
CC EMBL: AF032447; AAC39603.1; -
CC EMBL: AF032446; AAC39604.1; -
CC EMBL: AF032445; AAC39605.1; -
CC EMBL: AF032444; AAC39606.1; -
CC EMBL: AF032443; AAC39607.1; -
CC EMBL: AF032442; AAC39608.1; -
CC EMBL: AF032441; AAC39609.1; -
CC EMBL: AF032440; AAC39610.1; -
CC EMBL: AF032439; AAC39611.1; -
CC EMBL: AF032438; AAC39612.1; -
CC EMBL: AF032437; AAC39613.1; -
CC EMBL: AF032436; AAC39614.1; -
CC EMBL: AF032435; AAC39615.1; -
CC EMBL: AF032434; AAC39616.1; -
CC EMBL: AF032433; AAC39617.1; -
CC EMBL: AF032432; AAC39618.1; -
CC EMBL: AF032431; AAC39619.1; -
CC EMBL: AF032430; AAC39620.1; -
CC EMBL: AF032429; AAC39621.1; -
CC EMBL: AF032428; AAC39622.1; -
CC EMBL: AF032427; AAC39623.1; -
CC EMBL: AF032426; AAC39624.1; -
CC EMBL: AF032425; AAC39625.1; -
CC EMBL: AF032424; AAC39626.1; -
CC EMBL: AF032423; AAC39627.1; -
CC EMBL: AF032422; AAC39628.1; -
CC EMBL: AF032421; AAC39629.1; -
CC EMBL: AF032420; AAC39630.1; -
CC EMBL: AF032419; AAC39631.1; -
CC EMBL: AF032418; AAC39632.1; -
CC EMBL: AF032417; AAC39633.1; -
CC EMBL: AF032416; AAC39634.1; -
CC EMBL: AF032415; AAC39635.1; -
CC EMBL: AF032414; AAC39636.1; -
CC EMBL: AF032413; AAC39637.1; -
CC EMBL: AF032412; AAC39638.1; -
CC EMBL: AF032411; AAC39639.1; -
CC EMBL: AF032410; AAC39640.1; -
CC EMBL: AF032409; AAC39641.1; -
CC EMBL: AF032408; AAC39642.1; -
CC EMBL: AF032407; AAC39643.1; -
CC EMBL: AF032406; AAC39644.1; -
CC EMBL: AF032405; AAC39645.1; -
CC EMBL: AF032404; AAC39646.1; -
CC EMBL: AF032403; AAC39647.1; -
CC EMBL: AF032402; AAC39648.1; -
CC EMBL: AF032401; AAC39649.1; -
CC EMBL: AF032400; AAC39650.1; -
CC EMBL: AF032399; AAC39651.1; -
CC EMBL: AF032398; AAC39652.1; -
CC EMBL: AF032397; AAC39653.1; -
CC EMBL: AF032396; AAC39654.1; -
CC EMBL: AF032395; AAC39655.1; -
CC EMBL: AF032394; AAC39656.1; -
CC EMBL: AF032393; AAC39657.1; -
CC EMBL: AF032392; AAC39658.1; -
CC EMBL: AF032391; AAC39659.1; -
CC EMBL: AF032390; AAC39660.1; -
CC EMBL: AF032389; AAC39661.1; -
CC EMBL: AF032388; AAC39662.1; -
CC EMBL: AF032387; AAC39663.1; -
CC EMBL: AF032386; AAC39664.1; -
CC EMBL: AF032385; AAC39665.1; -
CC EMBL: AF032384; AAC39666.1; -
CC EMBL: AF032383; AAC39667.1; -
CC EMBL: AF032382; AAC39668.1; -
CC EMBL: AF032381; AAC39669.1; -
CC EMBL: AF032380; AAC39670.1; -
CC EMBL: AF032379; AAC39671.1; -
CC EMBL: AF032378; AAC39672.1; -
CC EMBL: AF032377; AAC39673.1; -
CC EMBL: AF032376; AAC39674.1; -
CC EMBL: AF032375; AAC39675.1; -
CC EMBL: AF032374; AAC39676.1; -
CC EMBL: AF032373; AAC39677.1; -
CC EMBL: AF032372; AAC39678.1; -
CC EMBL: AF032371; AAC39679.1; -
CC EMBL: AF032370; AAC39680.1; -
CC EMBL: AF032369; AAC39681.1; -
CC EMBL: AF032368; AAC39682.1; -
CC EMBL: AF032367; AAC39683.1; -
CC EMBL: AF032366; AAC39684.1; -
CC EMBL: AF032365; AAC39685.1; -
CC EMBL: AF032364; AAC39686.1; -
CC EMBL: AF032363; AAC39687.1; -
CC EMBL: AF032362; AAC39688.1; -
CC EMBL: AF032361; AAC39689.1; -
CC EMBL: AF032360; AAC39690.1; -
CC EMBL: AF032359; AAC39691.1; -
CC EMBL: AF032358; AAC39692.1; -
CC EMBL: AF032357; AAC39693.1; -
CC EMBL: AF032356; AAC39694.1; -
CC EMBL: AF032355; AAC39695.1; -
CC EMBL: AF032354; AAC39696.1; -
CC EMBL: AF032353; AAC39697.1; -
CC EMBL: AF032352; AAC39698.1; -
CC EMBL: AF032351; AAC39699.1; -
CC EMBL: AF032350; AAC39700.1; -
CC EMBL: AF032349; AAC39701.1; -
CC EMBL: AF032348; AAC39702.1; -
CC EMBL: AF032347; AAC39703.1; -
CC EMBL: AF032346; AAC39704.1; -
CC EMBL: AF032345; AAC39705.1; -
CC EMBL: AF032344; AAC39706.1; -
CC EMBL: AF032343; AAC39707.1; -
CC EMBL: AF032342; AAC39708.1; -
CC EMBL: AF032341; AAC39709.1; -
CC EMBL: AF032340; AAC39710.1; -
CC EMBL: AF032339; AAC39711.1; -
CC EMBL: AF032338; AAC39712.1; -
CC EMBL: AF032337; AAC39713.1; -
CC EMBL: AF032336; AAC39714.1; -
CC EMBL: AF032335; AAC39715.1; -
CC EMBL: AF032334; AAC39716.1; -
CC EMBL: AF032333; AAC39717.1; -
CC EMBL: AF032332; AAC39718.1; -
CC EMBL: AF032331; AAC39719.1; -
CC EMBL: AF032330; AAC39720.1; -
CC EMBL: AF032329; AAC39721.1; -
CC EMBL: AF032328; AAC39722.1; -
CC EMBL: AF032327; AAC39723.1; -
CC EMBL: AF032326; AAC39724.1; -
CC EMBL: AF032325; AAC39725.1; -
CC EMBL: AF032324; AAC39726.1; -
CC EMBL: AF032323; AAC39727.1; -
CC EMBL: AF032322; AAC39728.1; -
CC EMBL: AF032321; AAC39729.1; -
CC EMBL: AF032320; AAC39730.1; -
CC EMBL: AF032319; AAC39731.1; -
CC EMBL: AF032318; AAC39732.1; -
CC EMBL: AF032317; AAC39733.1; -
CC EMBL: AF032316; AAC39734.1; -
CC EMBL: AF032315; AAC39735.1; -
CC EMBL: AF032314; AAC39736.1; -
CC EMBL: AF032313; AAC39737.1; -
CC EMBL: AF032312; AAC39738.1; -
CC EMBL: AF032311; AAC39739.1; -
CC EMBL: AF032310; AAC39740.1; -
CC EMBL: AF032309; AAC39741.1; -
CC EMBL: AF032308; AAC39742.1; -
CC EMBL: AF032307; AAC39743.1; -
CC EMBL: AF032306; AAC39744.1; -
CC EMBL: AF032305; AAC39745.1; -
CC EMBL: AF032304; AAC39746.1; -
CC EMBL: AF032303; AAC39747.1; -
CC EMBL: AF032302; AAC39748.1; -
CC EMBL: AF032301; AAC39749.1; -
CC EMBL: AF032300; AAC39750.1; -
CC EMBL: AF032299; AAC39751.1; -
CC EMBL: AF032298; AAC39752.1; -
CC EMBL: AF032297; AAC39753.1; -
CC EMBL: AF032296; AAC39754.1; -
CC EMBL: AF032295; AAC39755.1; -
CC EMBL: AF032294; AAC39756.1; -
CC EMBL: AF032293; AAC39757.1; -
CC EMBL: AF032292; AAC39758.1; -
CC EMBL: AF032291; AAC39759.1; -
CC EMBL: AF032290; AAC39760.1; -
CC EMBL: AF032289; AAC39761.1; -
CC EMBL: AF032288; AAC39762.1; -
CC EMBL: AF032287; AAC39763.1; -
CC EMBL: AF032286; AAC39764.1; -
CC EMBL: AF032285; AAC39765.1; -
CC EMBL: AF032284; AAC39766.1; -
CC EMBL: AF032283; AAC39767.1; -
CC EMBL: AF032282; AAC39768.1; -
CC EMBL: AF032281; AAC39769.1; -
CC EMBL: AF032280; AAC39770.1; -
CC EMBL: AF032279; AAC39771.1; -
CC EMBL: AF032278; AAC39772.1; -
CC EMBL: AF032277; AAC39773.1; -
CC EMBL: AF032276; AAC39774.1; -
CC EMBL: AF032275; AAC39775.1; -
CC EMBL: AF032274; AAC39776.1; -
CC EMBL: AF032273; AAC39777.1; -
CC EMBL: AF032272; AAC39778.1; -
CC EMBL: AF032271; AAC39779.1; -
CC EMBL: AF032270; AAC39780.1; -
CC EMBL: AF032269; AAC39781.1; -
CC EMBL: AF032268; AAC39782.1; -
CC EMBL: AF032267; AAC39783.1; -
CC EMBL: AF032266; AAC39784.1; -
CC EMBL: AF032265; AAC39785.1; -
CC EMBL: AF032264; AAC39786.1; -
CC EMBL: AF032263; AAC39787.1; -
CC EMBL: AF032262; AAC39788.1; -
CC EMBL: AF032261; AAC39789.1; -
CC EMBL: AF032260; AAC39790.1; -
CC EMBL: AF032259; AAC39791.1; -
CC EMBL: AF032258; AAC39792.1; -
CC EMBL: AF032257; AAC39793.1; -
CC EMBL: AF032256; AAC39794.1; -
CC EMBL: AF032255; AAC39795.1; -
CC EMBL: AF032254; AAC39796.1; -
CC EMBL: AF032253; AAC39797.1; -
CC EMBL: AF032252; AAC39798.1; -
CC EMBL: AF032251; AAC39799.1; -
CC EMBL: AF032250; AAC39800.1; -
CC EMBL: AF032249; AAC39801.1; -
CC EMBL: AF032248; AAC39802.1; -
CC EMBL: AF032247; AAC39803.1; -
CC EMBL: AF032246; AAC39804.1; -
CC EMBL: AF032245; AAC39805.1; -
CC EMBL: AF032244; AAC39806.1; -
CC EMBL: AF032243; AAC39807.1; -
CC EMBL: AF032242; AAC39808.1; -
CC EMBL: AF032241; AAC39809.1; -
CC EMBL: AF032240; AAC39810.1; -
CC EMBL: AF032239; AAC39811.1; -
CC EMBL: AF032238; AAC39812.1; -
CC EMBL: AF032237; AAC39813.1; -
CC EMBL: AF032236; AAC39814.1; -
CC EMBL: AF032235; AAC39815.1; -
CC EMBL: AF032234; AAC39816.1; -
CC EMBL: AF032233; AAC39817.1; -
CC EMBL: AF032232; AAC39818.1; -
CC EMBL: AF032231; AAC39819.1; -
CC EMBL: AF032230; AAC39820.1; -
CC EMBL: AF032229; AAC39821.1; -
CC EMBL: AF032228; AAC39822.1; -
CC EMBL: AF032227; AAC39823.1; -
CC EMBL: AF032226; AAC39824.1; -
CC EMBL: AF032225; AAC39825.1; -
CC EMBL: AF032224; AAC39826.1; -
CC EMBL: AF032223; AAC39827.1; -
CC EMBL: AF032222; AAC39828.1; -
CC EMBL: AF032221; AAC39829.1; -
CC EMBL: AF032220; AAC39830.1; -
CC EMBL: AF032219; AAC39831.1; -
CC EMBL: AF032218; AAC39832.1; -
CC EMBL: AF032217; AAC39833.1; -
CC EMBL: AF032216; AAC39834.1; -
CC EMBL: AF032215; AAC39835.1; -
CC EMBL: AF032214; AAC39836.1; -
CC EMBL: AF032213; AAC39837.1; -
CC EMBL: AF032212; AAC39838.1; -
CC EMBL: AF032211; AAC39839.1; -
CC EMBL: AF032210; AAC39840.1; -
CC EMBL: AF032209; AAC39841.1; -
CC EMBL: AF032208; AAC39842.1; -
CC EMBL: AF032207; AAC39843.1; -
CC EMBL: AF032206; AAC39844.1; -
CC EMBL: AF032205; AAC39845.1; -
CC EMBL: AF032204; AAC39846.1; -
CC EMBL: AF032203; AAC39847.1; -
CC EMBL: AF032202; AAC39848.1; -
CC EMBL: AF032201; AAC39849.1; -
CC EMBL: AF032200; AAC39850.1; -
CC EMBL: AF032199; AAC39851.1; -
CC EMBL: AF032198; AAC39852.1; -
CC EMBL: AF032197; AAC39853.1; -
CC EMBL: AF032196; AAC39854.1; -
CC EMBL: AF032195; AAC39855.1; -
CC EMBL: AF032194; AAC39856.1; -
CC EMBL: AF032193; AAC39857.1; -
CC EMBL: AF032192; AAC39858.1; -
CC EMBL: AF032191; AAC39859.1; -
CC EMBL: AF032190; AAC39860.1; -
CC EMBL: AF032189; AAC39861.1; -
CC EMBL: AF032188; AAC39862.1; -
CC EMBL: AF032187; AAC39863.1; -
CC EMBL: AF032186; AAC39864.1; -
CC EMBL: AF032185; AAC39865.1; -
CC EMBL: AF032184; AAC39866.1; -
CC EMBL: AF032183; AAC39867.1; -
CC EMBL: AF032182; AAC39868.1; -
CC EMBL: AF032181; AAC39869.1; -
CC EMBL: AF032180; AAC39870.1; -
CC EMBL: AF032179; AAC39871.1; -
CC EMBL: AF032178; AAC39872.1; -
CC EMBL: AF032177; AAC39873.1; -
CC EMBL: AF032176; AAC39874.1; -
CC EMBL: AF032175; AAC39875.1; -
CC EMBL: AF032174; AAC39876.1; -
CC EMBL: AF032173; AAC39877.1; -
CC EMBL: AF032172; AAC39878.1; -
CC EMBL: AF032171; AAC39879.1; -
CC EMBL: AF032170; AAC39880.1; -
CC EMBL: AF032169; AAC39881.1; -
CC EMBL: AF032168; AAC39882.1; -
CC EMBL: AF032167; AAC39883.1; -
CC EMBL: AF032166; AAC39884.1; -
CC EMBL: AF032165; AAC39885.1; -
CC EMBL: AF032164; AAC39886.1; -
CC EMBL: AF032163; AAC39887.1; -
CC EMBL: AF032162; AAC39888.1; -
CC EMBL: AF032161; AAC39889.1; -
CC EMBL: AF032160; AAC39890.1; -
CC EMBL: AF032159; AAC39891.1; -
CC EMBL: AF032158; AAC39892.1; -
CC EMBL: AF032157; AAC39893.1; -
CC EMBL: AF032156; AAC39894.1; -
CC EMBL: AF032155; AAC39895.1; -
CC EMBL: AF032154; AAC39896.1; -
CC EMBL: AF032153; AAC39897.1; -
CC EMBL: AF032152; AAC39898.1; -
CC EMBL: AF032151; AAC39899.1; -
CC EMBL: AF032150; AAC39900.1; -
CC EMBL: AF032149; AAC39901.1; -
CC EMBL: AF032148; AAC39902.1; -
CC EMBL: AF032147; AAC39903.1; -
CC EMBL: AF032146; AAC39904.1; -
CC EMBL: AF032145; AAC39905.1; -
CC EMBL: AF032144; AAC39906.1; -
CC EMBL: AF032143; AAC39907.1; -
CC EMBL: AF032142; AAC39908.1; -
CC EMBL: AF032141; AAC39909.1; -
CC EMBL: AF032140; AAC39910.1; -
CC EMBL: AF032139; AAC39911.1; -
CC EMBL: AF032138; AAC39912.1; -
CC EMBL: AF032137; AAC39913.1; -
CC EMBL: AF032136; AAC39914.1; -
CC EMBL: AF032135; AAC39915.1; -
CC EMBL: AF032134; AAC39916.1; -
CC EMBL: AF032133; AAC39917.1; -
CC EMBL: AF032132; AAC39918.1; -
CC EMBL: AF032131; AAC39919.1; -
CC EMBL: AF032130; AAC39920.1; -
CC EMBL: AF032129; AAC39921.1; -
CC EMBL: AF032128; AAC39922.1; -
CC EMBL: AF032127; AAC39923.1; -
CC EMBL: AF032126; AAC39924.1; -
CC EMBL: AF032125; AAC39925.1; -
CC EMBL: AF032124; AAC39926.1; -
CC EMBL: AF032123; AAC39927.1; -
CC EMBL: AF032122; AAC39928.1; -
CC EMBL: AF032121; AAC39929.1; -
CC EMBL: AF032120; AAC39930.1; -
CC EMBL: AF032119; AAC39931.1; -
CC EMBL: AF032118; AAC39932.1; -
CC EMBL: AF032117; AAC39933.1; -
CC EMBL: AF032116; AAC39934.1; -
CC EMBL: AF032115; AAC39935.1; -
CC EMBL: AF032114; AAC39936.1; -
CC EMBL: AF032113; AAC39937.1; -
CC EMBL: AF032112; AAC39938.1; -
CC EMBL: AF032111; AAC39939.1; -
CC EMBL: AF032110; AAC39940.1; -
CC EMBL: AF032109; AAC39941.1; -
CC EMBL: AF032108; AAC39942.1; -
CC EMBL: AF032107; AAC39943.1; -
CC EMBL: AF032106; AAC39944.1; -
CC EMBL: AF032105; AAC39945.1; -
CC EMBL: AF032104; AAC39946.1; -
CC EMBL: AF032103; AAC39947.1; -
CC EMBL: AF032102; AAC39948.1; -
CC EMBL: AF032101; AAC39949.1; -
CC EMBL: AF032100; AAC39950.1; -
CC EMBL: AF032099; AAC39951.1; -
CC EMBL: AF032098; AAC39952.1; -
CC EMBL: AF032097; AAC39953.1; -
CC EMBL: AF032096; AAC39954.1; -
CC EMBL: AF032095; AAC39955.1; -
CC EMBL: AF032094; AAC39956.1; -
CC EMBL: AF032093; AAC39957.1; -
CC EMBL: AF032092; AAC39958.1; -
CC EMBL: AF032091; AAC39959.1; -
CC EMBL: AF032090; AAC39960.1; -
CC EMBL: AF032089; AAC39961.1; -
CC EMBL: AF032088; AAC39962.1; -
CC EMBL: AF032087; AAC39963.1; -
CC EMBL: AF032086; AAC39964.1; -
CC EMBL: AF032085; AAC39965.1; -
CC EMBL: AF032084; AAC39966.1; -
CC EMBL: AF032083; AAC39967.1; -
CC EMBL: AF032082; AAC39968.1; -
CC EMBL: AF032081; AAC39969.1; -
CC EMBL: AF032080; AAC39970.1; -
CC EMBL: AF032079; AAC39971.1; -
CC EMBL: AF032078; AAC39972.1; -
CC EMBL: AF032077; AAC39973.1; -
CC EMBL: AF032076; AAC39974.1; -
CC EMBL: AF032075; AAC39975.1; -
CC EMBL: AF032074; AAC39976.1; -
CC EMBL: AF032073; AAC39977.1; -
CC EMBL: AF032072; AAC39978.1; -
CC EMBL: AF032071; AAC39979.1; -
CC EMBL: AF032070; AAC39980.1; -
CC EMBL: AF032069; AAC39981.1; -
CC EMBL: AF032068; AAC39982.1; -
CC EMBL: AF032067; AAC39983.1; -
CC EMBL: AF032066; AAC39984.1; -
CC EMBL: AF032065; AAC39985.1; -
CC EMBL: AF032064; AAC39986.1; -
CC EMBL: AF032063; AAC39987.1; -
CC EMBL: AF032062; AAC39988.1; -
CC EMBL: AF032061; AAC39989.1; -
CC EMBL: AF032060; AAC39990.1; -
CC EMBL: AF032059; AAC39991.1; -
CC EMBL: AF032058; AAC39992.1; -
CC EMBL: AF032057; AAC39993.1; -
CC EMBL: AF032056; AAC39994.1; -
CC EMBL: AF032055; AAC39995.1; -
CC EMBL: AF032054; AAC39996.1; -
CC EMBL: AF032053; AAC39997.1; -
CC EMBL: AF032052; AAC39998.1; -
CC EMBL: AF032051; AAC39999.1; -
CC EMBL: AF032050; AAC40000.1; -
CC EMBL: AF032049; AAC40001.1; -
CC EMBL: AF032048; AAC40002.1; -
CC EMBL: AF032047; AAC40003.1; -
CC EMBL: AF032046; AAC40004.1; -
CC EMBL: AF032045; AAC40005.1; -
CC EMBL: AF032044; AAC40006.1; -
CC EMBL: AF032043; AAC40007.1; -
CC EMBL: AF032042; AAC40008.1; -
CC EMBL: AF032041; AAC40009.1; -
CC EMBL: AF032040; AAC40010.1; -
CC EMBL: AF032039; AAC40011.1; -
CC EMBL: AF032038; AAC40012.1; -
CC EMBL: AF032037; AAC40013.1; -
CC EMBL: AF032036; AAC40014.1; -
CC EMBL: AF032035; AAC40015.1; -
CC EMBL: AF032034; AAC40016.1; -
CC EMBL: AF032033; AAC40017.1; -
CC EMBL: AF032032; AAC40018.1; -
CC EMBL: AF032031; AAC40019.1; -
CC EMBL: AF032030; AAC40020.1; -
CC EMBL: AF032029; AAC40021.1; -
CC EMBL: AF032028; AAC40022.1; -
CC EMBL: AF032027; AAC40023.1; -
CC EMBL: AF032026; AAC40024.1; -
CC EMBL: AF032025; AAC40025.1; -
CC EMBL: AF032024; AAC40026.1; -
CC EMBL: AF032023; AAC40027.1; -
CC EMBL: AF032022; AAC40028.1; -
CC EMBL: AF032021; AAC40029.1; -
CC EMBL: AF032020; AAC40030.1; -
CC EMBL: AF032019; AAC40031.1; -
CC EMBL: AF032018; AAC40032.1; -
CC EMBL: AF032017; AAC40033.1; -
CC EMBL: AF032016; AAC40034.1; -
CC EMBL: AF032015; AAC40035.1; -
CC EMBL: AF032014; AAC40036.1; -
CC EMBL: AF032013; AAC40037.1; -
CC EMBL: AF032012; AAC40038.1; -
CC EMBL: AF032011; AAC40039.1; -
CC EMBL: AF032010; AAC40040.1; -
CC EMBL: AF032009; AAC40041.1; -
CC EMBL: AF032008; AAC40042.1; -
CC EMBL: AF032007; AAC40043.1; -
CC EMBL: AF032006; AAC40044.1; -
CC EMBL: AF032005; AAC40045.1; -
CC EMBL: AF032004; AAC40046.1; -
CC EMBL: AF032003; AAC40047.1; -
CC EMBL: AF032002; AAC40048.1; -
CC EMBL: AF032001; AAC40049.1; -
CC EMBL: AF032000; AAC40050.1; -
CC EMBL: AF031999; AAC40051.1; -
CC EMBL: AF031998; AAC40052.1; -
CC EMBL: AF031997; AAC40053.1; -
CC EMBL: AF031996; AAC40054.1; -
CC EMBL: AF031995; AAC40055.1; -
CC EMBL: AF031994; AAC40056.1; -
CC EMBL: AF031993; AAC40057.1; -
CC EMBL: AF031992; AAC40058.1; -
CC EMBL: AF031991; AAC40059.1; -
CC EMBL: AF031990; AAC40060.1; -
CC EMBL: AF031989; AAC40061.1; -
CC EMBL: AF031988; AAC40062.1; -
CC EMBL: AF031987; AAC40063.1; -
CC EMBL: AF031986; AAC40064.1; -
CC EMBL: AF031985; AAC40065.1; -
CC EMBL: AF031984; AAC40066.1; -
CC EMBL: AF031983; AAC40067.1; -
CC EMBL: AF031982; AAC40068.1; -
CC EMBL: AF031981; AAC40069.1; -
CC EMBL: AF031980; AAC40070.1
```


[illegible]

```

Query Match Similarity    37.0%; Score 51; DB 10; Length 231;
Best Local Similarity    44.4%; Pred. No. 11;
Matches    12; Conservative    3; Mismatches    4; Indels    8; Gaps    1.

QY      6 QRYG-----RELKMSDFEESER 24
          |||||:||||:||||:
DB     107 QRLGECLDKIDVGLADLDEWNTFR 133

RESULT 4
Q95703 PRELIMINARY; PRT; 232 AA.
NC_095703.1
AC   Q95703.1
DT   01-MAY-2000 (Tremblay, 13, Created)
PT   01-MAY-2000 (Tremblay, 13, Sequence update)
DR   01-JUN-2001 (Tremblay, 17, Last annotation update)
DE   FLORAL HOMEOTIC PROTEIN AP3.
GN   APERIALA3.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
SC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
SX   eurosid2.11; Brassicales; Brassicaceae; Arabidopsids.
NCBI_TaxID=3702.

Query Match    37.0%; Score 51; DB 10; Length 232;
Best Local Similarity    44.4%; Pred. No. 11;
Matches    12; Conservative    3; Mismatches    4; Indels    8; Gaps    1.

DY      6 QRYG-----RELKMSDFEESER 24
          |||||:||||:||||:
DB     107 QRLGECLDKIDVGLADLDEWNTFR 133

RESULT 5
Q9SQZ2 PRELIMINARY; PRT; 232 AA.
NC_09SQZ2.1
AC   Q9SQZ2.1
DT   01-MAY-2000 (Tremblay, 13, Created)
PT   01-MAY-2000 (Tremblay, 13, Last sequence update)
DR   01-DEC-2001 (Tremblay, 19, Last annotation update)
DE   FLORAL HOMEOTIC PROTEIN AP3.
GN   APERIALA3.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
SC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
SX   eurosid2.11; Brassicales; Brassicaceae; Arabidopsids.
NCBI_TaxID=3702.

```

```

RN [1]
RD SEQUENCE FROM N.A.
RX MEDLINE-CV: LI-8. PubMed-9927474;
RA Purganan M.D., Sudduth J.I.;
RT "Molecular population genetics of floral homeotic loci. Departures
RT from the equilibrium-neutral model at the APTALA3 and PISTILLATA
RT genes of Arabidopsis thaliana."
RL Genetics 151:839-848(1999).
CC -1- SUPRACELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SUPRACELLULAR LOCATION: NUCLEAR DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL: AF15801.1;
DR HSP: P11766; IWM.
DR InterPro: IPR002487; K-box.
DR Pfam: PF01486; K-box.
DR Pfam: PF00319; SRF-TP; 1.
DR PRINTS: PR00404; MADS1DOMAIN.
DR SMART: SM00432; MADS1_BOX_1; 1.
DR PROSITE: PS00656; MADS_BOX_2; 1.
DR PROSITE: PS00656; MADS_BOX_2; 1.
DR DNA-binding: Nuclear protein; Transcription regulation.
KW SEQUENCE 232 AA; 27267 MW; 42A852D697E22A65 CRC64;
SQ
Query Match 37.08; Score 51; DB 10; Length 232;
Best Local Similarity 44.48; Pred. No. 11;
Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;
QY 6 ORFG-----RELRRMSDFEGSGFK 24
DB 107 ORFGCLDLDIOELRLDEDMENFK 133
RESULT 6
ID 095021 PRELIMINARY; PRT; 232 AA.
AC 095021;
DT 01-MAY-2000 (TREMBLER, 13, Created)
DT 01-MAY-2000 (TREMBLER, 13, Last sequence update)
DT 01-DEC-2001 (TREMBLER, 19, Last annotation update)
DE FLORAL HOMEOTIC PROTEIN AP3.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RD SEQUENCE FROM N.A.
RX MEDLINE-CV: LI-8. PubMed-9927474;
RA Purganan M.D., Sudduth J.I.;
RT "Molecular population genetics of floral homeotic loci. Departures
RT from the equilibrium-neutral model at the APTALA3 and PISTILLATA
RT genes of Arabidopsis thaliana."
RL Genetics 151:839-848(1999).
CC -1- SUPRACELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SUPRACELLULAR LOCATION: NUCLEAR DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL: AF15801.1;
DR HSP: P11766; IWM.
DR InterPro: IPR002487; K-box.
DR Pfam: PF01486; K-box.
DR Pfam: PF00319; SRF-TP; 1.
DR PRINTS: PR00404; MADS1DOMAIN.
DR SMART: SM00432; MADS1_BOX_1; 1.
DR PROSITE: PS00656; MADS_BOX_2; 1.
DR PROSITE: PS00656; MADS_BOX_2; 1.
DR DNA-binding: Nuclear protein; Transcription regulation.
KW SEQUENCE 232 AA; 27267 MW; 66976305B8B63B3 CRC64;
SQ

```

```

Query Match 37.08; Score 51; DB 10; Length 232;
Best Local Similarity 44.48; Pred. No. 11;
Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;
QY 6 ORFG-----RELRRMSDFEGSGFK 24
DB 107 ORFGCLDLDIOELRLDEDMENFK 133
RESULT 7
ID 095020 PRELIMINARY; PRT; 232 AA.
AC 095020;
DT 01-MAY-2000 (TREMBLER, 13, Created)
DT 01-MAY-2000 (TREMBLER, 13, Last sequence update)
DT 01-DEC-2001 (TREMBLER, 19, Last annotation update)
DE FLORAL HOMEOTIC PROTEIN AP3.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RD SEQUENCE FROM N.A.
RX MEDLINE-CV: CONSCLDA. PubMed-9927474;
RA Purganan M.D., Sudduth J.I.;
RT "Molecular population genetics of floral homeotic loci. Departures
RT from the equilibrium-neutral model at the APTALA3 and PISTILLATA
RT genes of Arabidopsis thaliana."
RL Genetics 151:839-848(1999).
CC -1- SUPRACELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SUPRACELLULAR LOCATION: NUCLEAR DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL: AF15801.1;
DR HSP: P11766; IWM.
DR InterPro: IPR002487; K-box.
DR Pfam: PF01486; K-box.
DR Pfam: PF00319; SRF-TP; 1.
DR PRINTS: PR00404; MADS1DOMAIN.
DR SMART: SM00432; MADS1_BOX_1; 1.
DR PROSITE: PS00656; MADS_BOX_2; 1.
DR PROSITE: PS00656; MADS_BOX_2; 1.
DR DNA-binding: Nuclear protein; Transcription regulation.
KW SEQUENCE 232 AA; 27342 MW; BDPCB5B973FA601 CRC64;
SQ
Query Match 37.08; Score 51; DB 10; Length 232;
Best Local Similarity 44.48; Pred. No. 11;
Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;
QY 6 ORFG-----RELRRMSDFEGSGFK 24
DB 107 ORFGCLDLDIOELRLDEDMENFK 133
RESULT 8
ID 095019 PRELIMINARY; PRT; 232 AA.
AC 095019;
DT 01-MAY-2000 (TREMBLER, 13, Created)
DT 01-MAY-2000 (TREMBLER, 13, Last sequence update)
DT 01-JUN-2001 (TREMBLER, 17, Last annotation update)
DE FLORAL HOMEOTIC PROTEIN AP3.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RD SEQUENCE FROM N.A.

```


DR HSP: P11746; 1MM.
 DR InterPro: IPR002487; K-box.
 DR InterPro: IPR002100; MADS-box.
 DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SRP-TE; 1.
 DR PRINTS: PR00404; MADSOMAIN.
 DR SMART: SM00432; MADS; 1.
 DR PROSITE: PS00350; MADS_BOX_1; 1.
 DR PROSITE: PS50066; MADS_BOX_2; 1.
 DR DNA-binding: Nuclear protein; Transcription regulation.
 KW DBRCN1C835557D6 CRG64;
 SQ SEQUENCE 232 AA; 27314 MW; DBRCN1C835557D6 CRG64;

Query Match 37.0%; Score 51; DB 10; Length 232;
 Best Local Similarity 44.4%; Pred. No. 11;
 Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;

OY 6 ORYG-----RELRMSDEFGSGF 24
 DB 107 QRGRCUDELIDQELRLLEDMNTRK 133
 :||||:||||:|||||

RESULT 12

OS05 PRELIMINARY; PRT; 232 AA.

AC OS05:
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE FLORAL HOMEOTIC PROTEIN AP3.
 GN APERLAL3.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopses.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, KAS-1;
 RX MEDLINE=99126449; PubMed=9927474;
 RA Purugganan M.D., Sudduth J.I.;
 RT "Molecular population genetics of floral homeotic loci, departures
 from the equilibrium-neutral model at the APERLAL3 and PISTILLATA
 genes of Arabidopsis thaliana."
 RL Genetics 151:839-848(1999)
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
 DR HSP: P115812; AAD51901.1;
 DR HSP: P11746; 1MM.
 DR InterPro: IPR002487; K-box.
 DR InterPro: IPR002100; MADS-box.
 DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SRP-TE; 1.
 DR PRINTS: PR00404; MADSOMAIN.
 DR SMART: SM00432; MADS; 1.
 DR PROSITE: PS00350; MADS_BOX_1; 1.
 DR PROSITE: PS50066; MADS_BOX_2; 1.
 DR DNA-binding: Nuclear protein; Transcription regulation.
 KW DBRCN1C835557D6 CRG64;
 SQ SEQUENCE 232 AA; 27300 MW; 5CA05FD4F824DF0 CRG64;

Query Match 37.0%; Score 51; DB 10; Length 232;
 Best Local Similarity 44.4%; Pred. No. 11;
 Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;

OY 6 ORYG-----RELRMSDEFGSGF 24
 DB 107 QRGRCUDELIDQELRLLEDMNTRK 133
 :||||:||||:|||||

RESULT 13
 OS05 PRELIMINARY; PRT; 904 AA.

AC OS05:
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE NADH DEHYDROGENASE 1 SUBUNIT G.
 GN NUCG.
 OS Pseudomonas fluorescens.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae.
 OC Pseudomonas.
 OX NCBI_TaxID=294;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WC395;
 RA "Characterization of NADH dehydrogenases of Pseudomonas fluorescens
 WC395 and their role in competitive root colonization."
 RT Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
 RL EMBL: AF281148; AA897803.1;
 DR InterPro: IPR002283; Complex_L75K;
 DR PROSITE: PS00841; COMPLEX_L75K_1; 1.
 DR PROSITE: PS00842; COMPLEX_L75K_2; 1.
 DR PROSITE: PS00843; COMPLEX_L75K_3; 1.
 SQ SEQUENCE 904 AA; 98157 MW; C25B66C6DADF457 CRG64;

Query Match 36.6%; Score 50.5; DB 2; Length 904;
 Best Local Similarity 50.0%; Pred. No. 63;
 Matches 11; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

OY 1 NLMADRGRELRMSDEFGS 22
 DB 236 NISGGRG-ELRLINRFNS 256
 :||||:||||:|||||

RESULT 14

OS05 PRELIMINARY; PRT; 283 AA.

AC OS05:
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
 GN ENV.
 OS Chimpense immunodeficiency virus (SIVcpz) (CIV).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11723;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SVACMPRL185;
 RX MEDLINE=98343740; PubMed=9680146;
 RA von Hennburg E.J., Engelbrecht S., Mwenda J., Laten J.D., Robson B.A.,
 BA Steiner J., Chage G.K.;
 RT "African immunodeficiency viruses (SIVs) from eastern and southern
 Africa: detection of a SVAGmutant from a chacma baboon."
 RL J. Gen. Virol. 79:1882-1814(1998).
 DR EMBL: AF015909; AA536621.1;
 DR InterPro: IPR000772; GP120.
 DR Pfam: PF00516; GP120; 1.
 KW AIDS; coat protein; Glycoprotein.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 283 AA; 32477 MW; 49BD545018A2871 CRG64;

Query Match 36.2%; Score 50; DB 15; Length 283;
 Best Local Similarity 42.9%; Pred. No. 20;
 Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 5 AORRGRELRMSDEFGSGF 25
 DB 74 SOKINRLKNSCHFGNWK 94
 :|||:||||:|||||

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2002, 10:35:57 : Search time 228.86 seconds
(without alignments)

13,104 Million cell updates/sec

Title: US-09-544-664-14

Perfect score: 137

Sequence: 1 OEDINARHLAQVGSMDRIPPGL 27

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 11107396 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: A Genesec 032802.*

1: /SIDSI/gcgdata/hold-genesec/genesecp-emb1/AA1980.DAT.*
2: /SIDSI/gcgdata/hold-genesec/genesecp-emb1/AA1981.DAT.*
3: /SIDSI/gcgdata/hold-genesec/genesecp-emb1/AA1982.DAT.*
4: /SIDSI/gcgdata/hold-genesec/genesecp-emb1/AA1983.DAT.*
5: /SIDSI/gcgdata/hold-genesec/genesecp-emb1/AA1984.DAT.*
6: /SIDSI/gcgdata/hold-genesec/genesecp-emb1/AA1985.DAT.*
7: /SIDSI/gcgdata/hold-genesec/genesecp-emb1/AA1986.DAT.*
8: /SIDSI/gcgdata/hold-genesec/genesecp-emb1/AA1987.DAT.*
9: /SIDSI/gcgdata/hold-genesec/genesecp-emb1/AA1988.DAT.*
10: /SIDSI/gcgdata/hold-genesec/genesecp-emb1/AA1989.DAT.*
11: /SIDSI/gcgdata/hold-genesec/genesecp-emb1/AA1990.DAT.*
12: /SIDSI/gcgdata/hold-genesec/genesecp-emb1/AA1991.DAT.*
13: /SIDSI/gcgdata/hold-genesec/genesecp-emb1/AA1992.DAT.*
14: /SIDSI/gcgdata/hold-genesec/genesecp-emb1/AA1993.DAT.*
15: /SIDSI/gcgdata/hold-genesec/genesecp-emb1/AA1994.DAT.*
16: /SIDSI/gcgdata/hold-genesec/genesecp-emb1/AA1995.DAT.*
17: /SIDSI/gcgdata/hold-genesec/genesecp-emb1/AA1996.DAT.*
18: /SIDSI/gcgdata/hold-genesec/genesecp-emb1/AA1997.DAT.*
19: /SIDSI/gcgdata/hold-genesec/genesecp-emb1/AA1998.DAT.*
20: /SIDSI/gcgdata/hold-genesec/genesecp-emb1/AA1999.DAT.*
21: /SIDSI/gcgdata/hold-genesec/genesecp-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/hold-genesec/genesecp-emb1/AA2001.DAT.*

pred. No. is the number of results predicted by chance to have a score greater than the highest score of the alignment printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	137	100.0	27	21 AAB37014	Bcl2 polypeptide B
2	137	100.0	135	21 AAB4017	Amino acid sequence
3	137	100.0	135	21 AAB4018	Amino acid sequence
4	137	100.0	135	21 AAB4019	Amino acid sequence
5	137	100.0	135	21 AAB4020	Amino acid sequence
6	137	100.0	135	21 AAB4021	Amino acid sequence
7	137	100.0	135	21 AAB4022	Amino acid sequence
8	137	100.0	135	21 AAB4023	Amino acid sequence
9	137	100.0	135	21 AAB4024	Amino acid sequence
10	137	100.0	135	21 AAB4025	Amino acid sequence
11	137	100.0	135	21 AAB4026	Amino acid sequence
12	137	100.0	135	21 AAB4027	Amino acid sequence
13	137	100.0	135	21 AAB4028	Amino acid sequence
14	137	100.0	135	21 AAB4029	Amino acid sequence
15	137	100.0	135	21 AAB4030	Amino acid sequence
16	137	100.0	135	21 AAB4031	Amino acid sequence
17	137	100.0	135	21 AAB4032	Amino acid sequence
18	137	100.0	135	21 AAB4033	Amino acid sequence
19	137	100.0	135	21 AAB4034	Amino acid sequence
20	137	100.0	135	21 AAB4035	Amino acid sequence
21	137	100.0	135	21 AAB4036	Amino acid sequence
22	137	100.0	135	21 AAB4037	Amino acid sequence
23	137	100.0	135	21 AAB4038	Amino acid sequence
24	137	100.0	135	21 AAB4039	Amino acid sequence
25	137	100.0	135	21 AAB4040	Amino acid sequence
26	137	100.0	135	21 AAB4041	Amino acid sequence
27	137	100.0	135	21 AAB4042	Amino acid sequence
28	137	100.0	135	21 AAB4043	Amino acid sequence
29	137	100.0	135	21 AAB4044	Amino acid sequence
30	137	100.0	135	21 AAB4045	Amino acid sequence
31	137	100.0	135	21 AAB4046	Amino acid sequence
32	137	100.0	135	21 AAB4047	Amino acid sequence
33	137	100.0	135	21 AAB4048	Amino acid sequence
34	137	100.0	135	21 AAB4049	Amino acid sequence
35	137	100.0	135	21 AAB4050	Amino acid sequence
36	137	100.0	135	21 AAB4051	Amino acid sequence
37	137	100.0	135	21 AAB4052	Amino acid sequence
38	137	100.0	135	21 AAB4053	Amino acid sequence
39	137	100.0	135	21 AAB4054	Amino acid sequence
40	137	100.0	135	21 AAB4055	Amino acid sequence
41	137	100.0	135	21 AAB4056	Amino acid sequence
42	137	100.0	135	21 AAB4057	Amino acid sequence
43	137	100.0	135	21 AAB4058	Amino acid sequence
44	137	100.0	135	21 AAB4059	Amino acid sequence
45	137	100.0	135	21 AAB4060	Amino acid sequence

12	113	82.5	29	19	AAW50273
13	99	72.3	27	21	AAB37015
14	99	72.3	32	19	AAW50264
15	99	72.3	33	19	AAW50265
16	99	72.3	44	19	AAW50266
17	99	72.3	135	19	AAW50267
18	99	72.3	135	19	AAW50268
19	99	72.3	135	19	AAW50269
20	99	72.3	135	19	AAW50270
21	99	72.3	135	19	AAW50271
22	99	72.3	135	19	AAW50272
23	98	71.5	165	22	AAW50273
24	98	71.5	165	22	AAW50274
25	98	71.5	165	22	AAW50275
26	98	71.5	165	22	AAW50276
27	98	71.5	165	22	AAW50277
28	98	71.5	165	22	AAW50278
29	98	71.5	165	22	AAW50279
30	98	71.5	165	22	AAW50280
31	98	71.5	165	22	AAW50281
32	98	71.5	165	22	AAW50282
33	98	71.5	165	22	AAW50283
34	98	71.5	165	22	AAW50284
35	98	71.5	165	22	AAW50285
36	98	71.5	165	22	AAW50286
37	98	71.5	165	22	AAW50287
38	98	71.5	165	22	AAW50288
39	98	71.5	165	22	AAW50289
40	98	71.5	165	22	AAW50290
41	98	71.5	165	22	AAW50291
42	98	71.5	165	22	AAW50292
43	98	71.5	165	22	AAW50293
44	98	71.5	165	22	AAW50294
45	98	71.5	165	22	AAW50295

ALIGNMENTS

RESULT 1

AAB37014 standard: peptide: 27 AA.

AAB37014:

28-FEB-2001 (first entry)

Bcl2 polypeptide B13 domain peptide #14.

Cytostatic: neuroprotective; anti-HIV; virucide; cerebroprotective;

cardinal; Bcl-2 superfamily; Bcl-2 domain; cell death agonist; Bad;

apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;

colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;

melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;

stroke; myocardial infarction.

Homo sapiens.

WO200059526-A1.

12-OCT-2000.

06-APR-2000: 2000MO-US09352.

07-APR-1999: 9905-0128202.

(GIDE-) UNIV JEFFERSON THOMAS.

Huang Z, Wang J, Zhang Z, Shan S, Lu Z.

WPI: 2000-679325/66.

New peptide conjugates for modulating apoptosis or for inhibiting B

cell death.

PT

CC portion (e.g. AA00607) for increasing the stability of the fused
 CC protein as compared to the human protein only.
 CC The invention relates to 87 novel genes and their fragments (nucleic
 CC acid sequences: AA00611-X00724; amino acid sequences AA67807-W68094)
 CC which are useful for preventing, treating or ameliorating medical
 CC conditions e.g. by protein or gene therapy. Also, pathological
 CC polypeptides can be diagnosed by determining the amount of the new
 CC polypeptides in a sample or by determining the presence of mutations in
 CC the new polynucleotides. Specific uses are described for each of the 87
 CC polynucleotides, based on which tissues they are most highly expressed in
 CC (see AA00611 for described uses).

SO Sequence 195 AA:

Query Match 100.0%; Score 137; DB 20; Length 195;
 Best Local Similarity 100.0%; Pred. No. 8, 9e-14;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GEDIRNFARHLAQVDSMORSLPPGL 27
 Db 79 qedirnfarhlavqdsmsrslppgl 105

RESULT 8

AA084015 standard; protein: 195 AA.

AC AA084015:

DT 03-JUL-2000 (first entry)

XX Amino acid sequence of human BID polypeptide.

KM BID: p15 BID: cell death agonist; tumour necrosis factor; FAS signalling;
 KW cytochrome C.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Cleavage-site 60..61 /note= "caspase cleavage site"

FT Domain 50..98 /note= "BH3 domain"

XX MO200011162-A1.

XX 02-MAR-2000.

XX 28-JUL-1999; 99WO-US16966.

XX 19-AUG-1998; 98US-0136879.

XX 20-AUG-1998; 98US-0137038.

XX (UNIW) UNIV WASHINGTON.

XX Gross A. Korsmeyer SJ;

XX WPI: 2000-224697/19.

XX Human and murine p15 BID polypeptides with cell death agonist activity
 PT are produced by caspase cleavage of BID in cells undergoing FAS or
 PT tumour necrosis mediated cell death, useful as modulators of target cell
 PT death.

XX Claim 3, Fig 1, 55pp; English.

XX The present sequence represents a human BID polypeptide. The
 CC specification describes p15 BID polypeptides which have cell death
 CC agonist activity. Cell death mediated by tumour necrosis factor (TNF)
 CC and FAS signalling pathways includes the generation of p15 BID, which
 CC is translocated to the mitochondria where it exerts cell death agonist
 CC activity, probably by inducing release of cytochrome C. The p15 BID

CC polypeptides are useful in methods for modulating death of a target
 CC cell. Mutants of p15 BID, comprising an inactivating mutation in the
 CC BH3 domain, are used in methods for inhibiting death of a target cell.
 CC Agents that specifically inhibit caspase cleavage of p22 BID at the
 CC p15 cleavage site are also useful for inhibiting death of a target
 CC cell.

SO Sequence 195 AA:

Query Match 100.0%; Score 137; DB 21; Length 195;
 Best Local Similarity 100.0%; Pred. No. 8, 9e-14;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GEDIRNFARHLAQVDSMORSLPPGL 27
 Db 79 qedirnfarhlavqdsmsrslppgl 105

RESULT 9

AA050255 standard; protein: 200 AA.

AC AA050255:

DT 20-JUL-1998 (first entry)

XX Human BH3 interacting domain death agonist protein variant.

KM Human; BH3 interacting domain death agonist; BID; BCL-2 family;
 KW apoptosis; regulation; cell death; inflammation; cancer; arthritis;
 KW autoimmune disease; viral infection; lymphoproliferative.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 166 /note= "encoded by TRGS"

FT Misc-difference 175 /note= "encoded by GR"

XX WO9809980-A1.

XX 12-MAR-1998.

XX 09-SEP-1997; 97WO-US15872.

XX 09-SEP-1996; 96US-0706741.

XX (UNIW) UNIV WASHINGTON.

XX Korsmeyer SJ;

XX WPI: 1998-193546/17.

XX N-FSDB; AA022146.

XX BH3 interacting domain death agonist polypeptide - used for treating
 XX decreased apoptotic conditions resulting from inflammation etc.

XX Claim 4: Page 69; 118pp; English.

XX The present sequence represents a BH3 interacting domain death agonist
 CC (BID) protein given in the present invention. The protein, the DNA
 CC encoding it or antisense sequences can be used for preventing or treating
 CC a decreased apoptotic state of a cell. The decreased apoptotic state that
 CC is treated results from a disease such as cancer, viral infections,
 CC lymphoproliferative conditions, autoimmune disease, inflammation,
 CC autoimmune disease, viral infection, lymphoproliferative conditions,
 CC BID polypeptide in a cell or population of cell. The nucleic acid
 CC sequence and the BID protein can also be used for treating
 CC immunodeficiency disease (including AIDS), senescence, neurodegenerative
 CC disease, ischemic and reperfusion cell death, infertility and
 CC wound-healing. Primers derived from the nucleic acid encoding the BID

CC protein can be used for detecting/quantitating the protein and for
 CC detecting alterations in the nucleic acid encoding the BID protein.
 XX
 SO Sequence 200 AA;

Query Match 100.0%; Score 137; DB 19; Length 200;
 Best Local Similarity 100.0%; Pred. No. 9.1e-14;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IIRNIAHRLAOGDSMDRSLPPGL 27
 DB 79 qedllrniahrlaogdsmdrslppgl 105

RESULT 10

AAV96325 standard; Peptide: 26 AA.

AAV96325:

17-AUG-2000 (first entry)

Mammalian Bid Bcl-2 homology domain 3 domain.

Mammal: apoptosis; cell death; BPC3; apoptosis promotion; Bid;
 apoptosis inhibition; malignant cell; autoimmune disease.

Mammalia.

WO200026228-A1.

11-MAY-2000.

28-OCT-1999; 99NO-US25285.

02-NOV-1998; 98US-0184168.

(CLON-) CLOUTCH LAB INC.

Zhu L, Yin X, Chittenden T;

WPI: 2000-365560/31.

Novel polynucleotide encoding a BPC3 protein which is useful for
 treating diseases, especially in the treatment of cancer and
 autoimmune diseases.

Disclosure: Fig 4; 47pp; English.

The present sequence is the mammalian Bid Bcl-2 homology domain 3
 (BH3) domain, which was used in a sequence alignment with the same
 domain of a putative version of the mammalian apoptosis
 regulator BPC3, which was designated BPC3-ORF2. The BPC3 protein,
 nucleic acids and antibodies are suitable for use in promoting cell
 death or for preventing apoptosis in malignant cells and those causing
 autoimmune diseases.

Sequence 26 AA;

Query Match 88.3%; Score 121; DB 21; Length 26;
 Best Local Similarity 100.0%; Pred. No. 3.2e-12;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 IIRNIAHRLAOGDSMDRSLPPGL 27
 DB 1 IIRNIAHRLAOGDSMDRSLPPGL 24

RESULT 11

AAV70375 standard; Peptide: 26 AA.

AAV70375;
 02-MAY-2001 (first entry)

BID BH3 consensus peptide sequence SEQ ID NO:8.

Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
 immunostimulant; neuroprotective; necrotic; antileukemic; vulnery;
 cytostatic; antiviral; antitumor; antileukemic; wound healing;
 immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;
 immunodeficiency disease; neurodegenerative disease; viral infection;
 ischemic cell death; reperfusion cell death; arthritis; interstitial;
 lymphoproliferative condition; inflammation; autoimmune disease.

Unidentified.

WO200110888-A1.

15-FEB-2001.

30-MAY-2000; 2000WO-US11864.

28-MAY-1999; 99US-0136783.

(APOF-) APOPTOSIS TECHNOLOGY INC.

Zhou X;

WPI: 2001-138734/14.

New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,
 useful for screening for candidate compounds which induce or inhibit
 apoptosis, comprises amino acid substitutions at Ser18, Ser15 or
 Ser13.

Example 2; Fig 3e; 157pp; English.

The present invention describes an isolated or synthetic polypeptide
 (1) comprising a less than full length amino acid sequence of a mutant
 Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its
 fragment, which contains amino acid substitutions at Ser18 of a human
 BAD (Ser15 of a murine BAD (longer murine BAD) or Ser13 of a murine
 BAD (shorter murine BAD). (1) has immunostimulant, neuroprotective,
 necrotic, antileukemic, vulnery, cytostatic, antiviral, and
 antitumor, antileukemic, and immunosuppressive activities, and
 is useful for screening for candidate compounds which induce or inhibit
 apoptosis. Other uses include for active cell survival or apoptosis. Other uses include
 inducing or inhibiting apoptosis in a cell. Candidate compounds
 identified and (mutant) BAD polypeptides are useful in treating
 immunodeficiency diseases, neurodegenerative diseases, ischemic cell
 death, reperfusion cell death, wound healing, cancer, viral infections,
 lymphoproliferative conditions, arthritis, interstitial, inflammation and
 autoimmune diseases. The present sequence represents a Bcl family member
 BH3 domain consensus sequence which is used in an example from the
 present invention.

Sequence 26 AA;

Query Match 88.3%; Score 121; DB 22; Length 26;
 Best Local Similarity 100.0%; Pred. No. 3.2e-12;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 IIRNIAHRLAOGDSMDRSLPPGL 27
 DB 1 IIRNIAHRLAOGDSMDRSLPPGL 24

RESULT 12

AAV50273 standard; Peptide: 29 AA.

[illegible]

KW	colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
KM	melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
KN	stroke; myocardial infarction.
XX	
OS	homo sapiens .
PX	WC0200059526-A1 .
PN	
PD	12-OCT-2000 .
PF	06-APR-2000; 200OMO-W0809352 .
PI	
PR	07-APR-1999; : 99US-0128302 .
PA	(UYJE-Y) UNTV JEFFERSON THOMAS .
PZ	
PT	Huang Z , Wang Z , Zhang Z , Shan S , Lu Z ;
DR	WPI : 2000-6793325/66 .
XN	New peptide conjugates for modulating apoptosis or for inhibiting B
XX	cell lymphomaleukemia 2 (bel-2) function, especially useful for
PS	treating neurodegenerative disorders, stroke, or cancer
XX	
PL	Claim 18; Page 18; 74pp: English.
XX	
CC	The invention relates to a peptide conjugate having the formula:
CC	(R-X)-peptide where R = 1-10; X = C=O. When the R-X group is attached
CC	to the amino terminus of the peptide chain, the functional group of the
CC	functional group of the side chain is NH ₂ or OH; or X=O or NH,
CC	when the R-X group is attached to the C-terminus of the peptide, or a
CC	side chain of the peptide, where the side chain functional group is COOH
CC	or CONH ₂ , and R = 2-18c alky or alkoxy, 2-14c alkylenyl containing one
CC	or two double bonds, cyclohexyl, cyclopentyl, cyclohexenyl optionally
CC	monosubstituted with a methyl or ethyl substituent, or 1-5c straight or branched chain
CC	alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples
CC	of the peptide portion of the conjugate. The peptides represent analogues
CC	of a bel-2 superfamily polypeptide corresponding to amino acids 72-97 of
CC	the BH3 domain of the cell death agonist bcl-2. The peptide conjugate is
CC	useful for modulating apoptosis in the cells and tissues and for blocking of
CC	apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
CC	function. In particular, the peptide conjugate is useful for treating a
CC	disease afflicted with a cancer characterized by cancer cells that
CC	express Bcl-2. The cancer includes prostate, colorectal, gastric,
CC	non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
CC	acute or chronic lymphocytic and non-lymphocytic leukemias. The peptide
CC	conjugate is useful for inducing apoptosis in cancer cells characterized by
CC	increased apoptosis e.g., neurodegenerative disorders, acquired
CC	immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
XX	
SU	Sequence 27 AA:
OY	Query Match 72.3%; Score 99; DN 21; Length 27; Best Local Similarity 70.4%; Prod. No. 1,1e+08; Matches 19; Conservative 3; Mismatches 5; Indels 0; Gaps 0; DB 1 OEDTIRINHAAGVGDSMDKSTIPQI 27 II::III IIIIIIIIIII I ::I I 27
ID	AAM50264 standard; peptide: 32 AA.
AA	AAM50264;
DJ	20-JUL-1998 (first entry)
DE	Mouse BID BH3 domain peptide A.

```

XX Mouse: BH3 interacting domain death agonist; BID; BCL-2 family;
KW apoptosis; regulation; cell death; inflammation; cancer; arthritis;
KW autoimmune disease; viral infection; lymphoproliferative.
XX
XX Mus sp.
XX
XX W0980980-A1.
XX
XX PD 12-MAR-1998.
XX
XX 09-SEP-1997; 97MO-US15872.
XX
XX 09-SEP-1996; 96US-0706741.
XX
XX (UNIW ) UNIV WASHINGTON.
XX
XX Korsmeyer SJ.
XX
XX WPI: 1998-193546/17.
XX
XX BH3 interacting domain death agonist polypeptide - used for treating
XX decreased apoptotic conditions resulting from inflammation etc.
XX
XX Example 8; Page 85; 118pp; English.
XX
XX The present sequence represents a BH3 interacting domain death agonist
XX (BID) BH3 domain peptide given in the present invention. The protein, the
XX DNA encoding it or antisense sequences can be used for preventing or
XX treating a decreased apoptotic state of a cell. The decreased apoptotic
XX state can be used for treating a decreased apoptotic state of a cell.
XX infections, lymphoproliferative conditions arthritis inflammation and
XX autoimmune diseases. Antibodies against the BID protein can be used for
XX detecting a BID polypeptide in a cell or population of cell. The nucleic
XX acid sequence and the BID protein can also be used for treating
XX immunodeficiency disease (including AIDS), senescence, neurodegenerative
XX disease, cancer, viral infection, lymphoproliferative conditions, viral
XX infection, autoimmune disease. Antibodies against the BID protein can be used for
XX wound-healing. Primers derived from the nucleic acid encoding the BID
XX protein can be used for detecting/quantitating the protein and for
XX detecting alterations in the nucleic acid encoding the BID protein.
XX
XX Sequence 32 AA:
XX
XX Query Match 72.3%; Score 99; DB 19; Length 32;
XX Best Local Similarity 70.4%; Pred. No. 1.3e-08;
XX Matches 19; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
XX
XX 1 GEDIRIRARHAGVDSMPSRPT 27
XX ||:|||||:||||:|:|:|
XX DB 5 qeeIhnhtrhagjgdmhndhptcl 31
XX
XX RESULT 35
XX AAW50262 standard; Protein; 33 AA.
XX
XX AAW50262;
XX
XX 20-JUL-1998 (first entry)
XX
XX Mouse BID truncated protein BID 74-106.
XX
XX Mouse: BH3 interacting domain death agonist; BID; BCL-2 family;
XX apoptosis; regulation; cell death; inflammation; cancer; arthritis;
XX autoimmune disease; viral infection; lymphoproliferative.
XX
XX Mus sp.
XX
XX W0980980-A1.
XX
XX PD 12-MAR-1998.
XX

```

```

PR 09-SEP-1997; 97MO-US15872.
XX
XX 09-SEP-1996; 96US-0706741.
XX
XX (UNIW ) UNIV WASHINGTON.
XX
XX Korsmeyer SJ.
XX
XX WPI: 1998-193546/17.
XX
XX BH3 interacting domain death agonist polypeptide - used for treating
XX decreased apoptotic conditions resulting from inflammation etc.
XX
XX Example 8; Page 84; 118pp; English.
XX
XX The present sequence represents a BH3 interacting domain death agonist
XX (BID) truncated protein given in the present invention. The protein, the
XX DNA encoding it or antisense sequences can be used for preventing or
XX treating a decreased apoptotic state of a cell. The decreased apoptotic
XX state can be used for treating a decreased apoptotic state of a cell.
XX infections, lymphoproliferative conditions arthritis inflammation and
XX autoimmune diseases. Antibodies against the BID protein can be used for
XX detecting a BID polypeptide in a cell or population of cell. The nucleic
XX acid sequence and the BID protein can also be used for treating
XX immunodeficiency disease (including AIDS), senescence, neurodegenerative
XX disease, cancer, viral infection, lymphoproliferative conditions, viral
XX infection, autoimmune disease. Antibodies against the BID protein can be used
XX wound-healing. Primers derived from the nucleic acid encoding the BID
XX protein can be used for detecting/quantitating the protein and for
XX detecting alterations in the nucleic acid encoding the BID protein.
XX
XX Sequence 33 AA:
XX
XX Query Match 72.3%; Score 99; DB 19; Length 33;
XX Best Local Similarity 70.4%; Pred. No. 1.3e-08;
XX Matches 19; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
XX
XX 1 GEDIRIRARHAGVDSMPSRPT 27
XX ||:|||||:||||:|:|:|
XX DB 6 qeeIhnhtrhagjgdmhndhptcl 32
XX

```

Search completed: September 20, 2002, 10:35:58
Job time: 426 sec

Fri Sep 20 11:03:04 2002

us-09-544-664-14.rag

Page 9

Fri Sep 20 11:03:04 2002

us-09-544-664-14.ral

age 1

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OK protein - protein search, using sw model

Run on: September 20, 2002, 10:37:19 : Search time 75.64 seconds

(without alignments)
8,719 Million cell updates/sec

Title: US-09-544-664-14

Sequence: 137

Sequence: 1 OEDIRNIAHRLAQCDSNDRIPEPL 27

Scoring table:

Gapop 10.0, Gapext 0.5

Searched:

231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing:

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1: /cgn2.6/prodata/2/1aa/5A.COMB.pep.*

2: /cgn2.6/prodata/2/1aa/5B.COMB.pep.*

3: /cgn2.6/prodata/2/1aa/5A.COMB.pep.*

4: /cgn2.6/prodata/2/1aa/5A.COMB.pep.*

5: /cgn2.6/prodata/2/1aa/5A.COMB.pep.*

6: /cgn2.6/prodata/2/1aa/5A.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query length	DB ID	Description
1	137	100.0	US-09-136-879-4	Sequence 4, Appl
2	137	100.0	US-09-136-879-4	Sequence 4, Appl
3	137	100.0	US-08-706-741B-4	Sequence 4, Appl
4	137	100.0	US-08-924-695A-4	Sequence 4, Appl
5	137	100.0	US-09-136-879-1	Sequence 5, Appl
6	137	100.0	US-08-706-741B-5	Sequence 5, Appl
7	137	100.0	US-08-706-741B-5	Sequence 5, Appl
8	137	100.0	US-08-706-741B-5	Sequence 5, Appl
9	113	82.5	US-08-924-695A-33	Sequence 33, Appl
10	99	72.3	US-08-706-741B-55	Sequence 55, Appl
11	99	72.3	US-08-924-695A-55	Sequence 55, Appl
12	99	72.3	US-08-706-741B-53	Sequence 53, Appl
13	99	72.3	US-08-706-741B-53	Sequence 53, Appl
14	99	72.3	US-08-706-741B-53	Sequence 53, Appl
15	99	72.3	US-08-924-695A-56	Sequence 56, Appl
16	99	72.3	US-08-706-741B-52	Sequence 52, Appl
17	99	72.3	US-08-924-695A-52	Sequence 52, Appl
18	99	72.3	US-08-706-741B-51	Sequence 51, Appl
19	99	72.3	US-08-706-741B-51	Sequence 51, Appl
20	99	72.3	US-08-706-741B-51	Sequence 51, Appl
21	99	72.3	US-08-706-741B-51	Sequence 51, Appl
22	99	72.3	US-08-924-695A-6	Sequence 6, Appl
23	99	72.3	US-09-136-879-2	Sequence 2, Appl
24	99	72.3	US-08-706-741B-85	Sequence 85, Appl
25	99	72.3	US-08-706-741B-85	Sequence 85, Appl
26	99	72.3	US-08-706-741B-85	Sequence 85, Appl
27	99	72.3	US-08-924-695A-87	Sequence 87, Appl

28	66	48.2	15	2	US-08-706-741B-86	Sequence 86, Appl
29	66	48.2	15	2	US-08-924-695A-86	Sequence 86, Appl
30	66	48.2	15	2	US-08-706-741B-86	Sequence 86, Appl
31	66	48.2	15	2	US-08-924-695A-86	Sequence 86, Appl
32	53	38.7	13	2	US-08-706-741B-45	Sequence 45, Appl
33	53	38.7	13	2	US-08-924-695A-45	Sequence 45, Appl
34	53	38.7	13	2	US-08-706-741B-8	Sequence 8, Appl
35	44	32.1	9	2	US-08-706-741B-8	Sequence 8, Appl
36	44	32.1	9	2	US-08-924-695A-8	Sequence 8, Appl
37	44	32.1	9	2	US-08-706-741B-8	Sequence 8, Appl
38	44	32.1	9	2	US-08-924-695A-8	Sequence 8, Appl
39	43.5	31.8	901	2	US-08-884-681-5	Sequence 5, Appl
40	43.5	31.8	968	4	US-08-560-005-7	Sequence 7, Appl
41	43.5	31.8	968	4	US-09-418-540-7	Sequence 22, Appl
42	43.5	31.8	968	4	US-09-418-540-7	Sequence 22, Appl
43	43.5	31.8	968	4	US-09-418-540-7	Sequence 22, Appl
44	43.5	31.8	968	4	US-09-418-540-7	Sequence 22, Appl
45	41.5	30.3	1462	3	US-09-157-021-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-09-136-879-3
Sequence 3, Application US/091368798
Patent No. 6326354
GENERAL INFORMATION:
APPLICANT: Kozmeyer, Stanley J.
TITLE OF INVENTION: MODULATION OF APOPTOSIS WITH BID
FILE REFERENCE: 60296285Replacement
CURRENT APPLICATION NUMBER: US/09/136,879B
CURRENT FILING DATE: 1996-08-19
INVENTOR OF SEQ ID NOS:
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 135
TYPE: PRT
ORGANISM: Homo sapiens
US-09-136-879-5

Query Match 100.0%; Score 137; DB 4; Length 135;
Best Local Similarity 100.0%; Pred. No. 1,6e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
DB 19 OEDIRNIAHRLAQCDSNDRIPEPL 45
OY 1 OEDIRNIAHRLAQCDSNDRIPEPL 27
|||||
US-09-136-879-4
US-09-136-879-4
Sequence 4, Application US/09136879B
Patent No. 6326354
GENERAL INFORMATION:
APPLICANT: Kozmeyer, Stanley J.
TITLE OF INVENTION: MODULATION OF APOPTOSIS WITH BID
FILE REFERENCE: 60296285Replacement
CURRENT APPLICATION NUMBER: US/09/136,879B
CURRENT FILING DATE: 1996-08-19
INVENTOR OF SEQ ID NOS:
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 140
TYPE: PRT
ORGANISM: Homo sapiens
US-09-136-879-4
Query Match 100.0%; Score 137; DB 4; Length 140;

Best Local Similarity 100.0%; Pred. No. 1, 7e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QEDIRIRIRHIAQVDSMDRSIPGL 27
DB 19 QEDIRIRIRHIAQVDSMDRSIPGL 45

RESULT 3
US-08-706-741B-4
Sequence 4, Application US/08706741B
Patent No. 5985593
GENERAL INFORMATION:
APPLICANT: KORMSEYER, STANLEY J.
TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS: 88
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63146
COMPUTER READABLE FORM:
FILE: 08706741B.DAT
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706.741B
CLASSIFICATION: 514
FILING DATE: 09-SEP-1997
PRIORITY DATE: 09-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 195 amino acids
TYPE: amino acid
STRANDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-706-741B-4

Query Match 100.0%; Score 137; DB 2; Length 195;
Best Local Similarity 100.0%; Pred. No. 2, 5e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QEDIRIRIRHIAQVDSMDRSIPGL 27
DB 79 QEDIRIRIRHIAQVDSMDRSIPGL 105

RESULT 4
US-08-924-695A-4
Sequence 4, Application US/08924695A
Patent No. 5985593
GENERAL INFORMATION:
APPLICANT: KORMSEYER, STANLEY J.
TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS: 88
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/924.695A
FILING DATE: 09-SEP-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 195 amino acids
TYPE: amino acid
STRANDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-924-695A-4

Query Match 100.0%; Score 137; DB 2; Length 195;
Best Local Similarity 100.0%; Pred. No. 2, 5e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QEDIRIRIRHIAQVDSMDRSIPGL 27
DB 79 QEDIRIRIRHIAQVDSMDRSIPGL 105

RESULT 5
US-09-136-879-1
Sequence 1, Application US/09136879B
Patent No. 6226285
GENERAL INFORMATION:
APPLICANT: Gross, Alan
APPLICANT: KORMSEYER, Stanley J.
TITLE OF INVENTION: MODULATION OF APOPTOSIS WITH BID
FILE REFERENCE: 60296285Replacement
CURRENT FILING DATE: 09/13/96, 879B
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 195
TYPE: PRT
ORGANISM: Homo sapiens
US-09-136-879-1

Query Match 100.0%; Score 137; DB 4; Length 195;
Best Local Similarity 100.0%; Pred. No. 2, 5e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QEDIRIRIRHIAQVDSMDRSIPGL 27
DB 79 QEDIRIRIRHIAQVDSMDRSIPGL 105

RESULT 6
US-08-706-741B-5
Sequence 5, Application US/08706741B
Patent No. 5985593
GENERAL INFORMATION:
APPLICANT: KORMSEYER, STANLEY J.
TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS

```

ADDRESSSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63146
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,741B
FILING DATE: 09-SEP-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: Linear
MOLECULE TYPE: protein
US-08-706-741B-5

Query Match 100.0%; Score 137; DB 2; Length 200;
Best Local Similarity 100.0%; Pred. No. 2.6e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QEDIRNARIHQVDSMDRSIPGL 27
DB 79 QEDIRNARIHQVDSMDRSIPGL 105

RESULT 7
US-08-924-695A-5
Sequence 5, Application US/08924695A
Patent No. 598883
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSER: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/924,695A
FILING DATE: 09-SEP-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 971798
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 5:
GENERAL INFORMATION:

```

```

SEQUENCE CHARACTERISTICS:
LENGTH: 200 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: Linear
MOLECULE TYPE: protein
US-08-924-695A-5

Query Match 100.0%; Score 137; DB 2; Length 200;
Best Local Similarity 100.0%; Pred. No. 2.6e-14;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QEDIRNARIHQVDSMDRSIPGL 27
DB 79 QEDIRNARIHQVDSMDRSIPGL 105

RESULT 8
US-08-706-741B-33
Sequence 33, Application US/08706741B
Patent No. 595593
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSER: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63146
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,741B
FILING DATE: 09-SEP-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: Linear
MOLECULE TYPE: peptide
US-08-706-741B-33

Query Match 82.5%; Score 113; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 RNIRARHQVDSMDRSIPGL 27
DB 1 RNIRARHQVDSMDRSIPGL 22

RESULT 9
US-08-924-695A-33
Sequence 33, Application US/08924695A
Patent No. 598883
GENERAL INFORMATION:

```


US-08-706-741B-53
Sequence 53, Application US/08706741B
Patent No. 5955593
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63146
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,741B
FILING DATE: 09-SEP-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-706-741B-53

Query Match 72.3%; Score 99; DB 2; Length 33;
Best Local Similarity 70.4%; Pred. No. 3.4e-09;
Matches 19; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 QEDIRNRHRLAQVSDMSRSTPGL 27
DB 6 QEDIRNRHRLAQVSDMSRSTPGL 32

RESULT 13
US-08-924-695A-53
Sequence 53, Application US/08924695A
Patent No. 5998583
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/924,695A
FILING DATE: 09-SEP-1997
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 971798
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-924-695A-53

Query Match 72.3%; Score 99; DB 2; Length 33;
Best Local Similarity 70.4%; Pred. No. 3.4e-09;
Matches 19; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 QEDIRNRHRLAQVSDMSRSTPGL 27
DB 6 QEDIRNRHRLAQVSDMSRSTPGL 32

RESULT 14
US-08-706-741B-56
Sequence 56, Application US/08706741B
Patent No. 5955593
GENERAL INFORMATION:
APPLICANT: KORSMEYER, STANLEY J.
TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63146
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,741B
FILING DATE: 09-SEP-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-706-741B-56

Query Match 72.3%; Score 99; DB 2; Length 44;
Best Local Similarity 70.4%; Pred. No. 4.7e-09;
Matches 19; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 QEDIRNRHRLAQVSDMSRSTPGL 27
DB 6 QEDIRNRHRLAQVSDMSRSTPGL 32

DB 17 QEEIHNIAHIAOIGDEMDHNIQPTL 43

RESULT 15

US-08-924-695A-56

/ Sequence 56, Application US/08924695A

/ Patent No. 5998583

/ GENERAL INFORMATION:

/ APPLICANT: KORSMEYER, STANLEY J.

/ TITLE OF INVENTION: BH3 INTERACTING DOMAIN DEATH AGONIST

/ NUMBER OF SEQUENCES: 88

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: HOWELL & HAFERKAMP, L.C.

/ STREET: 7733 FORSYTH BLVD., SUITE 1400

/ CITY: ST. LOUIS

/ STATE: MISSOURI

/ COUNTRY: USA

/ ZIP: 63105

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: IBM PC compatible

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patent in Release #1.0, Version #1.30

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/08/924,695A

/ FILING DATE: 09-SEP-1997

/ CLASSIFICATION: 514

/ ATTORNEY/AGENT INFORMATION:

/ NAME: HOLLAND, DONALD R.

/ REGISTRATION NUMBER: 35,197

/ REFERENCE/DOCKET NUMBER: 971798

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (314) 727-5188

/ TELEFAX: (314) 727-6092

/ INFORMATION FOR SEQ ID NO: 56:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 44 amino acids

/ TYPE: amino acid

/ STRANDEDNESS:

/ TOPOLOGY: linear

/ MOLECULE TYPE: peptide

US-08-924-695A-56

Query Match 72.3%; Score 99; DB 2; Length 44;

Best Local Similarity 70.4%; Pred. No. 4.7e-09;

Matches 19; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 QEDIIHIAHIAOIGDSMDRISIPGL 27

DB 17 QEEIHNIAHIAOIGDEMDHNIQPTL 43

Search completed: September 20, 2002, 10:37:20
Job time: 408 sec

RESULT 11

AF2445
 C:Species: *Anabaena sp.* strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 11
 C:Accession: AF2445
 R:Kanehisa, T.; Nakamura, Y.; Miki, C. P.; Sasamoto, S.; Watanabe, A.; Itinuchi, N.; Shimizu, S.; Sugimoto, M.; Takekawa, M.; Yamada, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001
 A:Title: Complete genome sequence of the filamentous nitrogen-fixing cyanobacterium *Anabaena*
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AF2445
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-329 <NR>
 A:Cross-references: GB:BA000019; PTDN:BA076817.1; PTD:G17134256; GSPDB:GN00179
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: al15118
 C:Superfamily: stress response protein csbh

Query Match

33.6% Score 46; DB 2; Length 329;
 Best Local Similarity 39.1%; Pred. No. 35;
 Matches 9; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

OY 1 OEDIRNARHLAOGDSMDRSI 23
 DB 14 EEDITMNRRLSOVMDMGCV 36

RESULT 12

fix23-2 protein - Rhizobium meliloti
 S18954
 C:Species: *Rhizobium meliloti*
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 08-Oct-1999
 C:Accession: S18954
 R:Petrovich, G.; Putnoky, P.; Kondorosi, A.
 submitted to the EMBL Data Library, January 1992
 A:Description: A fatty acid synthase like gene cluster of *Rhizobium meliloti* is involved
 A:Reference number: S18953
 A:Accession: S18954
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-395 <NR>
 A:Cross-references: EMBL:X64131; NID:G1235585; PTDN:CAA45484.1; PTD:9465272
 C:Superfamily: lacyl-carrier-protein S-malonyltransferase homology
 F:44-327/Domain: [lacyl-carrier-protein] S-malonyltransferase homology <NR>

Query Match 33.6% Score 46; DB 2; Length 395;
 Best Local Similarity 30.0%; Pred. No. 43;
 Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 2 EDIRNARHLAOGDSM 19
 DB 13 EDIVRAINHLNLRGSDI 30

RESULT 13

hypothetical protein AT4G10730 [imported] - Arabidopsis thaliana
 N85112
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
 C:Accession: N85112
 R:Rambourg, T.; The European Union Arabidopsis Genome Sequencing Consortium, "The Cold Spring
 Nature 402, 759-777, 1999
 A:Title: Sequence and analysis of chromosome 4 of the plant *Arabidopsis thaliana*.
 A:Reference number: AB5001; MUID:20083488
 A:Accession: N85112
 A:Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-693 <NR>
 A:Cross-references: GB:NC_001268; NID:97267771; PTDN:CA881174.1; GSPDB:GN00140
 C:Genetics:
 A:Gene: AT4G10730
 A:Map position: 4

Query Match

33.6% Score 46; DB 2; Length 693;
 Best Local Similarity 34.5%; Pred. No. 84;
 Matches 10; Conservative 6; Mismatches 9; Indels 4; Gaps 1;

OY 1 OEDIRNARHLAOGDSMDRS---1P 25
 DB 584 QODLTMLNVTLOQAAETDGSQNKLP 612

RESULT 14

S18015
 C:Species: *Drosophila melanogaster*
 C:Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 18-Feb-2000
 C:Accession: S18015
 R:Shishido, E.; Emori, Y.; Saigo, K.
 FEBS Lett. 289, 235-238, 1991
 A:Title: Identification of seven novel protein-tyrosine kinase genes of *Drosophila* by
 A:Reference number: S17552; MUID:92008631
 A:Accession: S18015
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-35 <NR>
 C:Superfamily: unassigned ser/thr or tyr-specific protein kinases; protein kinase hom
 C:Keywords: Atp; phosphotransferase; tyrosine-specific protein kinase
 F:1-35/Domain: protein kinase homology (fragment) <NR>

Query Match 33.2% Score 45.5; DB 2; Length 55;
 Best Local Similarity 32.6%; Pred. No. 5.2;
 Matches 10; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

OY 9 ARHLAOGD-SMDRSIP 26
 DB 6 ARHQAISDSCMSRSLAP 24

RESULT 15

AS6764
 band 3-related protein, ileum - rabbit
 C:Species: *Oryctolagus cuniculus* (domestic rabbit)
 C:Date: 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 20-Aug-1999
 C:Accession: AS6764
 R:Chow, A.; Dobbins, J.W.; Aronson, P.S.; Igarashi, P.
 Am. J. Physiol. 263, G345-G352, 1992
 A:Title: cDNA cloning and localization of a band 3-related protein from ileum.
 A:Reference number: AS6764; MUID:93035730
 A:Accession: AS6764
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1237 <NR>
 A:Cross-references: GB:545791; NID:G256659; PTDN:AB23486.1; PTD:G256660
 A:Experimental source: New Zealand white rabbit, ileal epithelial cells
 A:Note: sequence extracted from NCBI backbone (NCBI:115180, NCBI:P115181)
 C:Superfamily: band 3 anion transport protein

Query Match 33.2% Score 45.5; DB 2; Length 1237;
 Best Local Similarity 31.0%; Pred. No. 26/02; 8; Indels 3; Gaps 1;

OY 2 EDIRNARHLAOGDSMDRSIPGL 27
 DB 616 EELISVNRHQRGMKREGRGRLPGL 644

Fri Sep 20 11:03:05 2002

us-09-544-664-14.rpt

Search completed: September 20, 2002, 10:39:07
Job time: 479 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2002, 11:04:30 ; Search time 44.99 Seconds*

(without alignments)
23.237 Million cell updates/sec

Title: US-09-544-664-14

Sequence: 1 OEDILINRIHIAQVGDMSRIPGL 27

Scoring table: BIOSGM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SWISSPROT_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	137	100.0	195	1 BID_HUMAN	P59597 homo sapien
2	99	72.3	195	1 BID_MOUSE	P70444 mus musculus
3	57	41.6	195	1 ARLY_HAIEIN	P44314 haemophilus
4	47	34.3	195	1 A2AB_TALBO	O19091 talpa europ
5	47	34.3	1129	1 RPA2_TALBO	P20028 dirosophila
6	46	33.6	159	1 CONO_SYNE7	O50435 drosophila
7	46	33.6	1239	1 B2A2_RABIT	P57763 sultrichia
8	45	33.2	1239	1 B2A2_RABIT	P57763 sultrichia
9	45	32.8	1164	1 YEL1_YEAST	P43104 mycobacteri
10	45	32.8	1513	1 DPOA_CORYNE	P38833 mycobacteri
11	45	32.8	1513	1 DPOA_CORYNE	O27152 oxytrichia
12	44.5	32.5	511	1 C6PD_PNEUM	P41764 emetrichia
13	44	32.1	148	1 VPZ2_MERTF	P25687 mechanobact
14	44	32.1	415	1 PROA_HAGCU	P38821 bacillus su
15	44	32.1	415	1 PROA_HAGCU	O98814 ratius norv
16	44	32.1	530	1 PDP2_RAT	O88444 ratius norv
17	44	32.1	794	1 SP5A_BOVIN	O95115 bos taurus
18	43.5	31.8	298	1 YMA2_MYCO	O02278 mycobacteri
19	43.5	31.8	350	1 SUB1_SYNE7	P27312 bacillus su
20	43.5	31.8	689	1 YVAL_BACCU	O01968 homo sapien
21	43.5	31.8	901	1 OCRL_HUMAN	P37512 bacillus su
22	43	31.4	227	1 PMKY_HAIEIN	P44865 haemophilus
23	43	31.4	229	1 RK1_PORPO	P45358 caenorhabd
24	43	31.4	317	1 YK68_CHEBI	P40339 saccharomyc
25	43	31.4	323	1 RRC4_YEAST	P20497 vacuola vi
26	43	31.4	324	1 VP35_VACCC	P07240 vacuola vi
27	43	31.4	324	1 VP35_VACCC	P33059 vacuola vi
28	43	31.4	325	1 RBYV_AACH	O45355 azococci
29	43	31.4	342	1 CRYA_BOUL	P27206 escherichia
30	43	31.4	452	1 R2B1_BOUL	P27206 escherichia
31	43	31.4	488	1 ARBP_PICOB	O47037 picobact
32	43	31.4	488	1 ARBP_PICOB	O47037 picobact
33	43	31.4	493	1 PCKA_AAPRE	O97668 atropium p

34	43	31.4	889	1 IREL_HUMAN	P21399 homo sapien
35	43	31.4	889	1 IREL_MOUSE	P28271 mus musculus
36	43	31.4	889	1 IREL_RABIT	O01059 oryctolagus
37	43	31.4	889	1 IREL_RAT	O63270 rattus norv
38	43	31.4	889	1 IREL_CHICK	O90875 gallus gall
39	43	31.4	963	1 IREL_RAT	O62751 rattus norv
40	43	31.4	1048	1 P100_HICMA	P06318 human cyclin
41	42.5	31.0	1117	1 TERT_TERTH	P07198 tetrahymena
42	42.5	31.0	354	1 AR05_DUCHA	P27198 tetrahymena
43	42.5	31.0	416	1 KCIE_HUMAN	P45372 dicisternap
44	42.5	31.0	416	1 KCIE_HUMAN	P45372 dicisternap
45	42.5	31.0	479	1 CARR_BORCI	P53304 botrytis cl

ALIGNMENTS

RESULT	ID	BID_HUMAN	STANDARD:	PRT:	195 AA.
AC	P59597:				
DT	01-NOV-1997 (rel. 35, Created)				
DT	01-NOV-1997 (rel. 35, Last sequence update)				
DT	16-OCT-2001 (rel. 40, Last annotation update)				
DE	BH3 interacting domain death agonist (bid).				
GN	BID.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RP	SEQUENCE FROM N.A.				
RP	NCBI_MOLFUNS=97076762;				
RP	Mand K. Yio X.-M. Chao D.T. Millman C.L. Korsmeyer S.J.;				
RT	"BID, a novel BH3 domain-only death agonist."				
RL	Genes Dev. 10:2859-2869(1996).				
RN	121				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=98389636; PubMed=9721221;				
RA	Footz T.K., Bitren B., Minoshima S., Asakawa S., Shimizu N.,				
RA	Riazi M.A., Mobernd H.E.;				
RT	"The gene for death agonist BID maps to the region of human 22q11.2				
RT	6." duplicated in cat eye syndrome chromosomes and to mouse chromosome				
RL	Genomics 51:472-475(1998).				
RP	SEQUENCE FROM N.A.				
RA	Hillier L., Li J.K.N., Dubugue T., Ellington K., Hawkins M.,				
RA	Hillier L., Li J.K.N., Dubugue T., Le M. Tomson G. Harris M.,				
RA	Paterson J., Rifkin L., Rohlfing T., Soares M. Tan F.;				
RA	Trevisan E. Waterston R., Williamson A., Woldmann P., Wilson R.;				
RT	Submitted (JUL-1995) to the EMBL/Genbank/DBJ databases.				
RN	141				
RP	SEQUENCE OF 1-110 FROM N.A.				
RA	Fujiwara T., Hirano H., Hishigaki H., Horie M., Kawa A., Kuga Y.,				
RA	Kiyashiki H., Nagata M., Okuno S., Ozaki K., Shimizu F.,				
RA	Shimada Y., Shinomiya H., Suzuki M., Takachi A., Takada S.,				
RA	Matsuda T., Maekawa H., Nakamura Y., Takahashi E.;				
RT	Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.				
RN	151				
RP	SEQUENCE OF 1-74.				
RA	MEDLINE=96159527; PubMed=8593609;				
RA	Trotter J.A., Long K.R., Murrell J.R., Stotler C.J.;				
RA	Guella J.F., Buckler A.J.;				
RT	"An expression-independent catalog of genes from human chromosome				
RT	22."				
RL	Genome Res. 5:214-224(1995).				
RN	161				
RP	STRUCTURE BY NMR.				
RA	MEDLINE=99189777;				
RA	Shimizu N., Li J.K.N., Solovson G.S., Yuan J., Warner G.;				
RT	"Solution structure of BID, an intracellular amplifier of apoptotic				
RT	signaling."				

```

CC Cell 96:615-624(1999).
CC -1- FUNCTION: INDUCES ICE-LIKE PROTEASES AND APOPTOSIS. COUNTERS THE
CC PROTECTIVE EFFECT OF BCL-2 (BY SIMILARITY).
CC -1- SUBUNIT: FORMS HETERODIMERS EITHER WITH THE PRO-APOPTOTIC PROTEIN
CC BAX OR THE ANTI-APOPTOTIC PROTEIN BCL-2 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: PREDOMINANTLY CYTOPLASMIC (BY SIMILARITY).
CC -1- DOMAIN: INTERACTS WITH BAX, BID, BAD AND
CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 3 (BH3).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF042083; AAC34365.1; -.
CC EMBL: H23042; -. NOT_ANNOTATED_CDS.
CC EMBL: R09550; -. NOT_ANNOTATED_CDS.
CC EMBL: R09537; -. NOT_ANNOTATED_CDS.
CC EMBL: C1508; -. NOT_ANNOTATED_CDS.
CC EMBL: C15483; -. NOT_ANNOTATED_CDS.
CC DR: PDB: 1DDB; 27-JAN-00.
CC DR: M19: 601997; 27-JAN-00.
CC DR: InterPro: IPR000712; Bcl_2.
CC DR: PROSITE: PS01259; BH3; 1.
CC KW: Apoptosis; 3D-structure.
CC FT: DOMAIN: 86-100.
CC SO: SEQUENCE 195 AA; 21994 MW; B17A07334C1A8BEF CRC64;

Query Match 100.0%; Score 137; DB 1; Length 195;
Best Local Similarity 100.0%; Pred. No. 1; Be-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CEDIRNIRRLAAGVDSMDRSIPGL 27
DB 79 CEDIRNIRRLAAGVDSMDRSIPGL 105

RESULT 2
BID_MOUSE STANDARD: PRT; 195 AA.
AC 01-NOV-1997 (rel. 35, Created)
DR 01-NOV-1997 (rel. 35, Last sequence update)
DR 16-OCT-2001 (rel. 40, Last annotation update)
DE BH3 interacting domain death agonist (BID).
DN BID.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sclurognathu; Muridae; Murinae; Mus.
CC NCBI_TaxId=10090;
CC 11
CC SEQUENCE FROM N.A., AND MUTAGENESIS OF BH3 DOMAIN.
CC TISSUE-T-cell;
CC MEDLINE=97078762; PubMed=8918887;
CC Wang K., Yin X.-M., Chao D.-T., Millman C.L., Korsmeyer S.J.;
CC "BID: a novel BH3 domain-only death agonist.";
CC Genes Dev. 10:2859-2869(1996).
CC 12
CC STRUCTURE BY NMR. PubMed=1008978;
CC McDermott J.M., Fushman D., Millman C.L., Korsmeyer S.J., Cowburn D.;
CC "Solution structure of the proapoptotic molecule BID: a structural
CC basis of specific agonists and antagonists.";
CC Cell 96:323-334(1999).
CC -1- FUNCTION: INDUCES CASPASES AND APOPTOSIS. COUNTERS THE PROTECTIVE
CC EFFECT OF BCL-2.

```

```

CC -1- SUBUNIT: FORMS HETERODIMERS EITHER WITH THE PRO-APOPTOTIC PROTEIN
CC BAX OR THE ANTI-APOPTOTIC PROTEIN BCL-2.
CC -1- SUBCELLULAR LOCATION: PREDOMINANTLY CYTOPLASMIC.
CC -1- DOMAIN: INTERACTS WITH BAX, BID, BAX, BAD AND
CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 3 (BH3).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U75506; AAC71064.1; -.
CC PDB: 1DDB; 30-AUG-99.
CC DR: MGI:108093; Bcl.
CC DR: InterPro: IPR000712; Bcl_2.
CC DR: PROSITE: PS01259; BH3; 1.
CC KW: Apoptosis; 3D-structure.
CC FT: DOMAIN: 86-100.
CC SO: SEQUENCE 195 AA; 21950 MW; BAD23C71A1BC1F7 CRC64;

Query Match 72.3%; Score 99; DB 1; Length 195;
Best Local Similarity 70.4%; Pred. No. 9; Se-08;
Matches 19; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 1 CEDIRNIRRLAAGVDSMDRSIPGL 27
DB 79 CEDIRNIRRLAAGVDSMDRSIPGL 105

RESULT 3
ARYL_HAERIN STANDARD: PRT; 457 AA.
AC P44314;
DR 01-NOV-1995 (rel. 32, Created)
DR 01-NOV-1995 (rel. 32, Last sequence update)
DR 16-OCT-2001 (rel. 40, Last annotation update)
DE Argininosuccinate lyase (EC 4.3.2.1) (Argininosuccinase) (ASAL).
DN ARGH OR H10811.
OS Haemophilus influenzae.
CC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
CC Haemophilus.
CC NCBI_TaxId=727;
CC 11
CC SEQUENCE FROM N.A.
CC STRAIN=RD / KW20 / ATCC 51907;
CC MEDLINE=9530630; PubMed=7542800;
CC Fleisigmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
CC Kerlavang A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Maitick J.M.,
CC McKenney K., Sutton G., Fitzhugh W., Fields C.A., Cooney J.D.,
CC Scott J.D., Shirley R., Liu L.-I., Glodex A., Kelley J.M.,
CC Woldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
CC Ulteirack T.R., Hanna M.C., Nguyen D.T., Sauek D.M., Brandon R.C.,
CC Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,
CC Gnehm C.L., McDonald L.A., Smal J.K.V., Fraser C.M., Smith H.O.,
CC Venter J.C.;
CC "Whole-genome random sequencing and assembly of Haemophilus
CC influenzae Rd.";
CC Science 269:496-512(1995).
CC -1- CATALYTIC ACTIVITY: N-(L-arginino)succinate = fumarate + L-
CC arginine.
CC -1- PATHWAY: THE LAST STEP IN ARGININE BIOSYNTHESIS.
CC -1- SIMILARITY: BELONGS TO THE LYSINE I FAMILY. ARGININOSUCCINATE LYASE
CC SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -

```


CC enucleate requires a license agreement (see <http://www.lsb-sib.ch/announce>
CC or send an email to license@lsb-sib.ch).

DR ENRL_I02128: CAA33185.11

DR PIR_I00354: J00354.

DR Flybase: FBgn003278; Rn133.

DR Interpro: IPRO01572; Rn1.POL.B.

DR Pfam: PF00662; Rn1.POL.B.1; Rn1.POL.B.2; Rn1.POL.B.3; Rn1.POL.B.4; Rn1.POL.B.5; Rn1.POL.B.6; Rn1.POL.B.7; Rn1.POL.B.8; Rn1.POL.B.9; Rn1.POL.B.10; Rn1.POL.B.11; Rn1.POL.B.12; Rn1.POL.B.13; Rn1.POL.B.14; Rn1.POL.B.15; Rn1.POL.B.16; Rn1.POL.B.17; Rn1.POL.B.18; Rn1.POL.B.19; Rn1.POL.B.20; Rn1.POL.B.21; Rn1.POL.B.22; Rn1.POL.B.23; Rn1.POL.B.24; Rn1.POL.B.25; Rn1.POL.B.26; Rn1.POL.B.27; Rn1.POL.B.28; Rn1.POL.B.29; Rn1.POL.B.30; Rn1.POL.B.31; Rn1.POL.B.32; Rn1.POL.B.33; Rn1.POL.B.34; Rn1.POL.B.35; Rn1.POL.B.36; Rn1.POL.B.37; Rn1.POL.B.38; Rn1.POL.B.39; Rn1.POL.B.40; Rn1.POL.B.41; Rn1.POL.B.42; Rn1.POL.B.43; Rn1.POL.B.44; Rn1.POL.B.45; Rn1.POL.B.46; Rn1.POL.B.47; Rn1.POL.B.48; Rn1.POL.B.49; Rn1.POL.B.50; Rn1.POL.B.51; Rn1.POL.B.52; Rn1.POL.B.53; Rn1.POL.B.54; Rn1.POL.B.55; Rn1.POL.B.56; Rn1.POL.B.57; Rn1.POL.B.58; Rn1.POL.B.59; Rn1.POL.B.60; Rn1.POL.B.61; Rn1.POL.B.62; Rn1.POL.B.63; Rn1.POL.B.64; Rn1.POL.B.65; Rn1.POL.B.66; Rn1.POL.B.67; Rn1.POL.B.68; Rn1.POL.B.69; Rn1.POL.B.70; Rn1.POL.B.71; Rn1.POL.B.72; Rn1.POL.B.73; Rn1.POL.B.74; Rn1.POL.B.75; Rn1.POL.B.76; Rn1.POL.B.77; Rn1.POL.B.78; Rn1.POL.B.79; Rn1.POL.B.80; Rn1.POL.B.81; Rn1.POL.B.82; Rn1.POL.B.83; Rn1.POL.B.84; Rn1.POL.B.85; Rn1.POL.B.86; Rn1.POL.B.87; Rn1.POL.B.88; Rn1.POL.B.89; Rn1.POL.B.90; Rn1.POL.B.91; Rn1.POL.B.92; Rn1.POL.B.93; Rn1.POL.B.94; Rn1.POL.B.95; Rn1.POL.B.96; Rn1.POL.B.97; Rn1.POL.B.98; Rn1.POL.B.99; Rn1.POL.B.100; Rn1.POL.B.101; Rn1.POL.B.102; Rn1.POL.B.103; Rn1.POL.B.104; Rn1.POL.B.105; Rn1.POL.B.106; Rn1.POL.B.107; Rn1.POL.B.108; Rn1.POL.B.109; Rn1.POL.B.110; Rn1.POL.B.111; Rn1.POL.B.112; Rn1.POL.B.113; Rn1.POL.B.114; Rn1.POL.B.115; Rn1.POL.B.116; Rn1.POL.B.117; Rn1.POL.B.118; Rn1.POL.B.119; Rn1.POL.B.120; Rn1.POL.B.121; Rn1.POL.B.122; Rn1.POL.B.123; Rn1.POL.B.124; Rn1.POL.B.125; Rn1.POL.B.126; Rn1.POL.B.127; Rn1.POL.B.128; Rn1.POL.B.129; Rn1.POL.B.130; Rn1.POL.B.131; Rn1.POL.B.132; Rn1.POL.B.133; Rn1.POL.B.134; Rn1.POL.B.135; Rn1.POL.B.136; Rn1.POL.B.137; Rn1.POL.B.138; Rn1.POL.B.139; Rn1.POL.B.140; Rn1.POL.B.141; Rn1.POL.B.142; Rn1.POL.B.143; Rn1.POL.B.144; Rn1.POL.B.145; Rn1.POL.B.146; Rn1.POL.B.147; Rn1.POL.B.148; Rn1.POL.B.149; Rn1.POL.B.150; Rn1.POL.B.151; Rn1.POL.B.152; Rn1.POL.B.153; Rn1.POL.B.154; Rn1.POL.B.155; Rn1.POL.B.156; Rn1.POL.B.157; Rn1.POL.B.158; Rn1.POL.B.159; Rn1.POL.B.160; Rn1.POL.B.161; Rn1.POL.B.162; Rn1.POL.B.163; Rn1.POL.B.164; Rn1.POL.B.165; Rn1.POL.B.166; Rn1.POL.B.167; Rn1.POL.B.168; Rn1.POL.B.169; Rn1.POL.B.170; Rn1.POL.B.171; Rn1.POL.B.172; Rn1.POL.B.173; Rn1.POL.B.174; Rn1.POL.B.175; Rn1.POL.B.176; Rn1.POL.B.177; Rn1.POL.B.178; Rn1.POL.B.179; Rn1.POL.B.180; Rn1.POL.B.181; Rn1.POL.B.182; Rn1.POL.B.183; Rn1.POL.B.184; Rn1.POL.B.185; Rn1.POL.B.186; Rn1.POL.B.187; Rn1.POL.B.188; Rn1.POL.B.189; Rn1.POL.B.190; Rn1.POL.B.191; Rn1.POL.B.192; Rn1.POL.B.193; Rn1.POL.B.194; Rn1.POL.B.195; Rn1.POL.B.196; Rn1.POL.B.197; Rn1.POL.B.198; Rn1.POL.B.199; Rn1.POL.B.200; Rn1.POL.B.201; Rn1.POL.B.202; Rn1.POL.B.203; Rn1.POL.B.204; Rn1.POL.B.205; Rn1.POL.B.206; Rn1.POL.B.207; Rn1.POL.B.208; Rn1.POL.B.209; Rn1.POL.B.210; Rn1.POL.B.211; Rn1.POL.B.212; Rn1.POL.B.213; Rn1.POL.B.214; Rn1.POL.B.215; Rn1.POL.B.216; Rn1.POL.B.217; Rn1.POL.B.218; Rn1.POL.B.219; Rn1.POL.B.220; Rn1.POL.B.221; Rn1.POL.B.222; Rn1.POL.B.223; Rn1.POL.B.224; Rn1.POL.B.225; Rn1.POL.B.226; Rn1.POL.B.227; Rn1.POL.B.228; Rn1.POL.B.229; Rn1.POL.B.230; Rn1.POL.B.231; Rn1.POL.B.232; Rn1.POL.B.233; Rn1.POL.B.234; Rn1.POL.B.235; Rn1.POL.B.236; Rn1.POL.B.237; Rn1.POL.B.238; Rn1.POL.B.239; Rn1.POL.B.240; Rn1.POL.B.241; Rn1.POL.B.242; Rn1.POL.B.243; Rn1.POL.B.244; Rn1.POL.B.245; Rn1.POL.B.246; Rn1.POL.B.247; Rn1.POL.B.248; Rn1.POL.B.249; Rn1.POL.B.250; Rn1.POL.B.251; Rn1.POL.B.252; Rn1.POL.B.253; Rn1.POL.B.254; Rn1.POL.B.255; Rn1.POL.B.256; Rn1.POL.B.257; Rn1.POL.B.258; Rn1.POL.B.259; Rn1.POL.B.260; Rn1.POL.B.261; Rn1.POL.B.262; Rn1.POL.B.263; Rn1.POL.B.264; Rn1.POL.B.265; Rn1.POL.B.266; Rn1.POL.B.267; Rn1.POL.B.268; Rn1.POL.B.269; Rn1.POL.B.270; Rn1.POL.B.271; Rn1.POL.B.272; Rn1.POL.B.273; Rn1.POL.B.274; Rn1.POL.B.275; Rn1.POL.B.276; Rn1.POL.B.277; Rn1.POL.B.278; Rn1.POL.B.279; Rn1.POL.B.280; Rn1.POL.B.281; Rn1.POL.B.282; Rn1.POL.B.283; Rn1.POL.B.284; Rn1.POL.B.285; Rn1.POL.B.286; Rn1.POL.B.287; Rn1.POL.B.288; Rn1.POL.B.289; Rn1.POL.B.290; Rn1.POL.B.291; Rn1.POL.B.292; Rn1.POL.B.293; Rn1.POL.B.294; Rn1.POL.B.295; Rn1.POL.B.296; Rn1.POL.B.297; Rn1.POL.B.298; Rn1.POL.B.299; Rn1.POL.B.300; Rn1.POL.B.301; Rn1.POL.B.302; Rn1.POL.B.303; Rn1.POL.B.304; Rn1.POL.B.305; Rn1.POL.B.306; Rn1.POL.B.307; Rn1.POL.B.308; Rn1.POL.B.309; Rn1.POL.B.310; Rn1.POL.B.311; Rn1.POL.B.312; Rn1.POL.B.313; Rn1.POL.B.314; Rn1.POL.B.315; Rn1.POL.B.316; Rn1.POL.B.317; Rn1.POL.B.318; Rn1.POL.B.319; Rn1.POL.B.320; Rn1.POL.B.321; Rn1.POL.B.322; Rn1.POL.B.323; Rn1.POL.B.324; Rn1.POL.B.325; Rn1.POL.B.326; Rn1.POL.B.327; Rn1.POL.B.328; Rn1.POL.B.329; Rn1.POL.B.330; Rn1.POL.B.331; Rn1.POL.B.332; Rn1.POL.B.333; Rn1.POL.B.334; Rn1.POL.B.335; Rn1.POL.B.336; Rn1.POL.B.337; Rn1.POL.B.338; Rn1.POL.B.339; Rn1.POL.B.340; Rn1.POL.B.341; Rn1.POL.B.342; Rn1.POL.B.343; Rn1.POL.B.344; Rn1.POL.B.345; Rn1.POL.B.346; Rn1.POL.B.347; Rn1.POL.B.348; Rn1.POL.B.349; Rn1.POL.B.350; Rn1.POL.B.351; Rn1.POL.B.352; Rn1.POL.B.353; Rn1.POL.B.354; Rn1.POL.B.355; Rn1.POL.B.356; Rn1.POL.B.357; Rn1.POL.B.358; Rn1.POL.B.359; Rn1.POL.B.360; Rn1.POL.B.361; Rn1.POL.B.362; Rn1.POL.B.363; Rn1.POL.B.364; Rn1.POL.B.365; Rn1.POL.B.36

```

SQ SEQUENC 159 AA: 17593 MW: 6509EBCPFCF151C CRC64:
Query Match 33.6% SCORE 46; DB 1: Length 159;
Best Local Similarity 33.6%; Pred. No. 7.2;
Matches 7; Conservative 7; Mismatches 7; Indels 0; Gaps 0

OY 7 RIARHLAQVDSMDRSIPPEL 27
Db 128 STYKELMFGSVGVLHVPPEI 148

RESULT 7
1. PCNA_SIN3D
AC PCNA_SIN3D STANDARD: PRT: 248 AA.
PS7763:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE homolog B (PCNA), A DNA binding clamp B (proliferating cell nuclear antigen
DE homolog B (PCNA).
DE PCNE OR PCNA.
OC Sulfiteisphaera oshimensis.
OC Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfurisphaera.
PC NCB1_TaxId=69596;
RX SSOURCE FROM N.A.
RC STRAIN-TA-1;
RX MEDLINE-2102025; PubMed-11139078;
RX 1ae1 T., Kurosaev N., Tsch Y.H., Hotzliu T.:
RX "The Sulfiteisphaera oshimensis PCNA homologues."
RX Extremophiles 4:157-164(2000).
CC - FUNCTION: SLIDING CLAMP SUBUNIT. RESPONSIBLE FOR TETHERING THE
CC CATALYTIC SUBUNIT OF DNA POLYMERASE TO DNA DURING HIGH-SPEED
CC REPLICATION (BY SIMILARITY).
CC - SUBUNIT: HOMODIMER (BY SIMILARITY).
CC - SIMILARITY: 33.6% IDENTITY.
CC - THIS SWISS-PROT entry is copyrighted. It is produced through a collaboration be-
CC tween the Swiss Institute of Bioinformatics and the EMBL Outstation in
CC the European Bioinformatics Institute. There are no restrictions on its
CC use. The sequence is provided on the condition that any copyright notice
CC modified and this statement is not removed.
CC entities requires a license agreement (see http://www.isb-sdb.ch/announcements/).
CC or send an email to license@isb-sdb.ch).
CC 1998-06-05000. 20010562.
DR InterPro: IPR000730; PCNA.
DR Pfam: PF00705; PCNA. 1.
DR ProDom: PD002673; PCNA. 1; PALSE_NEG.
DR PROSITE: PS01251; PCNA. 1; PALSE_NEG.
DR DNASIS: F800125; PCNA. 1; PALSE_NEG.
DR KX DNA11499.
SQ SEQUENCE 248 AA: 27681 MW: 86620C0C147E6E89 CRC64:

Query Match 33.6% SCORE 46; DB 1: Length 248;
Best Local Similarity 33.6%; Pred. No. 7.2;
Matches 7; Conservative 7; Mismatches 7; Indels 0; Gaps 0.

OY 3 DTRNARHLAQVDSMDRS 22
Db 141 DLRKDARDSDVGEVLEIS 160

RESULT 8
1. B3A2_RABAT
AC B3A2_RABAT STANDARD: PRT: 1237 AA.
PS7763:
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE 15-Jul-1999 (Rel. 38, Last annotation update)
DE Anion exchange protein 3 (Non-erythroid band 3-like protein) (N3BP)

```

GN SLCA2 OR AE2.
 OS Oryctolagus cuniculus (Rabbit).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OS Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 CC NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NEW ZEALAND WHITE;
 RX MEDLINE=93035730; PubMed=1415547;
 RA Chow A., Dobbins J.W., Aronson P.S., Igarashi P.;
 RT "CDNA cloning and localization of a band 3-related protein from
 RL human."
 CC Am. J. Physiol. 263:G345-G352(1992).
 CC 1- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
 CC DISTRIBUTION.
 CC 1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
 CC 1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: S45791; AAB23488.1; -
 CC DR HSSP: P02730; IATR.
 CC DR InterPro: IPR001717; Anion_exchanger.
 CC DR InterPro: IPR003020; HCO3_cotransp.
 CC DR Pfam: PF00955; HCO3_cotransp. 1.
 CC DR Pfam: PR01231; HCO3TRANSPO.
 CC DR PROSITE: PS00219; ANION_EXCHANGER_1. 1.
 CC DR PROSITE: PS00220; ANION_EXCHANGER_2. 1.
 CC KW Transmembrane; Glycoprotein; Anion exchange; Lipoprotein; Palmitate.
 CC
 CC DOMAIN 1 703
 CC FT DOMAIN 1 703
 CC FT TRANSMEM 704 1237 MEMBRANE (ANION EXCHANGER).
 CC FT TRANSMEM 733 770 POTENTIAL.
 CC FT TRANSMEM 790 812 POTENTIAL.
 CC FT TRANSMEM 822 843 POTENTIAL.
 CC FT DOMAIN 844 896 EXPONENTIAL LOOP (POTENTIAL).
 CC FT TRANSMEM 897 914 POTENTIAL.
 CC FT DOMAIN 915 929 CITOPLASMIC (POTENTIAL).
 CC FT TRANSMEM 930 950 POTENTIAL.
 CC FT TRANSMEM 984 1006 POTENTIAL.
 CC FT TRANSMEM 1032 1053 POTENTIAL.
 CC FT TRANSMEM 1087 1132 POTENTIAL.
 CC FT TRANSMEM 1159 1195 POTENTIAL.
 CC FT DOMAIN 1195 1237 PRO-RICH.
 CC FT TRANSMEM 1237 1255 HIS-RICH.
 CC FT CARBOHYD 855 855 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 864 864 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 878 878 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT LIPID 1169 1169 PALMITATE (BY SIMILARITY).
 CC FT SEQUENCE 1237 AA; 136535 MW; 2811D1051552BB2 CRC64;
 SO
 Query Match 33.2%; Score 45.5; DB 1; Length 1237;
 Best Local Similarity 31.0%; Pred. No. 77;
 Matches 9; Conservative 9; Mismatches 8; Indels 3; Gaps 1;
 2 EDITRNA---RHIAOVGDSMDRSPGL 27
 Db 616 EELLRSVAHQOMLKKREOGRLPGL 644
 RESULT 9
 YU87_MYCTU STANDARD; PRT; 472 AA.
 AC 053304;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical 52.6 kDa protein RV3087.
 GN RV3087 OR MT3172 OR MTV013.08.
 OS Bacterioides fragilis.
 OC Bacteria; Firmicutes; Actinobacteriia; Actinobacteridae;
 OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 CC NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Broesch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Hasham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Kellogg A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne K., Skelton J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutherford S., Seeger K., Skelton J., Squares S., Squares R.,
 RA Sultson J.E., Taylor K., Whitehead S., Barrett B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence."
 RL Nature 393:537-544(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., Deboy R., Dodson R., Gwin M.L., Haft D., Hickey S.L.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Esmailaei M.D., Salzberg S.L.,
 RA Delcher A.L., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishal W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains."
 RL Submitted (Apr-2001) to the EMBL/Genbank/DBJ databases.
 CC 1- SIMILARITY: BELONGS TO THE UPF003 FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AL021309; CA616145.1; -
 CC DR EMBL: AE007134; AA47508.1; ALT_INIT.
 CC DR TIGR: MT3172; -
 CC DR Tuberculosis; RV3087; -
 CC DR InterPro: IPR004255; UPF0089.
 CC DR Pfam: PF03007; UPF0089. 1.
 CC KW Hypothetical protein; Complete proteome.
 CC SEQUENCE 472 AA; 52597 MW; AC03BDB4970FC0 CRC64;
 SO
 Query Match 32.8%; Score 45; DB 1; Length 472;
 Best Local Similarity 44.8%; Pred. No. 33;
 Matches 13; Conservative 3; Mismatches 7; Indels 6; Gaps 2;
 3 DITRNARHIAOVGDS---SMDSRIPG 26
 Db 204 DYVR-TEERFAKQDNRVPRFDSAPG 231
 RESULT 10
 KELL_YEAST STANDARD; PRT; 1164 AA.
 AC P38853;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Kell repeats protein 1.
 GN KELL OR IRL18C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=528BC / AB972;
 RA MEDLINE=94378003; PubMed=8091229;
 RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
 Du Z., Favali A., Fulton L., Gallung S., Giesel C., Kirsten J.,
 Kucaba T., Hiller L., Jier M., Johnston L., Langston T.,
 Latrelle P., Louis E.J., Macri C., Mardis E., Meneses S., Mouser L.,
 Nhan M., Rifkin L., Riles L., St Peter H., Trevasakis E., Vaughan K.,
 Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
 Vaubin M.;
 RA "Complete nucleotide sequence of *Saccharomyces cerevisiae* chromosome
 VIII";
 RT Science 265:2077-2082(1994).
 CC [2]
 CC CHARACTERIZATION:
 RA MEDLINE=9903296; PubMed=9786949;
 RA Phillips J., Herskowitz I.;
 RA "Identification of Kel1p, a kelch domain-containing protein involved
 in cell fusion and morphology in *Saccharomyces cerevisiae*";
 RT J. Cell Biol. 143:375-389(1998).
 CC -1- FUNCTION: HAS A ROLE IN CELL MORPHOGENESIS AND CELL FUSION AND MAY
 ANTAGONIZE THE PKC1 PATHWAY.
 CC -1- SUBUNIT: INTERACTS WITH KEL2.
 CC -1- SIMILARITY: CONTAINS 5 KELCH REPEATS.
 CC -1- SIMILARITY: TO YEAST KEL2.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: U10397; AAB68991.1;
 DR PIR: S46769; S46769.
 DR COMPLEYEAST-2PAGE: P38853;
 DR SGD: S0001201; KEL1.
 DR InterPro: IPR001298; Kelch.
 DR Pfam: PF01344; Kelch. 3.
 KW Repeat: Colled coil.
 FT REPEAT 139 186 KELCH 1.
 FT REPEAT 253 307 KELCH 2.
 FT REPEAT 308 357 KELCH 3.
 FT REPEAT 359 409 KELCH 4.
 FT REPEAT 411 460 KELCH 5.
 FT REPEAT 777 931 COLLED COIL (POTENTIAL).
 FT DOMAIN 974 1163 COLLED COIL (POTENTIAL).
 FT DOMAIN 1164 131093 MW; 4300CE570FLDEAD CRC64;
 SO SEQUENCE

Query Match 32.88; Score 45; DB 1; Length 1164;
 Best Local Similarity 53.38; Pred. No. 86;
 Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 2 EDIIRNARIHLAQQV 16
 DB 920 EDIINNVANSSQLD 934
 |||||1:1:1:1:1:1

RESULT 11
 ID DPOA_OXYTR STANDARD; PRT; 1513 AA.
 AC D27152;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE DNA polymerase alpha catalytic subunit (EC 2.7.7.7).
 OS *Oxytricha trifallax*.
 CC Eukaryota; Alveolata; Ciliophora; hypotrichs; Stichotrichidae;

CC Oxytrichidae; Oxytricha.
 OX NCBI_TaxID=5946;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC MEDLINE=97451043; PubMed=9302325;
 RA Hoffman D.C., Prescott D.M.;
 RA "Phylogenetic relationships among hypotrichous ciliates determined
 RT with the macronuclear gene encoding the large, catalytic subunit of
 RT DNA polymerase alpha";
 RL J. Mol. Evol. 45:301-310(1997).
 CC -1- FUNCTION: POLYMERASE ALPHA IN A COMPLEX WITH DNA PRIMAASE IS A
 REPLICATIVE POLYMERASE.
 CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
 + (DNA)(N)
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- MISCELLANEOUS: IN EUKARYOTES, THERE ARE FIVE DNA POLYMERASES:
 ALPHA, BETA, GAMMA, DELTA, AND EPSILON WHICH ARE RESPONSIBLE FOR
 DIFFERENT REACTIONS OF DNA SYNTHESIS
 CC -1- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL: U59426; AAB5771.1;
 DR InterPro: IPR002054; DNA_POL_B.
 DR Pfam: PF00136; DNA_POL_B; 1.
 DR Pfam: PF03104; DNA_POL_B_exo; 1.
 DR PRINTS: PR00106; DNAPOB.
 DR SMART: SM00486; POLBc; 1.
 DR PROSITE: PS00116; DNA_POLYMERASE_B; 1.
 KW TRANSFERASE; DNA-directed DNA polymerase; DNA replication;
 KW DNA-binding; Nuclear protein.
 SO SEQUENCE 1513 AA; 173059 MW; 4DF832BDCFC4416E CRC64;

Query Match 32.88; Score 45; DB 1; Length 1513;
 Best Local Similarity 31.68; Pred. No. 11e+02;
 Matches 6; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

OY 1 QEDIIRNARIHLAQQVDSM 19
 DB 1151 REDVYINLNEYLSIDIGKM 1169
 |||||1:1:1:1:1:1

RESULT 12
 ID G6PD_EMEI STANDARD; PRT; 511 AA.
 AC P41764; Q92408;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) (G6PD).
 CN GSDA OR G6PD
 OS *Emmericella nidulans* (*Aspergillus nidulans*).
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 CC Eurotiales; Trichocomaceae; *Emeticella*.
 OX NCBI_TaxID=5072;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=FGSC 4;
 RA Schaepe P.J., Muller Y., Visser J.;
 RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=MC096;
 RA van den Broek P., Goosen T., Wennekes B., van den Broek H.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: D-glucose 6-phosphate + NADP(+) = D-glucono-

Fri Sep 20 11:03:05 2002

us-09-544-664-14.rsp

Page 9

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DE BID PROTEIN.
 GN BID.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_taxid=10090;
 RP SEQUENCE FROM N.A.
 RC TISSUE=MAMMARY TUMOR. MAP-TGF ALPHA MODEL. 7 MONTHS OLD. GROSS
 RC TISSUE:;
 RA Streusberg R.;
 DR Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC020311; AF020311;
 DR MGD: MGI:108093; LDB:14
 DR InterPro: IPRO00712; BCL-2.
 DR PROSITE: PS01259; BH3; 1-
 SO SEQUENCE 195 AA; 21951 MW; 52F412714FB667F3 CRC64;

Query Match 72.3%; Score 99; DB 11; Length 195;
 Best Local Similarity 72.4%; Pred. No. 3.7e-07;
 Matches 19; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 OY 1 QEDIRNARIHLAQVDSMDRSIPGL 27
 DB 79 QDEIINARIHLAQIDEDMDHIQPTL 105

RESULT 3
 ID 09JLT6 PRELIMINARY; PRT; 196 AA.
 AC 09JLT6;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-DEC-2000 (TREMBLrel. 15, Last sequence update)
 DE APOPTOTIC DEATH AGONIST BID.
 GN BID.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 NC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_taxid=10116;
 RP SEQUENCE FROM N.A.
 RC STRAUB-SPRAGUE-DANLEY;
 RA Chen D., Cao G., Chen J.;
 RT "Cloning of rat apoptotic death agonist (BID) and its different
 RT suppression in ischemia and normal rat brain."
 RT Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR HSSB: P70444; LDB:11;
 DR InterPro: IPRO00712; BCL-2.
 DR PROSITE: PS01259; BH3; UNKNOWN_1.
 SO SEQUENCE 196 AA; 22281 MW; C5F6AD3F442C02E3 CRC64;

Query Match 67.2%; Score 92; DB 11; Length 196;
 Best Local Similarity 63.0%; Pred. No. 8.5e-06;
 Matches 17; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 OY 1 QEDIRNARIHLAQVDSMDRSIPGL 27
 DB 80 QDEIINARIHLAQIDEDMDHIQPTL 106

RESULT 4
 ID 09JK60 PRELIMINARY; PRT; 196 AA.
 AC 09JK60;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE BID PROTEIN.
 GN BID.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_taxid=10116;
 RP SEQUENCE FROM N.A.
 RC STRAUB-SPRAGUE-DANLEY;
 RA Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF259503; AF071759; L.
 DR HSSB: P70444; LDB:11;
 DR InterPro: IPRO00712; BCL-2.
 DR PROSITE: PS01259; BH3; UNKNOWN_1.
 SO SEQUENCE 196 AA; 22249 MW; C5F6AD3F50952E3 CRC64;

Query Match 67.2%; Score 92; DB 11; Length 196;
 Best Local Similarity 63.0%; Pred. No. 8.5e-06;
 Matches 17; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 OY 1 QEDIRNARIHLAQVDSMDRSIPGL 27
 DB 80 QDEIINARIHLAQIDEDMDHIQPTL 106

RESULT 5
 ID 09AL07 PRELIMINARY; PRT; 336 AA.
 AC 09AL07;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DE METEYV-ACCEPTING CHEMOCRECEPTOR-LIKE PROTEIN ORF2 (FRAGMENT).
 OS Pseudomonas fluorescens.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 NC Pseudomonas.
 NCBI_taxid=294;
 RP SEQUENCE FROM N.A.
 RC STRAUB-ATCC 13525;
 RA Feng S.F., Rosebach S.;
 RT "A locus involved in metal homeostasis in Pseudomonas fluorescens
 RT encodes a proton/cation antiporter of the RND family and a two-
 RT component system."
 RT Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY007258; AAC09614.1;
 DR InterPro: IPRO00104; PAS.
 DR InterPro: IPRO00700; PAS-ASSOC_C.
 DR Pfam: PF00785; PAC; 1.
 DR SMART: SM00086; PAC; 2.
 DR SMART: SM00091; PAS; 2.
 DR KX Receptor.
 FT NON-TER 336
 SO SEQUENCE 336 AA; 38039 MW; 867FBE095D4C838 CRC64;

Query Match 40.9%; Score 56; DB 2; Length 336;
 Best Local Similarity 44.4%; Pred. No. 3.5;
 Matches 6; Conservative 7; Mismatches 3; Indels 0; Gaps 0;
 OY 3 DITIRNARIHLAQVDSMD 20
 DB 308 DVMRDARIHLAQVDSMD 325

RESULT 6
 ID 09X2X0 PRELIMINARY; PRT; 190 AA.
 AC 09X2X0;

```

DT 01-NOV-1996 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE HYPOHETICAL 19.7 KDA PROTEIN.
OS Rhodospirillum rubrum (Rhodocycla cententaria).
OC Bacteria; Proteobacteria; alpha subdivision; Rhodospirillaceae;
OC Rhodospirillum.
OX NCBI_TaxID=34018;
ID 124 LARHLYDCGSDRDAVWPC 142
AC 124 LARHLYDCGSDRDAVWPC 142
SC 124 LARHLYDCGSDRDAVWPC 142
Query Match 38.7%; Score 53; DB 2; Length 190;
Best Local Similarity 47.4%; Pred. No. 5.2;
Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 8 IARHLYDCGSDRDAVWPC 26
DB 124 LARHLYDCGSDRDAVWPC 142
RESULT 7
ID 09FPR4 PRELIMINARY; PRT; 957 AA.
AC 09FPR4;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE EDR1.
OS Rhodospirillum rubrum (Rhodocycla cententaria).
OC Bacteria; Proteobacteria; alpha subdivision; Rhodospirillaceae;
OC Rhodospirillum.
OX NCBI_TaxID=34018;
ID 111
AC 111
SC 111
Query Match 37.6%; Score 51.5; DB 10; Length 957;
Best Local Similarity 42.0%; Pred. No. 5.2;
Matches 13; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

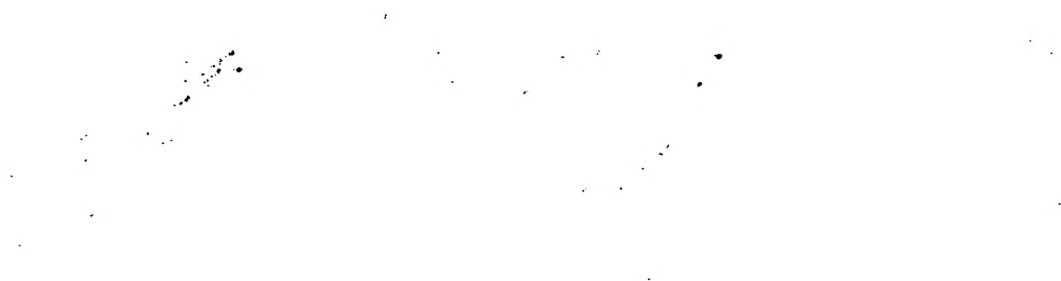
```

```

OY 4 IARHLYDCGSDRDAVWPC 27
DB 534 IOTANAKARSGCDSDRDAVWPC 558
RESULT 8
ID 022663 PRELIMINARY; PRT; 183 AA.
AC 022663;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE T22C1.2 PROTEIN.
OS Rhodospirillum rubrum (Rhodocycla cententaria).
OC Bacteria; Proteobacteria; alpha subdivision; Rhodospirillaceae;
OC Rhodospirillum.
OX NCBI_TaxID=34018;
ID 111
AC 111
SC 111
Query Match 37.2%; Score 51; DB 5; Length 183;
Best Local Similarity 28.6%; Pred. No. 9.9;
Matches 12; Conservative 6; Mismatches 4; Indels 20; Gaps 1;

OY 1 QEDIRNARHLYDCGSDRDAVWPC 22
DB 31 QEDIRNARHLYDCGSDRDAVWPC 22
RESULT 9
ID 09FPR4 PRELIMINARY; PRT; 251 AA.
AC 09FPR4;
DT 01-MAR-2001 (TREMBLrel. 13, Created)
DT 01-MAR-2001 (TREMBLrel. 13, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE EDR1.
OS Rhodospirillum rubrum (Rhodocycla cententaria).
OC Bacteria; Proteobacteria; alpha subdivision; Rhodospirillaceae;
OC Rhodospirillum.
OX NCBI_TaxID=34018;
ID 111
AC 111
SC 111
Query Match 37.2%; Score 51; DB 5; Length 183;
Best Local Similarity 28.6%; Pred. No. 9.9;
Matches 12; Conservative 6; Mismatches 4; Indels 20; Gaps 1;

```

PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
PS treating neurodegenerative disorders, stroke, or cancer -
XX
Claim 18, page 17, 74pp: English.

Claim 18; Page 17; 74pp; English

The invention relates to a peptide conjugate having the formula:
 $(R-X)_n$ -peptide where $n = 1-10$; $X = -CO-$, when the R-X group is attached to the N-terminals of the peptide, or a side chain of the peptide where the functional group of the side chain is NH_2 or OH; or $X = -O$ or $NH-$. When the R-X group is attached to the C-terminals of the peptide, or a side chain of the peptide, where the side chain functional group is COOH or CONH $_2$; and R = 2-18C alkylyl or alkoxy, 2-14C alkylenyl containing one or two double bonds, cyclopropyl, cyclopentenyl, cyclohexenyl optionally monosubstituted with a 1-5 straight or branched chain alkyl group, alternatively optionally monosubstituted with a 1-5 straight or branched chain alkyl group, or a 6-membered ring, the peptides AAb57001-AAb7058 represent analogues of the peptide Bortezomib, a proteasome conjugate. The peptides are useful for modulating apoptosis in the cells of the peptide conjugate is reversing B cell lymphoma/Leukemia 2 (Bcl-2)-mediated blockade of apoptosis in cancer cells. It is also useful for inhibiting Bcl-2 function. In particular, the peptide conjugate is useful for treating a subject afflicted with a cancer characterized by cancer cells that express Bcl-2. The cancer includes prostate, colorectal, gastric, non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or acute or chronic lymphocytic and non-lymphocytic leukemias. The peptide conjugate is also useful for treating disorders characterized by increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.

SQ Sequence 26 AA;

	Query Match	Similarity	100.0%	Score	138	DB	21	Length	26	
	Best Local	Similarity	100.0%	Pred. No.	1	de-14				
	Matches	26	Conservative	0	Mismatches	0	Indels	0	Gaps	0
QY	1	NLMAAQRGRLRMDSPEBSFKCL	26							
		1 nlwaaqrygrlrlmsdcgsgkygi	26							

```

RESULT      2
AAB37002
ID  AAB37002 standard; peptide; 26 AA

```

AC AAB37002

DT 28-FEB-2001 (first entry)

Bcl2 polypeptide BH3 domain peptide #2.

[illegible]

Homo sapiens

PN WO2000059526-A1

PD 12-OCT-2000

06-APR-2000; 2000WO-US09352.

07-APR-1999; 99US-0128202.

PA (UYJE-) UNIV JEFFERSON THOMAS.

PI Huang Z, Wang J, Zhang Z, Shan S, Lu Z,

XX
DF

WPI; 2000-679325/66.

PT New peptide conjugates for modulating apoptosis or for inhibiting B
PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
PT treating neurodegenerative disorders, stroke, or cancer -

PS Claim 18; page 17; 74pp; English.

The invention relates to a peptide conjugate having the formula:

(R-X)-peptide where n = 1-10; X = C=O, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is NH₂ or OH; or X = O or NH, when the R-X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COOH or CONH₂; and R = 2-18C alkyl or alkoxy, 2-14C alkynyl containing one or two double bonds, cyclohexyl, cyclopentyl, cycloheptyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, phenyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, benzyl, if the peptide has AHS3700A, HS3705B represent examples of the peptide sequence.

Peptides depending on amino acids 72-97 of the Hb3 domain of the cell death receptors in the cells of a subject are useful for modulating apoptosis in the cells of a subject. The peptide reversing B cell lymphoma/leukemia 2 (hc1-2)-mediated blockade of apoptosis in cancer cells. It is also useful for inhibiting hc1-2 function. In particular, the peptide conjugate is useful for treating a subject afflicted with a cancer characterized by cancer cells that express Bcl-2. The cancer includes prostate, colorectal, gastric, non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by increased apoptosis, e.g., neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.

SQ Sequence 26 AA;

Query Match	100.0%	Score 138;	DB 21;	Length 26;
Best Local Similarity	100.0%	Pred. No. 1,4e-14;		
Matches 26;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

```
Db      1 nlwaqrgyrelrrmsdefgsfkgl 26
RESULT 3
```

ID AAB37003

AC AAB37003;

DT 28-FEB-2001 (first entry)

KM Cystostatic; neuroprotective; anti-HIV; virinide; cerebroprotective;
KM cardant; Bcl-2 superfamily; B13 domain; cell death agonist; Bad;
KM apoptosis modulation; B cell lymphoma/leukemia 21; cancer; prostate;
KM colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
KM melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
KM stroke; myocardial infarction.

OS Homo sapiens

PN W0200059526-A1

PD 12-OCT-2000

06-APR-2000; 2000WO-US09352

PR 07-APR-1999; 99US-0128202

```

XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Huang Z., Wang J., Zhang Z., Shan S., Lu Z.;
XX
XX WPI: 2000-679325/66.
XX
XX New peptide conjugates for modulating apoptosis or for inhibiting B
XX cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
XX treating neurodegenerative disorders, stroke, or cancer.
XX
XX Claim 18: Page 17: 74pp; English.
XX
XX The invention relates to a peptide conjugate having the formula:
XX (R-X)n-peptide where n = 1-10; X = C=O, when the R-X group is attached
XX to the N-terminus of the peptide, or a side chain of the peptide where
XX the functional group of the side chain is NH2 or OH, or X = O or NH,
XX when the R-X group is attached to the C-terminus of the peptide, or a
XX side chain of the peptide, where the side chain functional group is COOH
XX or CONH2, and R = 2-18C alkyl or alkoxy, 2-14C alkenyl containing one
XX or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally
XX monosubstituted with a branched chain alkyl group,
XX monosubstituted with a branched chain alkyl group,
XX monosubstituted with a branched chain alkyl group,
XX alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples
XX of the peptide portion of the conjugate. The peptides represent analogues
XX of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
XX the Bcl-2 domain of the cell death agonist Bad. The peptide conjugate is
XX useful for modulating apoptosis in the cells of a subject, or for
XX reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of
XX apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
XX function. In particular, the peptide conjugate is useful for treating a
XX subject afflicted with a cancer characterized by cancer cells that
XX express Bcl-2. The cancer includes prostate, colorectal, gastric,
XX non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
XX acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
XX conjugate is also useful for treating disorders characterized by
XX increased apoptosis, e.g., neurodegenerative disorders, acquired
XX immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
XX
XX Sequence 27 AA:
XX
XX Query Match 100.0%; Score 138; DB 21; Length 27;
XX Best Local Similarity 100.0%; Pred. No. 1,4e-14;
XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Db 1 NMAAORYGRLPRMSDFEGSFKGL 26
XX I nlwaagrygrelrmdsfegsfkgl 26
XX
XX RESULT 4
XX AAB37056 standard; peptide: 27 AA.
XX ID AAB37056:
XX AC AAB37056:
XX AS 28-FEB-2001 (first entry)
XX DE Bcl2 polypeptide Bcl3 domain peptide #56.
XX
XX Cytostatic; neuroprotective; anti-HIV; virocidic; cerebroprotective;
XX cardiant; Bcl-2 superfamily; Bcl3 domain; cell death agonist; Bad;
XX apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;
XX colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
XX melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
XX stroke; myocardial infarction.
XX
XX Homo sapiens.
XX MO200059556-A1.
XX
XX 12-OCT-2000.

```

```

XX 06-APR-2000; 2000MO-US09352.
XX
XX 07-APR-1999; 99US-0128202.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Huang Z., Wang J., Zhang Z., Shan S., Lu Z.;
XX
XX WPI: 2000-679325/66.
XX
XX New peptide conjugates for modulating apoptosis or for inhibiting B
XX cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
XX treating neurodegenerative disorders, stroke, or cancer.
XX
XX Claim 18: Page 19: 74pp; English.
XX
XX The invention relates to a peptide conjugate having the formula:
XX (R-X)n-peptide where n = 1-10; X = C=O, when the R-X group is attached
XX to the N-terminus of the peptide, or a side chain of the peptide where
XX the functional group of the side chain is NH2 or OH, or X = O or NH,
XX when the R-X group is attached to the C-terminus of the peptide, or a
XX side chain of the peptide, where the side chain functional group is COOH
XX or CONH2, and R = 2-18C alkyl or alkoxy, 2-14C alkenyl containing one
XX or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally
XX monosubstituted with a 1-5C straight or branched chain alkyl group,
XX phenyl optionally monosubstituted with a 1-5C straight or branched chain
XX alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples
XX of the peptide portion of the conjugate. The peptides represent analogues
XX of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
XX the Bcl-2 domain of the cell death agonist Bad. The peptide conjugate is
XX useful for modulating apoptosis in the cells of a subject, or for
XX reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of
XX apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
XX function. In particular, the peptide conjugate is useful for treating a
XX subject afflicted with a cancer characterized by cancer cells that
XX express Bcl-2. The cancer includes prostate, colorectal, gastric,
XX non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
XX acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
XX conjugate is also useful for treating disorders characterized by
XX increased apoptosis, e.g., neurodegenerative disorders, acquired
XX immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
XX
XX Sequence 27 AA:
XX
XX Query Match 100.0%; Score 138; DB 21; Length 27;
XX Best Local Similarity 100.0%; Pred. No. 1,4e-14;
XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Db 1 NMAAORYGRLPRMSDFEGSFKGL 26
XX I nlwaagrygrelrmdsfegsfkgl 27
XX
XX RESULT 5
XX AAB37055 standard; peptide: 28 AA.
XX ID AAB37055:
XX AC AAB37055:
XX AS 28-FEB-2001 (first entry)
XX DE Bcl2 polypeptide Bcl3 domain peptide #55.
XX
XX Cytostatic; neuroprotective; anti-HIV; virocidic; cerebroprotective;
XX cardiant; Bcl-2 superfamily; Bcl3 domain; cell death agonist; Bad;
XX apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;
XX colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
XX melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
XX stroke; myocardial infarction.
XX
XX Homo sapiens.

```

XX W0200059526-A1.
 PN 12-OCT-2000.
 PD 06-APR-2000; 2000MO-US03352.
 XX 07-APR-1999; 99US-0128202.
 PR (UYDE-) UNIV JEFFERSON THOMAS.
 XX Huang Z, Zhang Z, Shan S, Lu Z;
 PI MPI; 2000-679325/66.
 DR
 XX New peptide conjugates for modulating apoptosis or for inhibiting B
 PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
 XX treating neurodegenerative disorders, stroke, or cancer.
 XX Claim 18; Page 19; 74pp: English.

XX The invention relates to a peptide conjugate having the formula:
 CC (R-X)-peptide where n = 1-10; X = C=O, when the R-X group is attached
 CC to the N-terminus of the peptide, or a side chain of the peptide where
 CC the functional group of the side chain is NH2 or OH; or X = O or NH,
 CC when the R-X group is attached to the C-terminus of the peptide, or a
 CC side chain of the peptide, where the side chain functional group is COOH
 CC or a double bond; R is a hydrophobic, hydrophilic, cationic, anionic,
 CC or nonsubstituted with a 1-5C straight or branched chain alkyl group,
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain
 CC alkyl group, or benzyl. The peptides AAB7001-837058 represent examples
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
 CC the BH3 domain of the cell death agonist Bad. The peptide conjugate is
 CC useful for modulating apoptosis in the cells of a subject, or for
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
 CC function in particular, the peptide conjugates are useful in treating a
 CC condition, such as cancer, neurodegenerative diseases, viral infections,
 CC stroke, and ischemic cell death. The peptide conjugates are also useful
 CC in treating B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of
 CC apoptosis in cancer cells. The cancer includes prostate, colorectal, gastric,
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
 CC conjugate is also useful for treating disorders characterized by
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
 CC
 XX Sequence 28 AA:

Query Match 100.0%; Score 138; DB 21; Length 28;
 Bcl-2 Local Similarity 100.0%; Pred. No. 1, 5e-14;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLMNAGRGRLRMSPDEFGSGFKL 26
 DB 2 nlmwagrygrlrmstdefsgsfkgl 27

RESULT 6
 AAB70370 standard: protein; 162 AA.
 ID AAB70370;
 AC AAB70370;
 XX 02-MAY-2001 (first entry)
 XX Shorter murine BAD mutant amino acid sequence SEQ ID NO:3.
 DE Bcl-XL/Bcl-2 associated cell death regulator; BAD; murine; apoptosis;
 KW immunostimulant; neuroprotective; neurotropic; antischismatic; vlnuagary;
 KW cytoskeletal; antiapoptotic; antiinflammatory; wound healing;
 KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;

KW Immunodeficiency disease; neurodegenerative disease; viral infection;
 KW ischemic cell death; reperfusion cell death; arthritis; infertility;
 KW lymphoproliferative condition; inflammation; autoimmune disease.
 XX Mur musculus.
 XX Synthetic.
 XX W0200110888-A1.
 XX 15-FEB-2001.
 PD 30-MAY-2000; 2000MO-US11864.
 XX 28-MAY-1999; 99US-0136783.
 PR (APOD-) APOPTOSIS TECHNOLOGY INC.
 XX Zhou X;
 PI MPI; 2001-138734/14.
 DR
 XX New mutant Bcl-XL/Bcl-2 associated cell death regulator polypeptide,
 PT useful for screening for candidate compounds which induce or inhibit
 PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
 XX Ser113.
 XX Claim 7; Page 148-149; 157pp: English.

XX The present invention describes an isolated or synthetic polypeptide
 CC (1) comprising a less than full length amino acid sequence of a mutant
 CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its
 CC fragment, which contains amino acid substitutions at Ser118 of a human
 CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine
 CC BAD (shorter murine BAD). (1) has immunostimulant, neuroprotective,
 CC neurotrophic, antischismatic, vulnerable, cytoskeletal, antiviral,
 CC anaplastic, antischismatic, vulnerable, cytoskeletal, antiviral,
 CC and can be used as an apoptosis inducer or inhibitor. BAD polypeptides and
 CC polynucleotides can be used for screening candidate compounds and drugs
 CC for the treatment of cancer, neurodegenerative diseases, viral infections,
 CC ischemic cell death, reperfusion cell death, wound healing, cancer, viral
 CC infections, lymphoproliferative conditions, arthritis, infertility, inflammation and
 CC autoimmune diseases. The present sequence represents a specifically
 CC claimed shorter murine BAD mutant amino acid sequence from the present
 CC invention.
 CC
 XX Sequence 162 AA:

Query Match 100.0%; Score 138; DB 22; Length 162;
 Bcl-2 Local Similarity 100.0%; Pred. No. 1, 1e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLMNAGRGRLRMSPDEFGSGFKL 26
 DB 98 nlmwagrygrlrmstdefsgsfkgl 123

RESULT 7
 AAR95168 standard: protein; 204 AA.
 ID AAR95168;
 AC AAR95168;
 XX 06-JAN-1997 (first entry)
 XX bcl-x(L)/bcl-2 associated death promoter protein.
 DE Bcl-XL/Bcl-2 associated death promoter; Bad; stroke;
 KW polypeptide; bcl-x; cell death; regulator; BH1; BH2; apoptotic cell death;
 KW cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS;

KM serine substituted mutant; apoptosis; cancer; viral infection.
 XX Mus sp.
 OS Synthetic.
 OS
 XX WO9817682-A1.
 PN
 XX 30-APR-1998.
 PD
 XX 17-OCT-1997: 97WO-US19175.
 XX
 XX 18-OCT-1996: 96US-0733505.
 XX
 PA (UNIV) UNIV WASHINGTON.
 PI
 PI Korsmeyer SJ.
 DR WPI: 1998-261422/23.
 DR N-PSDB: AAV27834.
 XX
 XX New mutant BAD polypeptide with phosphorylatable serine replaced -
 PT useful for, e.g. treating reduced apoptosis such as in cancer or
 PT viral infection
 PS
 PS Claim 7: Page 59; 95pp; English.
 XX
 CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
 CC death regulator) proteins, having an amino acid other than Ser at
 CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
 CC present sequence represents a mutant BAD protein. Also described are: (1)
 CC fragments of mutant BAD protein able to decrease cell viability; (2)
 CC fusion proteins of mutant BAD with a heterologous polypeptide that
 CC increases intracellular delivery. Mutant BAD proteins are used to treat
 CC or prevent diseases associated with reduced apoptosis, e.g. cancer,
 CC viral infection, lymphoproliferation, arthritis, infertility.
 CC Inflammation and autoimmune disease. Polynucleotide sequences encoding
 CC mutant BAD proteins can be used similarly by gene therapy or to produce
 CC transgenic animals for use as disease models or in drug screening. BAD
 CC proteins phosphorylated at specified Ser are used to screen for enhancers
 CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful
 CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,
 CC aging or ischemic cell death. The apoptotic status of cells is
 CC determined by measuring relative amounts of phosphorylated and non-
 CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
 CC greater death-promoting activity than wild-type BAD which can become
 CC phosphorylated on the specified Ser, forming a product that does not
 CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
 CC proteins in the cytosol, thus promoting cell survival. The mutants with
 CC Ser substituted cannot bind 14-3-3.
 XX
 XX Sequence 204 AA:
 SO

Query Match 100.0%; Score 138; DB 19; Length 204;
 Best Local Similarity 100.0%; Pred. No. 1,4e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DY 1 NLMAORYGRELRLRMSEDEGSPKGL 26
 DB 140 nlwaagrygrelrmsdegefskgl 165
 |||
 RESULT 10
 AAM61317 standard; Protein: 204 AA.
 XX
 XX AAM61317;
 AC
 XX
 XX 07-OCT-1998 (first entry)
 XX
 XX Mutant BCL-XL/BCL-2 associated cell death regulator #2.
 DE
 XX
 KM Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;

KM serine substituted mutant; apoptosis; cancer; viral infection.
 XX Mus sp.
 OS Synthetic.
 OS
 XX WO9817682-A1.
 PN
 XX 30-APR-1998.
 PD
 XX 17-OCT-1997: 97WO-US19175.
 XX
 XX 18-OCT-1996: 96US-0733505.
 XX
 PA (UNIV) UNIV WASHINGTON.
 PI
 PI Korsmeyer SJ.
 DR WPI: 1998-261422/23.
 DR N-PSDB: AAV27835.
 XX
 XX New mutant BAD polypeptide with phosphorylatable serine replaced -
 PT useful for, e.g. treating reduced apoptosis such as in cancer or
 PT viral infection
 PS
 PS Claim 7: Page 60; 95pp; English.
 XX
 CC The present invention describes mutant BAD (BCL-XL/BCL-2 associated cell
 CC death regulator) proteins, having an amino acid other than Ser at
 CC position 112 and/or 136, relative to the murine BAD 204 aa sequence. The
 CC present sequence represents a mutant BAD protein. Also described are: (1)
 CC fragments of mutant BAD protein able to decrease cell viability; (2)
 CC fusion proteins of mutant BAD with a heterologous polypeptide that
 CC increases intracellular delivery. Mutant BAD proteins are used to treat
 CC or prevent diseases associated with reduced apoptosis, e.g. cancer,
 CC viral infection, lymphoproliferation, arthritis, infertility.
 CC Inflammation and autoimmune disease. Polynucleotide sequences encoding
 CC mutant BAD proteins can be used similarly by gene therapy or to produce
 CC transgenic animals for use as disease models or in drug screening. BAD
 CC proteins phosphorylated at specified Ser are used to screen for enhancers
 CC and inhibitors of serine-phosphatase. Inhibitors are potentially useful
 CC in treatment of excessive apoptosis such as AIDS, neurodegeneration,
 CC aging or ischemic cell death. The apoptotic status of cells is
 CC determined by measuring relative amounts of phosphorylated and non-
 CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
 CC greater death-promoting activity than wild-type BAD which can become
 CC phosphorylated on the specified Ser, forming a product that does not
 CC heterodimerise with BCL-2 or BCL-XL but instead binds to 14-3-3 family
 CC proteins in the cytosol, thus promoting cell survival. The mutants with
 CC Ser substituted cannot bind 14-3-3.
 XX
 XX Sequence 204 AA:
 SO

Query Match 100.0%; Score 138; DB 19; Length 204;
 Best Local Similarity 100.0%; Pred. No. 1,4e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DY 1 NLMAORYGRELRLRMSEDEGSPKGL 26
 DB 140 nlwaagrygrelrmsdegefskgl 165
 |||
 RESULT 11
 AAM61318 standard; Protein: 204 AA.
 XX
 XX AAM61318;
 AC
 XX
 XX 07-OCT-1998 (first entry)
 XX
 XX Mutant BCL-XL/BCL-2 associated cell death regulator #3.
 DE
 XX
 KM Murine; mouse; BCL-XL/BCL-2 associated cell death regulator; BAD protein;

KM serine substituted mutant; apoptosis; cancer; viral infection.
 OS Mus sp.
 XX Synthetic.
 XX MO9817682-A1.
 XX
 PD 30-APR-1998.
 XX
 PD 17-OCT-1997; 97MO-US19175.
 XX
 PD 18-OCT-1996; 96US-0733505.
 XX
 PA (UNIV) UNIV WASHINGTON.
 XX
 PA Korsmeyer SJ;
 XX
 XI WP1: 1998-261422/23.
 DR N-PSDB; AAV27836.
 DR
 PT New mutant BAD polypeptide with phosphorylatable serine replaced
 PT useful for e.g. treating reduced apoptosis such as in cancer or
 PT viral infection
 PT
 PS Claim 7: Page 60-61; 95pp; English.
 XX
 XX The present invention describes mutant BAD (Bcl-XL/Bcl-2 associated cell
 CC death protein) proteins in which one or more serine residues are replaced
 CC with a threonine residue, resulting in a mutant BAD 304
 CC polypeptide having a post-translational modification site. The
 CC present sequence represents a mutant BAD protein. Also described are: (1)
 CC fragments of mutant BAD protein able to decrease cell viability; (2)
 CC fusion proteins of mutant BAD with a heterologous polypeptide that
 CC increases intracellular delivery. Mutant BAD proteins are used to treat
 CC cancer, including hematological malignancies, such as leukemia, lymphoma,
 CC virus-induced lymphoproliferation, testicular cancer, and
 CC inflammation and autoimmune disease. Polynucleotide sequences encoding
 CC mutant BAD proteins can be used similarly by gene therapy or to produce
 CC transgenic animals for use as disease models or in drug screening. BAD
 CC proteins phosphorylated at specified Ser are used to screen for enhancers
 CC and inhibitors of serine-phosphatase. Such mutants are potential useful
 CC in the treatment of cancer and other diseases. Mutant BAD proteins are
 CC used to study the role of BAD in apoptosis. Mutant BAD proteins are used
 CC to study the role of BAD in cell death. The apoptotic status of cells is
 CC determined by measuring relative amounts of phosphorylated and non-
 CC phosphorylated BAD, by usual immunoassays. Mutant BAD proteins have
 CC greater death-promoting activity than wild-type BAD which can become
 CC phosphorylated on the specified Ser, forming a product that does not
 CC inhibit Bcl-XL/Bcl-2. Mutant BAD proteins are used to study the role of
 CC BAD in the cytosol, thus promoting cell survival. The mutants with
 CC Ser substituted cannot bind 14-3-3.
 CC
 XX
 XX Sequence 204 AA:
 SO
 Query Match 100.0%; Score 138; DB 19; Length 204;
 Best Local Similarity 100.0%; Pred. NO. 1.4e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NIMAAOYRGELRRMSDEFGSPKGL 26
 DB 140 nlwaagrygrelrrmsdefgspgl 165
 RESULT 12
 AAM58832 standard; protein: 204 AA.
 XX
 XX AAM58832:
 AC
 XX 23-JUL-1998 (first entry)
 DT
 XX Murine BAD protein.
 DE
 XX BAD protein; Bcl-XL/Bcl-2 associated cell death regulator; 14-3-3;
 KM

KM serine phosphorylation; post-translational modification; apoptosis;
 KM signal transduction regulator; phosphoserine phosphatase; senescence;
 KM immunodeficiency disease; neurodegenerative disease; infertility;
 KM immunodeficiency disease; neurodegenerative condition; arthritis;
 KM inflammation; autoimmune diseases.
 XX
 OS Mus sp.
 XX
 XX MO9809643-A1.
 XX
 PD 12-MAR-1998.
 XX
 PD 09-SEP-1997; 97MO-US15871.
 XX
 PD 09-SEP-1996; 96US-0707868.
 XX
 PA (UNIV) UNIV WASHINGTON.
 XX
 PA Korsmeyer SJ;
 XX
 XI WP1: 1998-207049/18.
 DR
 PT serine-phosphorylated Bcl-X-L/Bcl-2 Associated cell Death regulator
 PT polypeptide - useful for modulation of apoptosis associated with,
 PT e.g. cancer and immunodeficiency diseases
 PT
 PS Claim 3: Fig 8; 61pp; English.
 XX
 XX This sequence represents a novel serine-phosphorylated protein, BAD
 CC (Bcl-XL/Bcl-2 associated cell death regulator). The serine residue is
 CC phosphorylated in a post-translational modification and allows binding
 CC to the 14-3-3 protein which is a signal transduction regulator.
 CC Modulators of phosphorylated BAD, which act through inhibition/activation
 CC of BAD, are used to study the role of BAD in apoptosis. Mutant BAD
 CC result from immunodeficiency diseases, senescence, neurodegenerative
 CC disease, ischemic cell death, reperfusion cell death, infertility and
 CC wound-healing. Decreased apoptosis may result from cancer, viral
 CC infection, lymphoproliferative conditions, arthritis, infertility,
 CC immunodeficiency disease, neurodegenerative disease, and/or total
 CC BAD in a cell is useful for determining the apoptotic state of a cell.
 CC
 XX
 XX Sequence 204 AA:
 SO
 Query Match 100.0%; Score 138; DB 19; Length 204;
 Best Local Similarity 100.0%; Pred. NO. 1.4e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NIMAAOYRGELRRMSDEFGSPKGL 26
 DB 140 nlwaagrygrelrrmsdefgspgl 165
 RESULT 13
 AAB70369 standard; protein: 204 AA.
 XX
 XX AAB70369:
 AC
 XX 02-MAY-2001 (first entry)
 DT
 XX Longer murine BAD mutant amino acid sequence SHQ ID NO:2.
 DE
 XX Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
 KM immunostimulant; neuroprotective; neotrophic; antileukemic; vulnerable;
 KM cyclostatic; antiviral; antitartaric; antileukemic; wound healing;
 KM immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;
 KM immunodeficiency disease; neurodegenerative disease; viral infection;
 KM ischemic cell death; reperfusion cell death; arthritis; infertility;
 KM lymphoproliferative condition; inflammation; autoimmune disease.
 KM

OS Mus musculus.
 OS Synthetic.
 XX W0200110888-A1.
 XX 15-FEB-2001.
 XX 30-MAY-2000; 2000MO-US11864.
 XX 28-MAY-1999; 99US-0136783.
 XX (APO-) APOPTOSIS TECHNOLOGY INC.
 XX Zhou X.
 XX WPI; 2001-138734/14.
 XX New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,
 PT useful for screening for candidate compounds which induce or inhibit
 PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
 PT Ser113 -
 XX
 XX Claim 4; Page 148; 157pp; English.
 CC The present invention describes an isolated or synthetic polypeptide
 CC (1) comprising a less than full length amino acid sequence of a mutant
 CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BMD) or its
 CC fragment, which contains an amino acid substitutions at Ser118 of human
 CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BMD) or its
 CC BMD (shorter murine BMD); (1) has immunostimulant, neuroprotective,
 CC antitoxic, antineoplastic, antiviral,
 CC antitubercular, antiinflammatory and immunosuppressive activities, and
 CC can be used as an apoptosis inducer or inhibitor. BMD polypeptides and
 CC polynucleotides can be used for screening candidate compounds and drugs
 CC inducing or inhibiting apoptosis in a cell. Candidate compounds include
 CC inducing or inhibiting apoptosis in a cell. Candidate compounds include
 CC identified and (mutant) BMD polypeptides are useful in treating cell
 CC immunodeficiency diseases, neurodegenerative diseases, ischemic cell
 CC death, reperfusion cell death, wound healing, cancer, viral infections
 CC and various other diseases. The present invention also provides a method
 CC for identifying and isolating BMD polypeptides and polynucleotides
 CC claimed longer murine BMD mutant amino acid sequence from the present
 CC invention.
 CC
 XX Sequence 204 AA:
 S0
 Query Match 100.0%; Score 138; DB 22; Length 204;
 Best Local Similarity 100.0%; Pred. No. 1,4e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Y0 1 NLMANRGCRGLRMSDEFGSFKGL 26
 DB 140 nlwaagtygrfclrmsdefgsfkyl 165

RESULT 14
 XX W0200110888-A1.
 ID AAM00220 standard; Protein; 567 AA.
 XX AAM00220;
 AC AAM00220;
 XX 31-MAY-2001 (first entry)
 DT
 XX Bad-DTR apoptosis-modifying fusion protein.
 XX Mouse; Bad-DTR; apoptosis; cancer; spinal muscular atrophy;
 KW diptheria toxin receptor binding domain; DTR; neoplasia; tumour;
 KW hyper-proliferation; Alzheimer's disease; neurodegenerative disorder;
 KW transient ischemic neuronal injury; stroke; spinal cord injury;
 KW Huntington's disease.
 XX Chimeric - Mus sp.
 OS

OS Chimeric - Corynebacterium diptheriae.
 OS Chimeric - Synthetic.
 XX Key Location/Qualifiers
 FT Region 3..12
 FT Region /note="10x histidine tag"
 XX W0200112661-A2.
 XX 22-FEB-2001.
 XX 15-AUG-2000; 2000MO-US22293.
 XX 16-AUG-1999; 99US-0149220.
 XX (HARD) HARVARD COLLEGE
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Youle RJ, Liu X, Collier RJ.
 XX WPI; 2001-218343/22.
 XX N-FSD03; AAS00248.
 XX Novel fusion protein for modifying apoptosis in target cell and
 PT reducing apoptosis after transient ischemic neuronal injury, has two
 PT domains which targets protein to a cell and modifies apoptotic response
 PT of cell -
 XX
 XX Claim 4; Page 59-61; 65pp; English.
 CC The sequence represents the amino acid sequence of Bad-DTR apoptosis-
 CC modifying fusion protein comprising Bad gene sequence fused via a short
 CC linker to diptheria toxin translocation domain (DTR). The binding a
 CC target cell and inducing apoptosis by crossing a cellular membrane of the
 CC target cell. The apoptosis-modifying fusion protein comprises at least
 CC two domains: the DTR domain, which targets the fusion protein to the
 CC target cell and the Bcl-XL domain, which modifies an apoptotic response
 CC of the target cell. The fusion protein is useful for modifying
 CC apoptosis in a subject after transient ischemic neuronal injury,
 CC lymphocyte cancer, neoplasia, epithelial, stem tumour or
 CC hyper-proliferative cell or an adipocyte. It is also useful for reducing
 CC apoptosis in a subject after transient ischemic neuronal injury,
 CC various diseases and injury condition through inhibition or enhancement
 CC of apoptosis in a subject after transient ischemic neuronal injury,
 CC such as Alzheimer's disease, Huntington's disease, spinal muscular
 CC atrophy, stroke episodes and unregulated cell growth as in tumours and
 CC various cancers. The apoptosis-modifying fusion protein can be delivered
 CC effectively throughout the body and targeted to selective tissue and
 CC cells.
 CC
 XX Sequence 567 AA:
 S0
 Query Match 100.0%; Score 138; DB 22; Length 567;
 Best Local Similarity 100.0%; Pred. No. 4.3e-13;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Y0 1 NLMANRGCRGLRMSDEFGSFKGL 26
 DB 161 nlwaagtygrfclrmsdefgsfkyl 186

RESULT 15
 XX AAM32476
 ID AAM32476 standard; Protein; 166 AA.
 XX AAM32476;
 AC AAM32476;
 XX 15-JAN-1998 (first entry)
 DT
 XX BAC6 protein for regulating cell death
 XX

XX BPC6 gene; cell death; cell cycle; bcl2; human.
 XX Homo sapiens.
 OS
 XX US5663316-A.
 PN
 XX 02-SEP-1997.
 PD
 XX 18-JUN-1996; 96US-0665617.
 PE
 XX 18-JUN-1996; 96US-0665617.
 PX
 XX (CLON-) CLONTECH LAB INC.
 PA
 XX Xudong Y;
 PI
 XX MPI: 1997-447980/41.
 DR
 XX N-PSDB: AAT91561.
 PT
 XX Isolated BPC6 gene - encodes a protein that regulates cell death
 XX through interaction with bcl-2.
 PS
 XX Claim 1: Column 11-12; 7pp; English.
 CC
 CC The present sequence represents a protein of 166 amino acids. The
 CC sequence is disclosed as being a protein called BPC6 which regulates
 CC cell death through interaction with Bcl-2. The DNA may be used for the
 CC production of the recombinant protein, which can be used in unspecified
 CC therapeutic or diagnostic procedures, as a molecular weight marker, and
 CC to raise antibodies that can be used in unspecified diagnostic or
 CC therapeutic applications and to reduce or eliminate the biological
 CC activity of the BPC6 protein in vivo.
 XX
 XX Sequence 166 AA:

Query Match 82.6%; Score 114; DB 18; Length 166;
 Best Local Similarity 91.7%; Pred. No. 6.1e-10;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 NLMAQRGRLRRKSDPEFGSFX 24
 |||||
 Db 101 nlwaqrygreilrmsdelfvdfk 124

Search completed: September 20, 2002, 10:35:56
 Job time: 424 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OK protein - protein search, using sw model

Run on: September 20, 2002, 10:37:18 Search time 75.64 Seconds
(without alignments)
8.396 Million cell updates/sec

Title: US-09-544-664-2
Perfect score: 138

Sequence: 1 NIMAAOYGRRLRMDSDEFESFGKL 26

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Lasting first 45 summaries

Database: Issued Patents: Aa*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/5C.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/5D.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/5E.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/5F.COMB.pep:*
7: /cgn2_6/ptodata/2/1aa/5G.COMB.pep:*
8: /cgn2_6/ptodata/2/1aa/5H.COMB.pep:*
9: /cgn2_6/ptodata/2/1aa/5I.COMB.pep:*
10: /cgn2_6/ptodata/2/1aa/5J.COMB.pep:*
11: /cgn2_6/ptodata/2/1aa/5K.COMB.pep:*
12: /cgn2_6/ptodata/2/1aa/5L.COMB.pep:*
13: /cgn2_6/ptodata/2/1aa/5M.COMB.pep:*
14: /cgn2_6/ptodata/2/1aa/5N.COMB.pep:*
15: /cgn2_6/ptodata/2/1aa/5O.COMB.pep:*
16: /cgn2_6/ptodata/2/1aa/5P.COMB.pep:*
17: /cgn2_6/ptodata/2/1aa/5Q.COMB.pep:*
18: /cgn2_6/ptodata/2/1aa/5R.COMB.pep:*
19: /cgn2_6/ptodata/2/1aa/5S.COMB.pep:*
20: /cgn2_6/ptodata/2/1aa/5T.COMB.pep:*
21: /cgn2_6/ptodata/2/1aa/5U.COMB.pep:*
22: /cgn2_6/ptodata/2/1aa/5V.COMB.pep:*
23: /cgn2_6/ptodata/2/1aa/5W.COMB.pep:*
24: /cgn2_6/ptodata/2/1aa/5X.COMB.pep:*
25: /cgn2_6/ptodata/2/1aa/5Y.COMB.pep:*
26: /cgn2_6/ptodata/2/1aa/5Z.COMB.pep:*
27: /cgn2_6/ptodata/2/1aa/5AA.COMB.pep:*
28: /cgn2_6/ptodata/2/1aa/5AB.COMB.pep:*
29: /cgn2_6/ptodata/2/1aa/5AC.COMB.pep:*
30: /cgn2_6/ptodata/2/1aa/5AD.COMB.pep:*
31: /cgn2_6/ptodata/2/1aa/5AE.COMB.pep:*
32: /cgn2_6/ptodata/2/1aa/5AF.COMB.pep:*
33: /cgn2_6/ptodata/2/1aa/5AG.COMB.pep:*
34: /cgn2_6/ptodata/2/1aa/5AH.COMB.pep:*
35: /cgn2_6/ptodata/2/1aa/5AI.COMB.pep:*
36: /cgn2_6/ptodata/2/1aa/5AJ.COMB.pep:*
37: /cgn2_6/ptodata/2/1aa/5AK.COMB.pep:*
38: /cgn2_6/ptodata/2/1aa/5AL.COMB.pep:*
39: /cgn2_6/ptodata/2/1aa/5AM.COMB.pep:*
40: /cgn2_6/ptodata/2/1aa/5AN.COMB.pep:*
41: /cgn2_6/ptodata/2/1aa/5AO.COMB.pep:*
42: /cgn2_6/ptodata/2/1aa/5AP.COMB.pep:*
43: /cgn2_6/ptodata/2/1aa/5AQ.COMB.pep:*
44: /cgn2_6/ptodata/2/1aa/5AR.COMB.pep:*
45: /cgn2_6/ptodata/2/1aa/5AS.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	138	100.0	204	1	US-08-333-565-2
2	138	100.0	204	2	US-08-661-479-2
3	138	100.0	204	2	US-08-733-505A-1
4	138	100.0	204	2	US-08-733-505A-12
5	138	100.0	204	2	US-08-733-505A-13
6	138	100.0	204	2	US-08-733-505A-14
7	135	97.8	204	2	US-08-717-123-3
8	114	82.6	166	1	US-08-665-617-2
9	114	82.6	168	2	US-08-717-123-2
10	114	82.6	168	3	US-08-985-335-1
11	114	82.6	168	3	US-08-985-335-7
12	114	82.6	168	4	US-09-410-372-1
13	114	82.6	168	4	US-09-410-372-7
14	113	81.9	23	1	US-08-333-565-10
15	113	81.9	23	2	US-08-661-479-10
16	113	81.9	23	2	US-08-733-505A-95
17	112	73.9	59	2	US-08-733-505A-56
18	102	73.9	59	2	US-08-733-505A-57
19	102	73.9	59	2	US-08-733-505A-58
20	86	62.3	16	1	US-08-333-565-26
21	86	62.3	16	2	US-08-661-479-26
22	61	44.2	11	2	US-08-733-505A-34
23	61	44.2	11	2	US-08-733-505A-35
24	51	37.2	6	2	US-08-661-479-58
25	51	37.2	6	2	US-08-661-479-59
26	33.3	33.3	946	3	US-09-074-779-3
27	46	33.3	946	4	US-09-386-774-3

ALIGNMENTS

28	44	31.9	263	4	US-09-651-656-27	Sequence 27, Appl
29	43	31.2	81	1	US-08-497-313-19	Sequence 19, Appl
30	43	31.2	213	3	US-08-718-738-18	Sequence 18, Appl
31	43	31.2	213	4	US-09-221-844-18	Sequence 18, Appl
32	43	31.2	380	1	US-08-153-848-40	Sequence 40, Appl
33	43	31.2	380	3	US-09-299-843A-40	Sequence 40, Appl
34	43	31.2	380	4	US-09-088-337B-40	Sequence 40, Appl
35	43	31.2	380	5	PCT-US93-11153-40	Sequence 40, Appl
36	42	30.4	322	4	US-09-359-161-7	Sequence 7, Appl
37	42	30.4	348	2	US-08-997-080-170	Sequence 170, App
38	42	30.4	348	2	US-08-997-362-170	Sequence 170, App
39	42	30.4	348	4	US-09-095-855-170	Sequence 170, App
40	42	30.4	348	4	US-09-324-542-170	Sequence 170, App
41	42	30.4	393	2	US-08-997-080-94	Sequence 94, Appl
42	42	30.4	393	3	US-08-997-362-94	Sequence 94, Appl
43	42	30.4	393	3	US-08-873-970-94	Sequence 94, Appl
44	42	30.4	393	4	US-09-095-855-94	Sequence 94, Appl
45	42	30.4	393	4	US-09-324-542-94	Sequence 94, Appl

RESULT 1
US-08-333-565-2
Sequence 2, Application US/08333565
Patent No. 5622822
GENERAL INFORMATION:
APPLICANT: KOSMEYER, Stanley I.
TITLE OF INVENTION: POLYMER-2 ASSOCIATED CELL DEATH
NUMBER OF INVENTIONS: 1
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Kounte and Crew
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,565
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15766A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2422
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..204
OTHER INFORMATION: /note- "Deduced amino acid sequence
OTHER INFORMATION: of mouse BMD."

Query Match 100.0% Score 138 DB 1 Length 204;
Best local similarity 100.0% Pred. No. 46-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NMAAORYGRELRLMSDEFGSFKGL 26
|||||
DB 140 NMAAORYGRELRLMSDEFGSFKGL 165

RESULT 2

US-08-661-479-2
Sequence 2, Application US/08661479
Patent No. 5834209
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-X/Bcl-2 ASSOCIATED CELL DEATH
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,479
FILING DATE: 11-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/333,565
FILING DATE: 31-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION/DOCKET NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: protein
LOCATION: 1..204
OTHER INFORMATION: /note= "Deduced amino acid sequence
OTHER INFORMATION: of mouse BAD."
US-08-661-479-2

Query Match 100.0%; Score 138; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 4e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NMAAORYGRELRLMSDEFGSFKGL 26
|||||
DB 140 NMAAORYGRELRLMSDEFGSFKGL 165

RESULT 3
US-08-733-505A-1
Sequence 1, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR

NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION/DOCKET NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5108
TELEFAX: (314) 727-5102
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-733-505A-1

Query Match 100.0%; Score 138; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 4e-14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NMAAORYGRELRLMSDEFGSFKGL 26
|||||
DB 140 NMAAORYGRELRLMSDEFGSFKGL 165

RESULT 4
US-08-733-505A-12
Sequence 12, Application US/08733505A
Patent No. 5856445
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MISSOURI
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,505A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION/DOCKET NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 727-5188
 TELEFAX: (314) 727-6092
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 204 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-733-505A-12

Query Match 100.0%; Score 138; DB 2; Length 204;
 Best Local Similarity 100.0%; Pred. No. 4e-14;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMAAORGYRELRMSDEFGSFKGL 26
 DB 140 NMAAORGYRELRMSDEFGSFKGL 165

RESULT 5
 US-08-733-505A-13
 ; Sequence 13, Application US/08733505A
 ; Patent No. 5856445
 ; GENERAL INFORMATION:
 ; APPLICANT: KORMEYER, STANLEY J.
 ; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
 ; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
 ; NUMBER OF SEQUENCES: 60
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
 ; STREET: 7733 FORSTH BLVD., SUITE 1400
 ; CITY: ST. LOUIS
 ; STATE: MISSOURI
 ; COUNTRY: USA
 ; ZIP: 63105
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/733,505A
 ; FILING DATE:
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: HOLLAND, DONALD R.
 ; REGISTRATION NUMBER: 35,197
 ; REFERENCE/DOCKET NUMBER: 965458
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (314) 727-5188
 ; TELEFAX: (314) 727-6092
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 204 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-733-505A-13

Query Match 100.0%; Score 138; DB 2; Length 204;
 Best Local Similarity 100.0%; Pred. No. 4e-14;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMAAORGYRELRMSDEFGSFKGL 26
 DB 140 NMAAORGYRELRMSDEFGSFKGL 165

RESULT 6

US-08-733-505A-14
 ; Sequence 14, Application US/08733505A
 ; Patent No. 5856445
 ; GENERAL INFORMATION:
 ; APPLICANT: KORMEYER, STANLEY J.
 ; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
 ; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
 ; NUMBER OF SEQUENCES: 60
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
 ; STREET: 7733 FORSTH BLVD., SUITE 1400
 ; CITY: ST. LOUIS
 ; STATE: MISSOURI
 ; COUNTRY: USA
 ; ZIP: 63105
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/733,505A
 ; FILING DATE:
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: HOLLAND, DONALD R.
 ; REGISTRATION NUMBER: 35,197
 ; REFERENCE/DOCKET NUMBER: 965458
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (314) 727-5188
 ; TELEFAX: (314) 727-6092
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 204 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-733-505A-14

Query Match 100.0%; Score 138; DB 2; Length 204;
 Best Local Similarity 100.0%; Pred. No. 4e-14;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMAAORGYRELRMSDEFGSFKGL 26
 DB 140 NMAAORGYRELRMSDEFGSFKGL 165

RESULT 7
 US-08-717-123-3
 ; Sequence 3, Application US/08717123
 ; Patent No. 5856703
 ; GENERAL INFORMATION:
 ; APPLICANT: Oltersdorf, William A.
 ; TITLE OF INVENTION: Human BAD polypeptides, Encoding Nucleic
 ; TITLE OF INVENTION: Acids and Methods of Use
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell and Flores
 ; STREET: 4370 La Jolla Village drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/717.123
 FILING DATE: 20-SEP-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-ID 1929
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9901
 TELEFAX: (619) 535-9949
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 204 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-717-123-3

Query Match 97.8%; Score 135; DB 2; Length 204;
 Best Local Similarity 96.2%; Pred. No. 1.2e-13;
 Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 NUNAAQRYGRLRMKSDPEFGSK 26
 DB 140 NUNAAQRYGRLRMKSDPEFGSK 165

RESULT 8
 US-08-665-617-2
 Sequence 2, Application US/0865617
 Patent No. 5653316
 GENERAL INFORMATION:
 APPLICANT: xudong, yin
 TITLE OF INVENTION: Gene and Protein for Regulation of Cell Death
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Saliwanchik & Saliwanchik
 STREET: 2421 N.W. 41st Street, Suite A-1
 CITY: Gainesville
 STATE: Florida
 COUNTRY: USA
 ZIP: 32606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/665.617
 FILING DATE: 08/23/96
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Saliwanchik, David R.
 REGISTRATION NUMBER: 31,794
 REFERENCE/DOCKET NUMBER: CL-8
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (352) 375-8100
 TELEFAX: (352) 372-5800
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 166 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-665-617-2

Query Match 82.6%; Score 114; DB 1; Length 166;
 Best Local Similarity 91.7%; Pred. No. 1.8e-10;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 NUNAAQRYGRLRMKSDPEFGSK 24

DB 101 NUNAAQRYGRLRMKSDPEFGSK 124

RESULT 9
 US-08-717-123-2
 Sequence 2, Application US/08717123
 Patent No. 5963703
 GENERAL INFORMATION:
 APPLICANT: Orye, William A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-ID 1929
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9901
 TELEFAX: (619) 535-9949
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 168 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-717-123-2

Query Match 82.6%; Score 114; DB 2; Length 168;
 Best Local Similarity 91.7%; Pred. No. 1.8e-10;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 NUNAAQRYGRLRMKSDPEFGSK 24
 DB 103 NUNAAQRYGRLRMKSDPEFGSK 126

RESULT 10
 US-08-985-335-1
 Sequence 1, Application US/08985335
 Patent No. 6080847
 GENERAL INFORMATION:
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Yue, Henry
 APPLICANT: Lal, Preeti
 APPLICANT: Shah, Purni
 APPLICANT: Corley, Neil C.
 TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Dr.
 CITY: Palo Alto
 STATE: CA

```

? COUNTRY: USA
? ZIP: 94304
? COMPUTER READABLE FORM:
? REGISTRATION NUMBER: 36,749
? TELEPHONE: 650-845-0555
? TELEFAX: 650-845-4166
? OPERATING SYSTEM: DOS
? SOFTWARE: FASTSEQ for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/985,335
? FILING DATE: Filed Herewith
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? REGISTRATION NUMBER: 36,749
? TELEPHONE: 650-845-0555
? TELEFAX: 650-845-4166
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 168 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? IMMEDIATE SOURCE:
? CLONE: SYNORAB01
? LIBRARY: SYNORAB01
? CLORE: 358673
?
? US-08-985-335-1
?
? Query Match 82.6%; Score 114; DB 3; Length 168;
? Best Local Similarity 91.7%; Pred. No. 1,8e-10;
? Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
?
? QY 1 NMAAQRGRELRRMSDEFYSFK 24
? Db 103 NMAAQRGRELRRMSDEFYSFK 126
?
? RESULT 11
? US-08-985-335-7
? Sequence 7, Application US/08983335
? Patent No. 606044
? GENERAL INFORMATION:
? APPLICANT: Hillman, Jennifer L.
? APPLICANT: Yue, Henry
? APPLICANT: Yee, Henry
? APPLICANT: Shah, Purni
? APPLICANT: Corley, Neil C.
? TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
? NUMBER OF SEQUENCES: 9
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Incyte Pharmaceuticals, Inc.
? STREET: 17400 Center Dr.
? CITY: Palo Alto
? STATE: CA
? COUNTRY: USA
? ZIP: 94304
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? OPERATING SYSTEM: IBM Compatible
? SOFTWARE: FASTSEQ for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/985,335
? FILING DATE: Filed Herewith
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? ATTORNEY/AGENT INFORMATION:

```

```

? NAME: Billings, Lucy J.
? REGISTRATION NUMBER: 36,749
? TELEPHONE: 650-845-0555
? TELEFAX: 650-845-4166
? INFORMATION FOR SEQ ID NO: 7:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 168 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? IMMEDIATE SOURCE:
? CLONE: SYNORAB01
? LIBRARY: SYNORAB01
? CLORE: 358673
?
? US-08-985-335-7
?
? Query Match 82.6%; Score 114; DB 3; Length 168;
? Best Local Similarity 91.7%; Pred. No. 1,8e-10;
? Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
?
? QY 1 NMAAQRGRELRRMSDEFYSFK 24
? Db 103 NMAAQRGRELRRMSDEFYSFK 126
?
? RESULT 12
? US-09-410-372-1
? Sequence 1, Application US/09410372
? Patent No. 6281334
? GENERAL INFORMATION:
? APPLICANT: Hillman, Jennifer L.
? APPLICANT: Yue, Henry
? APPLICANT: Yee, Henry
? APPLICANT: Shah, Purni
? APPLICANT: Corley, Neil C.
? TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
? NUMBER OF SEQUENCES: 9
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Incyte Pharmaceuticals, Inc.
? STREET: 3174 Porter Dr.
? CITY: Palo Alto
? STATE: CA
? COUNTRY: USA
? ZIP: 94304
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? OPERATING SYSTEM: IBM Compatible
? SOFTWARE: FASTSEQ for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/410,372
? FILING DATE:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Billings, Lucy J.
? REGISTRATION NUMBER: 36,749
? TELEPHONE: 650-845-0555
? TELEFAX: 650-845-4166
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 168 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? IMMEDIATE SOURCE:
? LIBRARY: SYNORAB01

```

Fri Sep 20 11:03:06 2002

us-09-544-664-2.rai

Page 6

CLONE: 358673
US-09-410-372-1

Query Match 82.6%; Score 114; DB 4; Length 168;
Best Local Similarity 91.7%; Pred. No. 1 Be-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 NLMAAORYGRELHMSDEFGSFK 24
DB 103 NLMAAORYGRELHMSDEFGSFK 126

RESULT 13
US-09-410-372-7
Sequence 7; Application US/09410372
Patent No. 6281334
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Shah, Parul C
APPLICANT: Korman, Stanley J
TITLE OF INVENTION: PROTEIN ASSOCIATED WITH CELL
TITLE OF INVENTION: PROLIFERATION
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Inocyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410.372
PUBLICATION DATE:
PUBLICATION DATA:
APPLICATION NUMBER: 08/985,335
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-853-0535
TELEFAX: 650-853-0536
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1683637
US-09-410-372-7

Query Match 82.6%; Score 114; DB 4; Length 168;
Best Local Similarity 91.7%; Pred. No. 1 Be-10;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 NLMAAORYGRELHMSDEFGSFK 24
DB 103 NLMAAORYGRELHMSDEFGSFK 126

RESULT 14

US-08-333-565-10
Sequence 10; Application US/08333565
Patent No. 562852
GENERAL INFORMATION:
APPLICANT: KORMAN, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourille and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,565
PUBLICATION DATE: 51,435,1594
PUBLICATION DATA: 435,1594
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-333-565-10

Query Match 81.9%; Score 113; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2 Be-11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NLMAAORYGRELHMSDEFG 21
DB 3 NLMAAORYGRELHMSDEFG 23

RESULT 15
US-08-661-479-10
Sequence 10; Application US/08661479
Patent No. 5814209
GENERAL INFORMATION:
APPLICANT: KORMAN, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourille and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,479

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: September 20, 2002, 10:39:02 ; Search time 55.59 seconds

(without alignments)
26.116 Million cell updates/sec

Title: US-09-544-664-2

Perfect score: 138

Sequence: 1 NIMAGRGRLRMNSDPFGSKGL 26

Scoring table:

RUSOM62
Gapop 10.0 , Gapext 0.5

Searched:

283138 seqs, 96089314 residues

Total number of hits satisfying chosen parameters:

283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing:

Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR.71:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	138	100.0	204	2	A55671	bad protein - mouse
2	138	100.0	204	2	A55671	inter-alpha-trypsin
3	53	38.4	223	2	D70760	inter-alpha-trypsin
4	53	38.4	223	2	S54354	inter-alpha-trypsin
5	52	37.7	370	2	S38185	2-dehydro-3-deoxyp
6	51	37.0	232	2	A42095	floral homeotic pr
7	50	36.2	374	2	C83338	serpinin-like prote
8	49	35.5	453	2	A81517	probable chitinase
9	48.5	35.1	314	2	S40376	inter-alpha-trypsin
10	48.5	35.1	314	2	T02975	annexin p35 - malz
11	48.5	35.1	314	2	T02975	transforming prote
12	48.5	35.1	314	2	C36365	oxidoreductase, so
13	48.5	35.1	314	2	F72829	oxidoreductase, so
14	48.5	35.1	314	2	F72829	oxidoreductase, so
15	48.5	35.1	314	2	G82308	oxoglutarate dehyd
16	47	34.1	597	2	P82668	hypothetical prote
17	47	34.1	597	2	P82668	hypothetical prote
18	47	34.1	597	2	P82668	hypothetical prote
19	46.5	33.7	314	2	T02961	annexin p33 - malz
20	46.5	33.7	314	2	T02961	annexin p33 - malz
21	46.5	33.7	314	2	T02961	annexin p33 - malz
22	46.5	33.7	314	2	T02961	annexin p33 - malz
23	46.5	33.7	314	2	T02961	annexin p33 - malz
24	46.5	33.7	314	2	T02961	annexin p33 - malz
25	46.5	33.7	314	2	T02961	annexin p33 - malz
26	46.5	33.7	314	2	T02961	annexin p33 - malz
27	46.5	33.7	314	2	T02961	annexin p33 - malz
28	46.5	33.7	314	2	T02961	annexin p33 - malz
29	46.5	33.7	314	2	T02961	annexin p33 - malz

30	45	32.6	165	2	S59889	chlorocruorin chain
31	45	32.6	295	2	F83201	conserved hypothet
32	45	32.6	346	2	H93406	sodium ion pump ox
33	45	32.6	591	2	B44465	oxalacetate decar
34	45	32.6	591	2	A80309	oxalacetate decar
35	45	32.6	596	2	A28088	oxalacetate decar
36	45	32.6	596	2	A28088	oxalacetate decar
37	45	32.6	715	2	S52675	env polyprotein -
38	45	32.6	864	1	VCL064	hypothetical prote
39	45	32.6	1263	2	T19472	hypothetical prote
40	45	32.6	1263	2	T19472	hypothetical prote
41	45	32.6	1263	2	T19472	hypothetical prote
42	44.5	32.2	75	2	T01993	hypothetical prote
43	44.5	32.2	455	2	D83264	hypothetical prote
44	44.5	32.2	536	2	AG1482	hypothetical prote
45	44.5	32.2	910	2	G91024	NADH dehydrogenase

ALIGNMENTS

RESULT 1
Query Match 100.0% Score 138.76 Length 204:
Bad protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-Mar-1995 #sequence-revision 03-Mar-1995 #text-change 05-Nov-1999
C:Accession: A55671
R:Yang, B.; Zhai, J.; Jockey, J.; Boise, L.R.; Thompson, C.B.; Korsmeyer, S.J.
A:Title: Bad -291 heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and promotes apoptosis
A:Accession: A55671
A:Reference number: MIMD:95136361
A:Status: preliminary: not compared with conceptual translation
A:Accession: A55671
A:Keywords: heterodimer

Query Match 100.0% Score 138.76 Length 204:
Bad protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-Mar-1995 #sequence-revision 03-Mar-1995 #text-change 05-Nov-1999
C:Accession: A55671
R:Yang, B.; Zhai, J.; Jockey, J.; Boise, L.R.; Thompson, C.B.; Korsmeyer, S.J.
A:Title: Bad -291 heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and promotes apoptosis
A:Accession: A55671
A:Reference number: MIMD:95136361
A:Status: preliminary: not compared with conceptual translation
A:Accession: A55671
A:Keywords: heterodimer

DB 140 NIMAGRGRLRMNSDPFGSKGL 165

OY 1 NIMAGRGRLRMNSDPFGSKGL 26

DB 140 NIMAGRGRLRMNSDPFGSKGL 165

OY 1 NIMAGRGRLRMNSDPFGSKGL 26

DB 140 NIMAGRGRLRMNSDPFGSKGL 165

OY 1 NIMAGRGRLRMNSDPFGSKGL 26

DB 140 NIMAGRGRLRMNSDPFGSKGL 165

OY 1 NIMAGRGRLRMNSDPFGSKGL 26

DB 140 NIMAGRGRLRMNSDPFGSKGL 165

OY 1 NIMAGRGRLRMNSDPFGSKGL 26

DB 140 NIMAGRGRLRMNSDPFGSKGL 165

OY 1 NIMAGRGRLRMNSDPFGSKGL 26

DB 140 NIMAGRGRLRMNSDPFGSKGL 165

OY 1 NIMAGRGRLRMNSDPFGSKGL 26

DB 140 NIMAGRGRLRMNSDPFGSKGL 165

OY 1 NIMAGRGRLRMNSDPFGSKGL 26

DB 140 NIMAGRGRLRMNSDPFGSKGL 165

OY 1 NIMAGRGRLRMNSDPFGSKGL 26

DB 140 NIMAGRGRLRMNSDPFGSKGL 165

OY 1 NIMAGRGRLRMNSDPFGSKGL 26

DB 140 NIMAGRGRLRMNSDPFGSKGL 165

OY 1 NIMAGRGRLRMNSDPFGSKGL 26

DB 140 NIMAGRGRLRMNSDPFGSKGL 165

[illegible]

C.Date: 31-Dec-1999 #sequence-revision 31-Dec-1999 #text-change 22-Jun-1999
C.Accession: S88185; S46126; S46130; JN0322; B48651
R.Donlgton, F.; Bileau, N.; Aigle, M.; Crouzet, M.
Feat 9, 1131-1177, 1999, sequence of a 5794 bp segment located on the right arm of chr
A.Reference number: S88185; M01D:940786/5
A.Accession: S38185
A.Status: translation not shown
A.Molecule type: DNA
A.Residues: 1-370 <MD>
A.Cross-references: DBI:120236; MID:g311101; PIDR:A465607.1; PTD:g311102
Submitted to the Protein Sequence database, August 1994
A.Reference number: S45906
A.Accession: S46126
A.Molecule type: DNA
A.Residues: 1-370 <ALC>
A.Cross-references: EMBL:D33118; MID:g536664; PIDR:CA485212.1; PTD:g536665; MIPS:YBR
submitted to the Protein Sequence database, August 1994
A.Reference number: S45940
A.Accession: S46130
A.Molecule type: DNA
A.Residues: 1-370 <ACS>
R.Kuenzler, M.; Parvayichin, G.; Egli, C.M.; Imiger, S.; Braue, G.H.
Gene 113, 67-74, 1992
A.Title: Cloning, primary structure and regulation of the AR04 gene, encoding the tyrosine
A.Reference number: JN0322; M01D:922534/9
A.Accession: JN0322
A.Residues: 1-370 <AR04>
A.Cross-references: EMBL:X63107
R.Kuenzler, M.; Balmeill, T.; Eggli, C.M.; Parvayichin, G.; Brans, G.H.
Bacteriol 175, 5548-5558, 1993
A>Title: Cloning, primary structure, and regulation of the HIS7 gene encoding a bifum
A.Accession: B48651
A.Molecule type: DNA
A>Status: preliminary
A.Molecule type: DNA
A.Cross-references: GB:X63107
C.Commentary: This enzyme catalyzes the condensation of phosphoenolpyruvate and D-erythr
A.Gene: SGD:AR04
A.Cross-references: SGD:S000453; MIPS:YBR249c
A.Map position: 2R
C.Function:
Description: aldehyde-lyase; carbon-carbon lyase
Reaction: 2-phosphoglycerate + H₂O = pyruvate + H₂
A.Note: first step in shikimate pathway
C.Superfamily: phospho-2-dehydro-3-deoxyheptonate aldolase
C.Keywords: aldehyde-lyase; aromatic amino acid biosynthesis; carbon-carbon lyase; cy

C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40376
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin cbl genes and their hypermutation.
A:Reference number: S40372; MUID:94080891
A:Accession: S40376
A:Status: preliminary; translation not shown
A:Residues: 1-111
A:Molecule type: mRNA
A:Cross-references: EMBL:X72486; NID:9441440; PTD:CAA51154.1; PTD:9441441
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterodimer; immunoglobulin
F:34-113/Domain: immunoglobulin homology <IMM>

Query Match 35.1%; Score 48.5; DB 2; Length 134;
Best Local Similarity 38.2%; Pred. No. 7.8;
Matches 13; Conservative 1; Mismatches 9; Indels 11; Gaps 1;
OY 3 MAAGVGRRLRRM-----SDEGSPFG 25
DB 58 WFRGRGSPRRRLRYNSKDSGVSHFGSGSG 91

RESULT 11
T02975
annexin P35 - maize
C:Species: Zea mays (maize)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
A:Accession: T02975
R:Greenland, A.J.
Plant Physiol. 112, 1391-1396, 1996
A:Title: cDNA isolation and gene expression of maize annexins P33 and P35.
A:Reference number: 214796; MUID:97032863
A:Accession: T02975
A:Status: preliminary; translated from GB/EWBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-314 <AAT>
A:Cross-references: EMBL:X98245; NID:91370602; PTD:CAA66901.1; PTD:91370603
A:Experimental source: cultivar clipper; root clip
A:Superfamily: annexin I; annexin repeat homology
F:14-85/Domain: annexin repeat homology <ANN>

Query Match 35.1%; Score 48.5; DB 2; Length 314;
Best Local Similarity 47.6%; Pred. No. 19;
Matches 10; Conservative 4; Mismatches 6; Indels 1; Gaps 1;
OY 5 AQRVGR-LRRMSDEFSGSK 24
DB 54 AEVQKELRLAADSHIKFE 74

RESULT 12
C36365
transforming protein homolog MRAS3 - Rhizomucor racemosus
C:Species: Rhizomucor racemosus
C:Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 19-Jan-2001
C:Accession: C36365
R:Caestele, W.L.; McConnell, D.G.; Wang, S.Y.; Lee, Y.T.; Linz, J.E.
Mol. Cell. Biol. 10, 6654-6663, 1990
A:Title: Expression of a gene family in the dimorphic fungus Mucor racemosus which exhibit
A:Reference number: A36365; MUID:91061774
A:Accession: C36365
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-206 <CA>
A:Cross-references: GB:MS5177
A:Experimental source: transforming protein; translation elongation factor Tu homology
C:Superfamily: GTP-binding P-loop
F:11-126/Domain: translation elongation factor Tu homology <TGF>

F:17-24/Region: nucleotide-binding motif A (P-loop)
F:123-126/Region: GTP-binding NKXD motif
F:153-155/Region: GTP-binding SAK/L motif
F:23,24,42,123,124,126,153/Binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser) #

Query Match 34.8%; Score 48; DB 2; Length 206;
Best Local Similarity 62.5%; Pred. No. 14;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
OY 10 RLRRMDEGSPFG 25
DB 169 RLRRMKNKDSGRSKG 184

RESULT 13
F72289
oxidoreductase, sol/deh family - Thermococcus maritima (strain MS88)
C:Species: Thermococcus maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
A:Accession: F72289
R:Neilson, K.E.; Clayton, R.A.; Gill, S.R.; Gwynn, M.L.; Dodson, R.J.; Hafl, D.H.; Hic
C.M.; Hic, M.M.; Stewart, A.M.; Cotton, M.D.; Pratic, M.S.; Phillips, C.A.; Richardson,
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A:Reference number: A72200; MUID:99287316
A:Accession: F72289
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-220 <ARN>
A:Cross-references: GB:AE001772; GB:AE000512; NID:94981693; PTD:AA036230.1; PTD:9498
A:Experimental source: strain MS88
A:Gene: TM1154
C:Superfamily: yeast SOL3 protein

Query Match 34.8%; Score 48; DB 2; Length 220;
Best Local Similarity 34.8%; Pred. No. 15;
Matches 8; Conservative 8; Mismatches 7; Indels 0; Gaps 0;
OY 4 AQRVGR-LRRMSDEFSGSK 26
DB 111 ACERVENKSHNTDFDLALIM 133

RESULT 14
T08545
threonine synthase (EC 4.2.99.2) precursor - Arabidopsis thaliana
N:Alternate names: protein F27813.80
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 07-Dec-1999
C:Accession: T08545; S71362; S74307
R:Bevan, M.; Zimmermann, M.; Gruenewald, A.; Wandlitz, R.; Bancroft, I.; Newes, H.W.;
submitted to the Protein Sequence database, May 1999
A:Reference number: 214742
A:Accession: T08545
A:Molecule type: DNA
A:Residues: 1-526 <REV>
A:Cross-references: EMBL:AL050352; GSPDB:GM00062; ATSP:F27813.80
A:Experimental source: cultivar Columbia; BAC clone F27813
R:Curien, G.; Dumas, R.; Ravanel, S.; Douce, R.
FEBS Lett. 390, 85-90, 1996
A:Title: Characterization of an Arabidopsis thaliana cDNA encoding an S-adenosylmethi
A:Reference number: S71362; MUID:96314555
A:Accession: S71362
A:Molecule type: mRNA
A:Residues: 1-1,3-526 <CUR>
A:Cross-references: EMBL:L41666; NID:91448916; PTD:AA04607.1; PTD:91448917
A:Accession: S74307
A:Molecule type: protein
A:Residues: 40-54 <CUR>

100

100

100

100

100

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2002, 11:04:28 ; Search time 44.99 Seconds

(without alignments)
22.376 Million cell updates/sec

Title: US-09-544-664-2

Perfect score: 139

Sequence: 1 NIMAAQRYGRLRMNDPEFGFKL 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40.4

Pred. No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	138	100.0	204	BAD_MOUSE	061337 mus musculus
2	138	100.0	205	BAD_MOUSE	035147 rattus norv
3	114	82.6	168	1BAD_HUMAN	Q92934 homo sapien
4	54	39.1	946	1TRH2_MOUSE	P92729 mesocricetu
5	53	38.4	946	1TRH2_MOUSE	061703 mus musculu
6	52	37.7	370	1AROG_YEAST	P32449 saccharomyc
7	51	37.0	232	1AP3_ARATH	P35632 arabidopsis
8	49	35.5	453	1RWDG_PSEAE	091403 pseudomonas
9	48	34.8	205	1RAS3_HIERA	P22280 rhizomucor
10	48	34.8	220	1GRLI_THESA	094008 thermotoga
11	48	34.8	519	1THRC_SOLTU	096728 atalapha
12	48	34.8	526	1TRHC_ARATH	094321 homo sapien
13	48	34.8	128	1BIR_HUMAN	043421 antipoleira
14	46.5	33.1	128	1BIR_HUMAN	043421 antipoleira
15	46.5	33.7	432	1PBR2_MOUSE	P13823 campylobact
16	46	33.3	946	1TRH2_HUMAN	046122 campylobact
17	46	33.3	1378	1RPOB_CAMEF	P21259 polychocis
18	45.5	33.0	287	1PRPA_POLPE	001133 calloritis
19	45.5	33.0	328	1PMRA_CALPA	009669 kluyveromyc
20	45	32.6	328	1SNR4_KIUTA	003030 salmonella
21	45	32.6	590	1PCOA_SALTY	003030 salmonella
22	45	32.6	595	1DKOA_RLEPN	013347 klebsiella
23	45	32.6	653	1HT2A_HUMAN	013347 homo sapien
24	45	32.6	865	1ENV_SIVAT	P05868 simian immu
25	45	32.6	1557	1LMLI_CAEEL	018823 caenorhabdi
26	44.5	32.2	907	1NDOG_ECOLI	P33602 escherichia
27	44.5	32.2	907	1NDOG_ECOLI	P33602 escherichia
28	44	31.9	196	1BIR_MOUSE	054918 ratu musculu
29	44	31.9	196	1BIR_MOUSE	054918 ratu musculu
30	44	31.9	262	1END8_ECOLI	P27757 simian immu
31	44	31.9	768	1ENV_SIVAT	P27757 simian immu
32	44	31.9	877	1ENV_SIVAT	P27757 simian immu
33	43.5	31.5	217	1URRF_SYNVS	P73327 synecchocyst

ALIGNMENTS

RESULT	1	STANDARD	PRY	204 AA.
BAD_MOUSE				
AC	Q61337:			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	Bcl2-antagonist of cell death (BAD) (Bcl-2 binding component 6) (Bcl-xL/Bcl-2 associated death promoter).			
DE	BAD OR BDC6.			
GN	BAD OR BDC6.			
OS	mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid:10090;			
RN	[1]			
RN	REFERENCE FROM N.A.			
RP	PROTEIN FROM R.A. THYMUS.			
RP	MDLINB-95136361. PubMed-7834748.			
RX	Yang E. 2ha 1. Jockey J. Boise L.H. Thompson C.B., Kormeyer S.J.			
RA	"Bad" a heterodimeric partner for Bcl-XL and Bcl-2, displaces Bax and			
RT	promotes cell death."			
RL	Cell 80:285-291(1995).			
RL	[2]			
RP	PHOSPHORYLATION, AND MDTAGENESIS OF SER-112 AND SER-136.			
RP	MDLINB-96022383. PubMed-9381178.			
RA	Del Peso L., Gonzalez-Garcia M., Page C., Herrera R., Nunez G.;			
RT	"Interleukin-3-induced phosphorylation of BAD through the protein			
RT	kinase Akt."			
RL	Science 278:687-689(1997).			
RN	[3]			
RP	MUTAGENESIS OF SERINE RESIDUES.			
RP	MDLINB-20403302. PubMed-10949026;			
RA	Datta S.R., Katsov A., Hu L., Petros A., Fesik S.W., Yaffe M.B.,			
RA	Greenberg M.E.;			
RT	"14-3-3 proteins and survival kinases cooperate to inactivate BAD by			
RT	BH3 domain phosphorylation."			
RL	Cell 96:611-612(2000).			
-1-	EVIDENCE FOR Bcl-2 and Bcl-XL phosphorylation of BAX. Can reverse the			
CC	binding to Bcl-2 and Bcl-XL, thereby affecting the level			
CC	of heterodimerization of these proteins with BAX. Can reverse the			
CC	death repressor activity of Bcl-XL, but not that of Bcl-2.			
CC	Appears to act as a link between growth factor receptor signaling			
CC	and the apoptotic pathways.			
CC	-1- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-			
CC	X(L), Bcl-2 and Bcl-XL. Also binds protein S100A10 (By similarity).			
CC	The Ser-112/Ser-136 phosphorylated form binds 14-3-3 proteins.			
CC	-1- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon			
CC	phosphorylation, localizes to the cytoplasm.			
CC	-1- DOMAIN: Interact BH3 domain is required by BIR, BID, BAK, BAD AND			
CC	BAX for their pro-apoptotic activity and for their interaction			
CC	with anti-apoptotic members of the Bcl-2 family.			
CC	-1- PTM: Phosphorylated on Ser-112 in response to survival stimuli.			
CC	Subsequent phosphorylation on Ser-136 promotes heterodimerization			
CC	with 14-3-3 proteins. This interaction then facilitates the			
CC	phosphorylation at Ser-135, a site within the BH3 domain, leading			
CC	to the release of Bcl-X(L) and the promotion of cell survival.			

34	43.5	31.5	1014	1	QVRA_STRCO	Q94507 streptomyces
35	43	31.2	377	1	APJ_MOUSE	Q94508 mus musculus
36	43	31.2	380	1	APJ_HUMAN	P35414 homo sapien
37	43	31.2	380	1	APJ_MOUSE	Q97656 macaca mula
38	43	31.2	578	1	ACER_ECOLI	P11071 escherichia
39	43	31.2	583	1	ACER_SALTY	P51057 salmonella
40	43	31.2	905	1	MDLI_TFAST	P33310 saccharomyc
41	43	31.2	905	1	MDLI_MOUSE	Q94501 mus musculu
42	42	30.4	202	1	PRIR_PRRM	Q94502 pyrococcus
43	42	30.4	202	1	PRIR_YEEN	Q94503 yeastia en
44	42	30.4	322	1	SRRA_YEEN	P13904 saccharomyc
45	42	30.4	463	1	Y030_NMYMC	P41434 autographa

QY 1 NMAAORYGRELRLMSDEFECSFKGL 26
 DB 141 NMAAORYGRELRLMSDEFECSFKGL 166

RESULT 3
 BAD_HUMAN STANDARD: PRT: 168 AA.

AC Q92934; O14803;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Bcl-2 antagonist of cell death (BAD) (Bcl-2 binding component 6) (Bcl-XL/Bcl-2 associated death promoter).
 GN BAD OR BCL6 OR BCL2L8.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCB1_TaxID=9606;
 OX [1]
 RN RP SEQUENCE FROM N.A.
 RA Yin D.-X., Li Z., Huang B., Chen S., Zhou H.;
 RT "A human protein that interacts with Bcl-2 and have homology to mouse BAD";
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.; AND PHOSPHORYLATION BY RAF-1.
 RX MEDLINE=97083574; PubMed=8929532;
 RA Wang H.-G., Rapp U.R., Reed J.C.;
 RT "Bcl-2 targets the protein kinase Raf-1 to mitochondria";
 RL Cell 87:628-638(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Takayama S., Reed J.C.;
 RT Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RL [4]
 RP SEQUENCE FROM N.A.; AND DIMERIZATION.
 RC TISSUE=Bone marrow; PubMed=9388232;
 RX MEDLINE=98049534; PubMed=9388232;
 RA Ohtsuka S., Diaz J.-L., Horne W., Chang J., Wang Y., Wilson G.;
 RT Chang S., Weeks S., Fritz L.C., Oltersdorf T.;
 RL "Dimerization properties of human BAD";
 J. Biol. Chem. 272:30866-30872(1997).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP STRUCTURE BY NMR OF 103-127.
 RX MEDLINE=21073561; PubMed=11206074;
 RA Petros A.M., Nettesheim D.G., Wang Y., Olejniczak E.T., Meadows R.P., Mack J., Swift K., Matayoshi E.D., Zhang H., Thompson C.B., Fesik S.W.;
 RT "Rationale for Bcl-xL/Bad peptide complex formation from structure, mutagenesis, and biophysical studies";
 RL Protein Sci. 9:2528-2534(2000).
 CC -1- FUNCTION: Promotes cell death. Successfully competes for the binding to Bcl-x(L), Bcl-2 and Bcl-w, thereby affecting the level of heterodimerization of these proteins with BAX. Can reverse the death repressor activity of Bcl-x(L), but not that of Bcl-2 (By similarity). Appears to act as a link between growth factor receptor signaling and the apoptotic pathways.
 CC -1- SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-x(L), Bcl-2 and Bcl-w. Also binds protein S100A10 (By similarity).
 CC The Ser-75/Ser-99 phosphorylated form binds 14-3-3 proteins (By similarity).
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon phosphorylation, localizes to the cytoplasm.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
 CC -1- DOMAIN: Interact BH3 domain is required by BAX, BAD AND BAX for their proapoptotic activity and for their interaction with anti-apoptotic members of the Bcl-2 family.

CC -1- PTH: Phosphorylated on Ser-75 in response to survival stimuli. Subsequent phosphorylation on Ser-99 promotes heterodimerization with 14-3-3 proteins. This interaction then facilitates the phosphorylation at Ser-118, a site within the BH3 domain, leading to the release of Bcl-x(L) and the promotion of cell survival. Ser-99 is the major site of AK7/PKB phosphorylation. Ser-118 the major site of protein kinase A (CAK) phosphorylation (by similarity).
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.1ab-sib.ch/announce/> or send an email to license@sib.ch).
 CC EMBL; U66879; AAB36516.1; -
 DR EMBL; AF021792; AAB72092.1; -
 DR EMBL; AF031523; AAB88124.1; -
 DR EMBL; BC001901; AAH01901.1; -
 DR PDB; 1G5J; 07-FEB-01.
 DR MIM; 603167; -
 DR InterPro; IPR000712; Bcl_2.
 DR PROSITE; PS01259; BH3; FALSE.NEG.
 DR Apoptosis; Phosphorylation; 3D-structure.
 FT MOD_RES 110 124
 FT MOD_RES 75 75 PHOSPHORYLATION (BY CAK AND PKB) (BY SIMILARITY)
 FT MOD_RES 99 99 PHOSPHORYLATION (BY CAK AND PKB) (BY SIMILARITY)
 FT MOD_RES 118 118 PHOSPHORYLATION (BY CAK AND PKB) (BY SIMILARITY)
 FT CONFLICT 64 91 AGAVATIRSRSSVPGAGFDEPCMGERS -> RMCGDPPSS POLIPDCGSRGRCGCAO (IN REF. 1).
 FT SQ SEQUENCE 168 AA; 18392 MW; 69PDDD27DDEB32A1 CRC64;

QY 1 NMAAORYGRELRLMSDEFECSFK 24
 DB 103 NMAAORYGRELRLMSDEFECSFK 126

Query Match 82.68; Score 114; DB 1; Length 168;
 Best Local Similarity 91.78; Pred. No. 3e-10; 2; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 4
 ITH2_MESAU STANDARD: PRT: 946 AA.

AC P97279;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DE 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy chain H2) (HC2).
 GN ITH2.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Mesocricetus.
 NC NCB1_TaxID=10036;
 OX [1]
 RN RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=97420688; PubMed=9276673;
 RA Nakatani T., Suzuki Y., Yamamoto T., Sinohara H.;
 RT "Molecular cloning and sequencing of cDNAs encoding three heavy-chain precursors of the inter-alpha-trypsin inhibitor in Syrian hamster: implications for the evolution of the inter-alpha-trypsin inhibitor heavy chain family";

RL	ZJ	Blochem.	122:71-82(1997).
RN	[2]	SEQUENCE OF 55-64; 140-146; 151-156; 424-447; 500-528 AND 577-605,	
RP	AND SUBUNITS.		
RC	TTSUE-plasma:		
RX	MEDLINE=97018241; PubMed=8864857;		
RA	Yamamoto T., Yamamoto K., Shiochima H. ;		
RT	Intraerythrocytic trypsin inhibitor and its related proteins in Syrian hamster urine and plasma.*		
RU	J. Biochem 120:1145-1152(1996).		
CC	-1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN, INCLUDING THOSE ON CELL SURFACES AND DEGRADATION OF HYALURONAN THE LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY SIMILARITY).		
CC	-1- SUBUNIT: -1- ALPHA-1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN, BIKRIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2 AND BIKRIN, INTER-ALPHA-LIKE INHIBITOR (I'-ALPHA-LI) OF H2 AND BIKRIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKRIN.		
CC	-1- PM: HEAVY CHAINS ARE INTERLINKED WITH BIKRIN VIA A CHONDROITIN 4-SULFATE BRIDGE TO THEIR C-TERMINAL ASPARTATE (BY SIMILARITY).		
CC	-1- SIMILARITY: BELONGS TO THE ITIH FAMILY.		
CC	-1- SIMILARITY: CONTAINS 1 WFA DOMAIN.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on ways CC can use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lbb-slb.ch/announce/ or send an email to llicense@slb.slb.ch).		
CC			
DR	EMBL; D89286; BAAL1939.1; -		
DR	InterPro: IPR002035; wfaA.		
DR	pfam: PF00092; wfa_1.		
DR	SMART: SM00327; wfa_1.		
DR	PROSITE: PSS0234; wfaA; 1.		
KW	Serine protease inhibitor; Repeat; Signal; Multigene family; Glycoprotein.		
KM	GlycoSignal.		
FT	SYMBOL	1	18
FT	PROPEP	19	54
FT	CHAIN	55	702
FT		H2.	
FT	PROPER	703	946
FT	DOMAIN	308	468
FT	CARBOHYD	118	118
FT	CARBOHYD	263	263
FT	CARBOHYD	445	445
FT	CARBOHYD	578	578
FT	BINDING	702	702
FT	CONFLICT	510	510
FT	CONFLICT	595	595
SO	SEQUENCE	946 AA;	106580 MW; CAB8F565458BF7B2E CRC64;
Oy	Query Match	39.1%; Score 54;	DB 1; Length 946;
	Best Local Similarity	34.6%;	Pred. No. 2.6;
	Matches	9; Conservative	5; Mismatches 12; Indels 0; Gaps 0;
Db	1 NMANORGRELRMSDEPGSPGIC 26 : : : : : : 212 NMVIVELQMRFLHPDPFEHQGV 237		
ID	RESULT 5		
ID	ITIH_MOUSE		
ID	ITIH_MOUSE	STANDARD: PRT; 946 AA.	
AC	061703;		
TC	15-JUL-1998 (Rel. 36, Created)		

DT	15-JUL-1998 (rel. 36, last sequence update)
DR	Inter-alpha-trypsin inhibitor heavy chain H2 precursor (ITI heavy chain H2).
GN	ITIH2.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Knemidaria; Euteheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
OK	NCBT_TaxID=10090;
RN	(1)
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6N; TISSUE=Liver;
RX	MEDLINE=95194326; PubMed=7534067;
RT	Chan P., Risler J.-L., Raguenes G., Sallier J.-P.;
RM	"The three heavy-chain precursors for the inter-alpha-inhibitor family in mouse: new members of the multicopper oxidase protein group with differential transcriptions in liver and brain";
RL	Blochem. J. 306:505-512(1995).
CC	-1- FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SEMO OR AS A BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,
CC	INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE ESSENTIALIZATION, SYNTHESIS AND DEGRADATION OF HYALURON WHICH ARE
CC	ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (BY SIMILARITY).
CC	-1- SUBUNIT: I-ALPHA-I PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,
CC	BIKRIN. INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2 AND BIKRIN. INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-II) OF H3 AND BIKRIN..
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN BOTH LIVER AND BRAIN
CC	-1- PMW: HEAVY CHAINS ARE INTERLINKED WITH BIKRIN VIA A CHONDROITIN 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (BY SIMILARITY).
CC	-1- SIMILARITY: BELONGS TO THE ITIH FAMILY.
CC	-1- SIMILARITY: CONTAINS 1 WFAA DOMAIN.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@sib-sb.ch).
CC	-----
DR	EMBL; X70392; CAA49842.1; ..
DR	MGD; MGI:96619; Tlth2.
DR	InterPro; IPRO02035; WFAA.
DR	Pfam; PF00092; wva; 1.
DR	SMART; SM00327; WVA; 1.
DR	ProSite; PS50234; WFAA; 1.
KM	Serine protease inhibitor; Repeat; signal; Multigene family;
KW	Glycoprotein.
FT	SIGNAL
FT	PROPER
FT	CHAIN
FT	PROPER
FT	CHAIN
FT	PROPER
FT	DOMAIN
FT	CARBOHYD
FT	CARBOHYD
FT	CARBOHYD
FT	BINDING
FT	SEQUENCE
SO	SEQUENCE

Query Match 38.4%; Score 53; DB 1; Length 946;
 Best local similarity 34.6%; Pred. No. 3.7;
 Matches 9; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

1 NIMAARYGRELKMSDEFGSEGL 26
 :|:|:|:|:|:|:|:|:|:|:|:|:
 212 NWATLEPGQMFLLVDPDFEGCHGV 237

```

RESULT 6
AARG_YEAST STANDARD; PRT: 370 AA.
ID AARG_YEAST
AC P32449;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited
DE (EC 4.1.2.15) (Phospho-2-keto-3-deoxyheptonate aldolase) (DHP
DE synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase).
GN ARO4 OR YBR249C OR YBR1701.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
NCBI_TaxID=4932.
[1]
SEQUENCE FROM N.A.
MEDLINE=92225349; PubMed=1348717;
Kuenzler M., Paravicini G., Egli C., Irniger S., Braus G.-H.;
"Cloning, primary structure and regulation of the ARO4 gene, encoding
the tyrosyl-3-phospho-2-deoxy-3-deoxy-D-arabino-heptulosonate-7-phosphate
synthase from Saccharomyces cerevisiae."
Gene 113:67-74(1992).
[2]
REVIEWS TO 205-207.
Kuenzler M.;
Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
MEDLINE=94078675; PubMed=8256522;
Daignon F., Bileau N., Aigle M., Crouzet M.;
"The complete sequence of a 6794 bp segment located on the right arm
of chromosome II of Saccharomyces cerevisiae. Finding of a putative
duplicase in a yeast."
Yeast 9:1131-1137(1993).
[4]
SEQUENCE FROM N.A.
STRAIN=S288C;
RA Allinovic G., Pohl F.M., Pohl T.M.;
Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
-1- FUNCTION: STEREOSPECIFIC CONDENSATION OF PHOSPHOENOLPYRUVATE (PEP).
AND D-BRYTHROSE-4-PHOSPHATE (D4P) GIVING RISE TO 3-DEOXY-D-
ARABINO-HEPTULOSONATE-7-PHOSPHATE (D4HP).
-1- CATALYTIC ACTIVITY: 2-dehydro-3-deoxy-D-arabino-heptonate 7-
phosphate + phosphate = phosphoenolpyruvate + D-erythrose 4-
phosphate + H(2)O.
-1- ENZYME REGULATION: INHIBITED BY TYROSINE.
-1- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN
THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).
-1- INDUCTION: BY AMINO ACID STARVATION.
-1- SIMILARITY: BELONGS TO CLASS-I DHP SYNTHETASE FAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL: X61107; CAA3419.1; -
DR EMBL: L20296; AAA65607.1; -
DR EMBL: Z36118; CAA85212.1; -
DR FIRM: S38185; S38185.
DR HSRP: P00886; IQRV.
DR SGD: S0000453; ARO4.
DR InterPro: IPR001785; DHP_synth_1.
DR Pfam: PF00793; DHP_synth_1; 1.
DR ProDom: PD005060; DHP_synth_1; 1.
Atomic amino acid biosynthesis: lyase; Multigene family.

```

```

SO SEQUENCE 370 AA: 39749 MW: 5948DA8F2A175579 CRC64:
Query Match 37.7%; Score 52; DB 1; Length 370;
Best Local Similarity 47.6%; Pred. No. 1.8;
Matches 10; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
OY 1 NIMANORYGRELIRMSDFEG 21
: 1111 : 1111 : 1
Db 80 DLEAAOEVALRLKISBELNG 100
RESULT 7
AP3_ARATH STANDARD; PRT: 232 AA.
ID AP3_ARATH
AC P35632; Q39003;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Floral homeotic protein APEPAL3.
AP3 OR ATG54340 OR T12E18.30.
GN Arabidopsis thaliana (Mouse-ear cress).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Esermatophyta; Magnoliophyta; eudicotyledons; core eudicotids; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
NCBI_TaxID=3702;
[1]
SEQUENCE FROM N.A.
TISSEUR-PETAL;
MEDLINE=92154682; PubMed=1346756;
Tack T., Brockman L.L., Meyerowitz E.M.;
"The homeotic gene APEPAL3 of Arabidopsis thaliana encodes a MADS
box and is expressed in petals and stamens."
Cell 68:683-697(1992).
[2]
SEQUENCE FROM N.A.
STRAIN=CV LANDSBERG EFFECT;
RC MEDLINE=95305018; PubMed=7948893;
Okamoto H., Yano A., Shirahata H., Okada K., Shimura Y.;
"Genetic complementation of a floral homeotic mutation, apetal3,
with an Arabidopsis thaliana gene homologous to DEFICIENS of
Antirrhinum majus."
Plant Mol. Biol. 26:465-472(1994).
[3]
SEQUENCE FROM N.A.
STRAIN-VARIOUS STRAINS;
RC MEDLINE=99126449; PubMed=9927474;
Purugganan M.D., Sudhith J.I.;
"Molecular population genetics of floral homeotic loci. Departures
from the equilibrium-neutral model at the APEPAL3 and PISTILLATA
genes of Arabidopsis thaliana."
Genetics 151:839-848(1999).
[4]
SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
RX MEDLINE=21016720; PubMed=11130713;
Salatnoubat M., Lemcke K., Rieger M., Ansonger W., Unseld M.,
Fatmanou B., Valle G., Bloeker H., Perez-Alonso M., Obermayer B.,
Dalsem M., Boutry M., Grivell L.A., Maché R., Pulgomech P.,
Winkler P., Catolico L., Weissenbach J., Saurin W., Queller F.,
Schaefer M., Mueller-Auer S., Cabal C., Fuchs M., Benes V.,
Wumbach E., Drzonek H., Erle H., Jordan N., Bangert S.,
Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simonet B.,
Corrad A., Hornischer K., Kaver G., Loehner T.-H., Nordstiek G.,
Reichelt J., Schaefer M., Schoen O., Bargues M., Terol J., Glment J.,
Navarro P., Collado C., Perez-Perez A., Ottenweider B., Duchemin D.,
Cooke R., Landie M., Berger-Llauro C., Purnelle B., Masuy D.,
de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacubeta E.,
Monfort A., Argirou A., Flores M., Liqiori R., Vitale D.,
Mannhant G., Haase D., Schoof H., Ridd S., Zaccaria P., Mewes H.-W.,
Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,

```

RA Rooney T., Rizzo M., Walts A., Uterback T., Fujii C.Y., Shea T.P.,
 RA Cressy T.H., Haas B., Maitl R., Wu D., Peterson J., Van Aken S.,
 RA Pal G., Millscher J., Sellers P., Gill J.E., Feldblum T.V.,
 RA Preus D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
 RA Fraser C.M., Kanko T., Nakamura Y., Sato S., Kato T., Asanizu E.,
 RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
 RA Kiyakawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,
 RA Matsumae A., Yamada M., Yasuda M., Tabata S.,
 RT Sequence and analysis of chromosome 3 of the plant Arabidopsis
 RL thaliana. ;
 CC Nature 408:820-822(2000).
 CC -1- FUNCTION: TRANSCRIPTION FACTOR INVOLVED IN THE GENETIC CONTROL OF
 CC FLOWER DEVELOPMENT.
 CC -1- SUBUNIT: FORMS AN HETERODIMER WITH PISTILLATA.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN PETALS AND STAMENS.
 CC -1- MISCELLANEOUS: MUTATIONS IN AP3 CAUSE TRANSFORMATION OF PETALS
 CC INTO SEEDS AND STAMINA INTO CARPELS.
 CC -1- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
 CC FACTORS.
 CC -1- SIMILARITY: CONTAINS A PROBABLE DIMERIZATION DOMAIN FOUND IN
 CC SRF-TYPE TRANSCRIPTION FACTORS (K-BOX).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-slb.ch/announce/>
 CC or send an email to license@isb-slb.ch).
 CC -----
 DR EMBL: M66357; AAA32740.1; -
 DR EMBL: D21325; BAA04665.1; -
 DR EMBL: AF115799; AAD51888.1; -
 DR EMBL: AF115800; AAD51889.1; -
 DR EMBL: AF115802; AAD51891.1; -
 DR EMBL: AF115804; AAD51893.1; -
 DR EMBL: AF115811; AAD51900.1; -
 DR EMBL: AF115814; AAD51903.1; -
 DR EMBL: AL132971; CAB81799.1; -
 DR PIR: A42095; A42095.
 DR HSSP: P11746; 1NM.
 DR TRANSFAC: T01776; -
 DR InterPro: IPR002487; K-box.
 DR InterPro: IPR002100; MADS-box.
 DR Pfam: PF01486; K-box; 1.
 DR Pfam: PF00319; SRF-TF; 1.
 DR PRINTS: PR00404; MADSDOMAIN.
 DR SMART: SM00433; MADS; 1.
 DR PROSITE: PS00350; MADS_BOX_1; 1.
 DR PROSITE: PS00065; MADS_BOX_2; 1.
 KM Transcription regulation; DNA-binding; Activator; Nuclear protein;
 KW Developmental protein.
 FT DOMAIN 3 MADS.
 FT DOMAIN 93 165 K-BOX.
 FT CONFLICT 198 199 A 62 R (1N REF. 2)
 FT SEQUENCE 232 AA: 27341 MW: 663070319F9857C3 CRC64;

Query Match 37.0% Score 51; DB 1; Length 232;
 Best Local Similarity 44.4% Pred. No. 1.5;
 Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1;

OY 6 ORTG-----RELMSDEEGSEFK 24
 DB 107 ORTGCELDLEIDQLTRLEDEMENTFK 133

RESULT 8
 RMQC_PSEAE STANDARD: PRT: 453 AA.
 ID RMQC_PSEAE
 AC O91403;

DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE DNA recombination protein rmcD homolog.
 GN rmcD OR PA1031.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 ON NCBI_TaxID=287;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01.
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Phan X.-O.T., Ervin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Huftnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Gollery L., Tolentino E., Westbrook-Madhen S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Keller J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT Complete genome sequence of Pseudomonas aeruginosa PA01, an
 RT opportunistic pathogen. ;
 RL Nature 406:959-964(2000).
 CC -1- FUNCTION: Involved in DNA recombination (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE RMCD FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-slb.ch/announce/>
 CC or send an email to license@isb-slb.ch).
 CC -----
 DR EMBL: AE004535; AAG04420.1; -
 DR InterPro: IPR003798; DUF195.
 DR Pfam: PF02646; DUF195; 1.
 KM DNA recombination; Coiled coil; Complete proteome.
 FT DOMAIN 16 201 COILED COIL (PORENTNL).
 FT SEQUENCE 453 AA: 51539 MW: 1E7BA7B2E2C54B CRC64;

Query Match 35.5% Score 49; DB 1; Length 453;
 Best Local Similarity 55.6% Pred. No. 6.5;
 Matches 10; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

OY 3 MAORGR-ELRMSDE 18
 DB 65 WABRGRGRFLRNLASE 82

RESULT 9
 RA53_SHIRA STANDARD: PRT: 205 AA.
 ID RA53_SHIRA
 AC P22280;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Ras-like protein 3.
 DE Ras3.
 GN Rho3.
 OS Rhizomucor racemosus (Mucor circinelloides f. lusitanicus).
 OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
 OC Mucor.
 ON NCBI_TaxID=4841;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 1216B;
 RX MEDLINE=91061774; PubMed=1701021;
 RA Casale W.L., McConnell D.G., Wang S.-Y., Lee Y.-J., Linz J.E.;
 RT "Expression of a gene family in the dimorphic fungus Mucor racemosus
 RT which exhibits striking similarity to human ras genes."
 RL Mol. Cell. Biol. 10:6654-6663(1990).
 CC -1- RAYZYE REGULATION: ALTERNATE BETWEEN AN INACTIVE FORM BOUND TO GDP
 CC AND AN ACTIVE FORM BOUND TO GTP. ACTIVATED BY A GUANINE

CC NUCLEOTIDE-EXCHANGE FACTOR (GEF) AND INACTIVATED BY A GTPASE-
 CC ACTING PROTEIN (GAP).
 CC -1- SUBCELLULAR LOCATION: PLASMA MEMBRANE.
 CC -1- DEVELOPMENTAL STAGE: IN SPORULATING MYCELIUM AND MUCH LESS IN
 CC GERMLING AND YEAST.
 CC -1- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RAS FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M55177; AA83379.1; -
 CC FIP: C36365; C36365.
 CC DR HSSP: P01112; IPIL
 CC DR InterPro: IPR001806; 1_RAS_cnsfsmg.
 CC DR Pfam: PF000172; RAS_1_RAS_STRINGSFAMG.
 CC DR SMART: SM00173; RAS; 1.
 CC DR GTP binding: P_cys141; LipoProtein.
 CC KM NP_BIND: 16 63 GTP (BY SIMILARITY).
 CC FT NP_BIND: 63 63 GTP (BY SIMILARITY).
 CC FT NP_BIND: 125 125 GTP (BY SIMILARITY).
 CC FT DOMAIN: 38 144 EFFECTOR REGION (PROBABLE).
 CC FT LID: 202 202 FANNESID (BY SIMILARITY).
 CC FT SEQUENCE: 205 AA; 23408 MW; DE06466090F50 CRC64;

Query Match 34.8%; Score 48; DB 1; Length 205;
 Best Local Similarity 62.5%; Pred. No. 3.8; Mismatches 4; Indels 0; Gaps 0;
 Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 10 REIKMSDEFGSFG 25
 DB 168 REIKMSDEFGSFG 183

RESULT 10
 6RCL:THEMA STANDARD; PRT; 220 AA.
 AC 09YON8; 2000 (Rel. 39. Created)
 DT 30-MAY-2000 (Rel. 39. Last sequence update)
 DT 16-OCT-2001 (Rel. 40. Last annotation update)
 DE 6-phosphogluconolactonase (EC 3.1.1.31) (6PGL).
 GN PGL OR DPGA OR PM154.
 OS Thermotoga maritima.
 OC Bacteriota; Thermotogales; Thermotoga.
 OX NCBI_TaxId=2386;
 RN 1
 RC SEQUENCE FROM N.A.
 RC STRAIN=MS8 / DSM 3109;
 RC MEDLINE=9287316; PubMed=10360571.
 RA Nelson R.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,
 RA Halt D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
 RA McDonald L., Overback T.R., Patel M.S., Phillips C.A., Richardson D.,
 RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser J.C.M.;
 RT Evidence for lateral gene transfer between Archaea and Bacteria from
 RT genome sequences of the thermococcus maritima.
 RL Nature 391:2325-2326 (1998).
 CC -1- PHOSPHOGLUCONOLACTONASE
 CC -1- CATALYTIC ACTIVITY: 6-phospho-D-glucono-1,5-lactone + H(2)O -> 6-
 CC -1- phospho-D-glucconate.
 CC -1- PATHWAY: SECOND STEP IN PENTOSE PHOSPHATE PATHWAY.
 CC -1- SIMILARITY: BELONGS TO THE GLUCONAMINE/GALACTOSAMINE-6-PHOSPHATE
 CC ISOMERASE FAMILY. 6-PHOSPHOGLUCONOLACTONASE SUPERFAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF001772; MAD36230.1; -
 CC DR TIGR: TM154; -
 CC DR InterPro: IPR000457; Glucosamine Iso.
 CC DR Pfam: PF01182; Glucosamine Iso; 1.
 CC DR HydroLase: Complete proteome
 CC KM SEQUENCE: 220 AA; 25325 MW; 9B0PD07E01B60C3 CRC64;

Query Match 34.8%; Score 48; DB 1; Length 220;
 Best Local Similarity 34.8%; Pred. No. 4.1; Mismatches 8; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 4 AMOYGREIKMSDEFGSFGCL 26
 DB 111 ACENTERIKMSDEFGSFGCL 133

RESULT 11
 THRC:SOULTU STANDARD; PRT; 519 AA.
 AC 09HT26; 2002 (Rel. 41. Created)
 DT 01-MAR-2002 (Rel. 41. Last sequence update)
 DT 01-MAR-2002 (Rel. 41. Last annotation update)
 DE Threonine synthase, chloroplast precursor (EC 4.2.99.2) (TS).
 OS Solanum tuberosum (potato).
 OC Saururales; Vitellaceae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC Asteridae; Gentianales; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxId=4113;
 RN 11
 RC SEQUENCE FROM N.A.
 RC Casazza P., Kaiser S., Willmitzer L., Hoefgen R., Hesse H.;
 RT Isolation and characterization of a cDNA encoding threonine synthase
 RT from Solanum tuberosum.
 RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: O-phospho-L-homoserine + H(2)O -> L-threonine +
 CC -1- phosphate. Pyridoxal phosphate (by similarity).
 CC -1- COFACTOR: Pyridoxal phosphate (by similarity).
 CC -1- ENZYME REGULATION: Allosterically activated by S-adenosyl-
 CC -1- methionine (SAM) (by similarity).
 CC -1- PATHWAY: Threonine biosynthesis; last step.
 CC -1- SUBUNIT: Homodimer (by similarity).
 CC -1- SUBCELLULAR LOCATION: Chloroplast (by similarity).
 CC -1- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF028294; MAF74984.1; -
 CC DR InterPro: IPR001926; EC_enzyme_delta.
 CC DR Pfam: PF02581; PDR.
 CC DR PROSITE: PS00165; DEHYDRATASE_SPT_TH_1.
 CC KM Threonine biosynthesis; lysase; pyridoxal phosphate; Allosteric enzyme;
 CC KM Chloroplast; Transient peptide; CHLOROPLAST (BY SIMILARITY).
 CC FT TRANSIT: 1 519
 CC FT CHAIN: 1 519 THREONINE SYNTHASE (BY SIMILARITY).
 CC FT BINDING: 196 199 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 CC FT SEQUENCE: 519 AA; 57412 MW; 11AC0979CD23164 CRC64;

Query Match 34.8% Score 48; DB 1; Length 519;
 Best Local Similarity 35.3% Pred. No. 11;
 Matches 12; Conservative 6; Mismatches 8; Indels 8; Gaps 1;
 Oy 1 NLMARCYGRELBMSPD-----EFGSGFGL 26
 Db 165 NLMARCYGRELBMSPD-----EFGSGFGL 198

RESULT 12
 THRC ARATH STANDARD; PRT: 526 AA.
 AC 095785: 039144: (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Threonine synthase, chloroplast precursor (EC 4.2.99.2) (TS).
 GN ATG29840 OR F27B13.80.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Euphorbiales; Brassicales; Brassicaceae; Arabidopsida.
 OX NCBI_TaxId=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Wassilewskija;
 RX MEDLINE=99418329; PubMed=10490396;
 RA Bartlam D., Tamaki Y., Malto S.;
 RT "Genomic nucleotide sequence of the Arabidopsis threonine synthase
 gene.";
 RL (in) Plant Gene Register PCR99-108.
 RN [12]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. COLUMBIA;
 RX MEDLINE=20083488; PubMed=10617198;
 RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
 RA Pohl T., Duesterhoeft A., Stiekema W., Entlan K.-D., Terry N.,
 RA Harris B., Ansoerje W., Brandt P., Grivell L.A., Rieger M.,
 RA Melchelsberger M., de Simone V., Obermayer B., Maecher M., Mueller M.,
 RA Krels M., Delany M., Pulgomech P., Watson M., Schmidheini T.,
 RA Reichert B., Portetelle D., Perez-Alonso M., Bouly M., Bancroft I.,
 RA Vos P., Hobeisel J., Zimmermann W., Medler H., Ridley P.,
 RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
 RA Van der Schueren J., GYmonpriez B., Chung Y.-J., Vandenbussche F.,
 RA Bracken M., Wellings I., Voet M., Bastiens I., Aert R., Defoor E.,
 RA Welzenegger T., Bothe G., Ransperger U., Hilbert H., Braun M.,
 RA Holzer E., Brandt A., Peters S., van Stevenen A., Dikse W.,
 RA Moollman P., Klein Lankhorst R., Rose M., Haut J., Koetter P.,
 RA Bernreiser S., Hempel S., Feldpausch M., Lambrecht S., Van den Daele H.,
 RA De Keyser A., Buyssehaert C., Cronin A., Quail M., Bray-Allen S.,
 RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
 RA Clark L., Dagggett J., Hall S., Kay M., Leonard N., McKay K., Mayes R.,
 RA Pettelt A., Ralanderam M.-A., Lyne M., Benes V., Reichmann S.,
 RA Borrova D., Bloeker H., Scharfe M., Giam M., Loehner T.-H.,
 RA Dose S., de Haan M., Maarse A.C., Schaefer K., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
 RA Neumann S., Aguilou A., Vitale D., Liguori R., Pleyadri E.,
 RA Masenun S., Hillier F., Clabaud G., Mendenhall A., Felber R.,
 RA Schaefer S., Hillier R., Schmidt W., Lechery A., Aubourg S.,
 RA Chedoi F., Cooke R., Berger C., Monfort A., Casachubeta E.,
 RA Gibbons T., Weber N., Vandenhol M., Burgess M., Terol J., Torres A.,
 RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
 RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bialke C.,
 RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
 RA Zaccarello P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
 RA Sakhon M., Murray J., Sheet P., Cordes M., Abi-Threideh J.,
 RA Stokeling T., Kalicki J., Graves T., Hartom G., Edwards J.,
 RA Lattelle P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
 RA Mink P., Bentley D., Fulton B., Miller T., Greco T., Kemp K.,
 RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,

RA Nelson J., Spleth J., Ryan E., Andrews S., Giesel C., Layman D.,
 RA Du H., All J., Berghoff A., Jones K., Dione K., Cotton M., Joshi C.,
 RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Jordan C.,
 RA Ma P., Zhong J., Preston R., Vill D., Shaker M., Maturo A., Shah R.,
 RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Tili S.,
 RA Granat S., Shohdy N., Hasegawa A., Hamed A., Lodhi M., Johnson A.,
 RA Chen E., Merri M., Martensen R., McCombie W.R.;
 RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
 thaliana.";
 RL Nature 402:769-777(1999).
 RN [13]
 RP SEQUENCE OF 2-526 FROM N.A., AND CHARACTERIZATION.
 RC STRAIN=cv. Columbia;
 RX PubMed=8706836;
 RA Curien G., Dumas R., Ravanel S., Douce R.;
 RT "Characterization of an Arabidopsis thaliana cDNA encoding an
 S-adenosylmethionine-sensitive threonine synthase. Threonine synthase
 from higher plants.";
 RL FEBS Lett. 390:85-90(1996).
 RN [14]
 RP CHARACTERIZATION.
 RX PubMed=9748328;
 RA Curien G., Job D., Douce R., Dumas R.;
 RT "Allosteric activation of Arabidopsis threonine synthase by
 S-adenosylmethionine.";
 RL Biochemistry 37:13212-13221(1998).
 RN [15]
 RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 41-526.
 RX PubMed=11344332;
 RA Thomazeau K., Curien G., Dumas R., Blou V.;
 RT "Crystal structure of threonine synthase from Arabidopsis thaliana.";
 RL Protein Sci. 10:638-648(2001).
 CC -1- CATALYTIC ACTIVITY: O-phospho-L-homoserine + H(2O) = L-threonine +
 phosphate.
 CC -1- COFACTOR: Pyridoxal phosphate.
 CC -1- ENZYME REGULATION: Allosterically activated up to 20-fold by S-
 adenosyl-methionine (SAM).
 CC -1- PATHWAY: Threonine biosynthesis: last step.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Chloroplast.
 CC -1- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@lsb-sib.ch).
 CC -----
 CC EMBL: AB027151; BAA77707.1; -
 CC EMBL: AL050352; CAB3659.1; -
 CC EMBL: AL161575; CAB9742.1; -
 CC EMBL: LA1666; AAB04607.1; -
 CC PDB: 1E5X; 02-AUG-01.
 CC InterPro: IPR001926; PALP.
 CC Pfam: PF00291; PALP.1.
 CC ProSite: PS00165; DEHYDRATASE_SSP_THR.1.
 CC Threonine biosynthesis: lysase, pyridoxal phosphate; Allosteric enzyme;
 CC Chloroplast; Transil peptide; 3D-structure.
 CC TRANSIT 1 40
 CC CHAIN 41 526
 CC THREONINE SYNTHASE.
 CC BINDING 203 203
 CC PYRIDOXAL PHOSPHATE.
 CC CONFLICT 2 2
 CC A -> L (IN REF. 3).
 CC SEQUENCE 526 AA: 57776 MW: 82787857882AD0 CMC64;

Query Match 34.8% Score 48; DB 1; Length 526;
 Best Local Similarity 35.3% Pred. No. 11;
 Matches 12; Conservative 6; Mismatches 8; Indels 8; Gaps 1;
 Oy 1 NLMARCYGRELBMSPD-----EFGSGFGL 26
 Db 165 NLMARCYGRELBMSPD-----EFGSGFGL 198


```

DB 172 NLFMAERKGFGLGNDLWVHCGISHTGSKDL 205

RESULT 13
BIM_HUMAN
ID BIM_HUMAN STANDARD; PRT: 198 AA.
AC 043521; 043522;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DB BCL2-like protein 11 (BCL2 interacting mediator of cell death).
GN BCL2L1 OR BIM.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, AND ALTERNATIVE SPLICING.
RX TISSUE-Peripheral blood, and spleen;
RX MEDLINE=98094360; PubMed=9420630;
RA O'Connor L., Strasser A., O'Reilly L.A., Hausmann G., Adams J.M.,
RA Cory S., Huang D.C.S.;
RA Bim: a novel member of the Bcl-2 family that promotes apoptosis.";
RL EMBL J. 17:384-395(1998).
CC -1- FUNCTION: INDUCES APOPTOSIS. ISOFORM BIML IS MORE POTENT THAN
CC ISOFORM BIMEL.
CC -1- SUBUNIT: FORMS HETERODIMERS WITH A NUMBER OF ANTIAPOPTOTIC BCL-2
CC PROTEINS INCLUDING MCL-1, BCL-2, BCL-XL, BFL-1, AND BHRF-1. DOES
CC NOT HETERODIMERIZE WITH PROAPOPTOTIC PROTEINS SUCH AS BAD, BAX,
CC BAX OR BAK (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: ASSOCIATED WITH INTRACYTOSOLIC MEMBRANES
CC (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: BIMEL (SHOWN HERE) AND
CC BIML. ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- DOMAIN: THE BH3 DOMAIN IS REQUIRED FOR BCL-2 BINDING AND
CC CYTOTOXICITY.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 3 (BH3).
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC
CC EMBL: AF032457; AAC39593.1; -
CC EMBL: AF032458; AAC39594.1; -
CC DR MIR: 603827; -
CC DR InterPro: IPR00712; BCL-2.
CC DR PROSITE: PS01259; BH3; FALSE NEG.
CC KM Apoptosis; Alternative splicing; Membrane.
CC FT DOMAIN 148 162 BH3;
CC FT VASPSPLIT 42 101 MISSING (IN ISOFORM BIML).
CC FT MOD_RES 198 AA; 22171 MW; D75735E469CA6997 CRC64;
CC SO SEQUENCE

Query Match 34.18; Score 47; DB 1; Length 198;
Best Local Similarity 45.58; Pred. No. 5.1;
Matches 10; Conservative 3; Mismatches 5; Indels 4; Gaps 1;

OY 2 LMAAQRGRELRLMSDEFGSF 23
DB 146 IWLIAQ-----ELRRIGDEFNAYV 163

RESULT 14
PMR2_ANTEL STANDARD; PRT: 429 AA.
AC Q16994;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Antho-Rfamidae neuropeptides type 2 precursor.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actinaria;
OC Nynantheae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93054550; PubMed=1429603;
RA Schmutzler C., Darmer D., Diekhoff D., Grimmelikhuijsen C.J.P.;
RT Identification of a novel type of processing sites in the precursor
RT for the sea anemone neuropeptide Antho-Rfamidae (<Glu-Gly-Arg-Phe-NH2)
RT from Anthopleura elegantissima.";
RL J. Biol. Chem. 267:22534-22541(1992).
CC -1- FUNCTION: NOT KNOWN BUT IT COULD ACT AS A TRANSMITTER AT
CC NEUROMUSCULAR SYNAPSES.
CC -1- SUBCELLULAR LOCATION: Secreted
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC
CC EMBL: M99170; AAA27739.1; -
CC DR Neuropeptide; Amidation; Repeat; Signal.
CC KW
CC FT SIGNAL 1 32
CC FT PEPTIDE 234 232
CC FT PEPTIDE 234 232 POTENTIAL.
CC FT PEPTIDE 242 245 ANTHO-RFAMIDE.
CC FT PEPTIDE 242 245 ANTHO-RFAMIDE.
CC FT PEPTIDE 258 253 ANTHO-RFAMIDE.
CC FT PEPTIDE 258 261 ANTHO-RFAMIDE.
CC FT PEPTIDE 266 259 ANTHO-RFAMIDE.
CC FT PEPTIDE 274 277 ANTHO-RFAMIDE.
CC FT PEPTIDE 290 293 ANTHO-RFAMIDE.
CC FT PEPTIDE 298 301 ANTHO-RFAMIDE.
CC FT PEPTIDE 306 309 ANTHO-RFAMIDE.
CC FT PEPTIDE 322 325 ANTHO-RFAMIDE.
CC FT PEPTIDE 330 333 ANTHO-RFAMIDE.
CC FT PEPTIDE 343 346 ANTHO-RFAMIDE.
CC FT PEPTIDE 356 359 ANTHO-RFAMIDE.
CC FT PEPTIDE 369 372 ANTHO-RFAMIDE.
CC FT MOD_RES 237 237 PROVIDE AMIDE GROUP).
CC FT MOD_RES 245 245 AMIDATION (G-248 PROVIDE AMIDE GROUP).
CC FT MOD_RES 245 245 AMIDATION (G-254 PROVIDE AMIDE GROUP).
CC FT MOD_RES 253 253 AMIDATION (G-262 PROVIDE AMIDE GROUP).
CC FT MOD_RES 261 261 AMIDATION (G-270 PROVIDE AMIDE GROUP).
CC FT MOD_RES 269 269 AMIDATION (G-278 PROVIDE AMIDE GROUP).
CC FT MOD_RES 277 277 AMIDATION (G-294 PROVIDE AMIDE GROUP).
CC FT MOD_RES 293 293 AMIDATION (G-302 PROVIDE AMIDE GROUP).
CC FT MOD_RES 301 301 AMIDATION (G-310 PROVIDE AMIDE GROUP).
CC FT MOD_RES 309 309 AMIDATION (G-326 PROVIDE AMIDE GROUP).
CC FT MOD_RES 325 325 AMIDATION (G-334 PROVIDE AMIDE GROUP).
CC FT MOD_RES 333 333 AMIDATION (G-347 PROVIDE AMIDE GROUP).
CC FT MOD_RES 346 346 AMIDATION (G-360 PROVIDE AMIDE GROUP).
CC FT MOD_RES 359 359 AMIDATION (G-373 PROVIDE AMIDE GROUP).
CC FT MOD_RES 372 372 AMIDATION (G-373 PROVIDE AMIDE GROUP).
CC SO SEQUENCE 429 AA; 50564 MW; 7C54F5C606537F4 CRC64;

Query Match 33.78; Score 46.5; DB 1; Length 429;
Best Local Similarity 52.44; Pred. No. 15;
Matches 11; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

OY 4 AAQRYGRRLR-RMSDEFGSF 23
DB 209 AAGRGRLRGRLRGRLRGRLRG 229

RESULT 15
PMR1_ANTEL STANDARD; PRT: 435 AA.
AC P10419;
DT 01-MAR-1985 (Rel. 10, Created)

```

DT 01-OCT-1993 (rel. 27, last sequence update)
 DT 16-OCT-2001 (rel. 40, last annotation update)
 DE Antho-Rfamidae neuropeptides type 1 precursor.
 OS Anthopleura elegantissima (See anemone).
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actinoptera;
 OC Nymphaeaceae; Actinellidae; Anthopleura.
 ON NCU_Taxid-6110;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=3054550; Pubmed1429603;
 RA Schmeitzler C., Barmer D., Diekhoff D., Grimmelikhuijzen C.J.P.;
 RT Identification of a novel type of processing sites in the precursor
 RT for the sea anemone neuropeptide Antho-Rfamidae (<Glu-Gly-Arg-Phe-NH2)
 RT from Anthopleura elegantissima.".
 RL J. Biol. Chem. 267:22534-22541(1992).
 RN [2]
 RP SEQUENCE OF MATURE PEPTIDE.
 RX MEDLINE=87092339; Pubmed2679288;
 RA Grimmelikhuijzen C.J.P., Graff D.;
 RT Isolation of PYROGLU-Gly-Arg-Phe-NH2 (Antho-Rfamidae), a neuropeptide
 RT from sea anemone.".
 RL Proc. Natl. Acad. Sci. U.S.A. 83:9817-9821(1986).
 CC -1- FUNCTION: NOT KNOWN BUT IT COULD ACT AS A TRANSMITTER AT
 CC NEURONAL LOCATION.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC
 DR EMBL: M98269; AAA27738.1; -
 DR PIR: A26666; ECXAA.
 DR PIR: A44308; A44308.
 DR InterPro: IPR002544; FARP.
 DR Pfam: PF01581; FARP; 13.
 KW Neuropeptide; Amidation; Repeat; Signal.
 FT SIGNAL 1 22
 FT PEPTIDE 194 197
 FT PEPTIDE 202 205
 FT PEPTIDE 210 213
 FT PEPTIDE 218 221
 FT PEPTIDE 226 229
 FT PEPTIDE 234 237
 FT PEPTIDE 242 245
 FT PEPTIDE 250 253
 FT PEPTIDE 258 261
 FT PEPTIDE 266 269
 FT PEPTIDE 274 277
 FT PEPTIDE 282 285
 FT PEPTIDE 290 293
 FT PEPTIDE 298 301
 FT PEPTIDE 306 309
 FT PEPTIDE 314 317
 FT PEPTIDE 322 325
 FT PEPTIDE 330 333
 FT PEPTIDE 338 341
 FT PEPTIDE 346 349
 FT PEPTIDE 354 357
 FT PEPTIDE 362 365
 FT PEPTIDE 370 373
 FT PEPTIDE 378 381
 FT PEPTIDE 386 389
 FT PEPTIDE 394 397
 FT PEPTIDE 402 405
 FT PEPTIDE 410 413
 FT PEPTIDE 418 421
 FT PEPTIDE 426 429
 FT PEPTIDE 434 437
 FT PEPTIDE 442 445
 FT PEPTIDE 450 453
 FT PEPTIDE 458 461
 FT PEPTIDE 466 469
 FT PEPTIDE 474 477
 FT PEPTIDE 482 485
 FT PEPTIDE 490 493
 FT PEPTIDE 498 501
 FT PEPTIDE 506 509
 FT PEPTIDE 514 517
 FT PEPTIDE 522 525
 FT PEPTIDE 530 533
 FT PEPTIDE 538 541
 FT PEPTIDE 546 549
 FT PEPTIDE 554 557
 FT PEPTIDE 562 565
 FT PEPTIDE 570 573
 FT PEPTIDE 578 581
 FT PEPTIDE 586 589
 FT PEPTIDE 594 597
 FT PEPTIDE 602 605
 FT PEPTIDE 610 613
 FT PEPTIDE 618 621
 FT PEPTIDE 626 629
 FT PEPTIDE 634 637
 FT PEPTIDE 642 645
 FT PEPTIDE 650 653
 FT PEPTIDE 658 661
 FT PEPTIDE 666 669
 FT PEPTIDE 674 677
 FT PEPTIDE 682 685
 FT PEPTIDE 690 693
 FT PEPTIDE 698 701
 FT PEPTIDE 706 709
 FT PEPTIDE 714 717
 FT PEPTIDE 722 725
 FT PEPTIDE 730 733
 FT PEPTIDE 738 741
 FT PEPTIDE 746 749
 FT PEPTIDE 754 757
 FT PEPTIDE 762 765
 FT PEPTIDE 770 773
 FT PEPTIDE 778 781
 FT PEPTIDE 786 789
 FT PEPTIDE 794 797
 FT PEPTIDE 802 805
 FT PEPTIDE 810 813
 FT PEPTIDE 818 821
 FT PEPTIDE 826 829
 FT PEPTIDE 834 837
 FT PEPTIDE 842 845
 FT PEPTIDE 850 853
 FT PEPTIDE 858 861
 FT PEPTIDE 866 869
 FT PEPTIDE 874 877
 FT PEPTIDE 882 885
 FT PEPTIDE 890 893
 FT PEPTIDE 898 901
 FT PEPTIDE 906 909
 FT PEPTIDE 914 917
 FT PEPTIDE 922 925
 FT PEPTIDE 930 933
 FT PEPTIDE 938 941
 FT PEPTIDE 946 949
 FT PEPTIDE 954 957
 FT PEPTIDE 962 965
 FT PEPTIDE 970 973
 FT PEPTIDE 978 981
 FT PEPTIDE 986 989
 FT PEPTIDE 994 997
 FT PEPTIDE 1002 1005
 FT PEPTIDE 1010 1013
 FT PEPTIDE 1018 1021
 FT PEPTIDE 1026 1029
 FT PEPTIDE 1034 1037
 FT PEPTIDE 1042 1045
 FT PEPTIDE 1050 1053
 FT PEPTIDE 1058 1061
 FT PEPTIDE 1066 1069
 FT PEPTIDE 1074 1077
 FT PEPTIDE 1082 1085
 FT PEPTIDE 1090 1093
 FT PEPTIDE 1098 1101
 FT PEPTIDE 1106 1109
 FT PEPTIDE 1114 1117
 FT PEPTIDE 1122 1125
 FT PEPTIDE 1130 1133
 FT PEPTIDE 1138 1141
 FT PEPTIDE 1146 1149
 FT PEPTIDE 1154 1157
 FT PEPTIDE 1162 1165
 FT PEPTIDE 1170 1173
 FT PEPTIDE 1178 1181
 FT PEPTIDE 1186 1189
 FT PEPTIDE 1194 1197
 FT PEPTIDE 1202 1205
 FT PEPTIDE 1210 1213
 FT PEPTIDE 1218 1221
 FT PEPTIDE 1226 1229
 FT PEPTIDE 1234 1237
 FT PEPTIDE 1242 1245
 FT PEPTIDE 1250 1253
 FT PEPTIDE 1258 1261
 FT PEPTIDE 1266 1269
 FT PEPTIDE 1274 1277
 FT PEPTIDE 1282 1285
 FT PEPTIDE 1290 1293
 FT PEPTIDE 1298 1301
 FT PEPTIDE 1306 1309
 FT PEPTIDE 1314 1317
 FT PEPTIDE 1322 1325
 FT PEPTIDE 1330 1333
 FT PEPTIDE 1338 1341
 FT PEPTIDE 1346 1349
 FT PEPTIDE 1354 1357
 FT PEPTIDE 1362 1365
 FT PEPTIDE 1370 1373
 FT PEPTIDE 1378 1381
 FT PEPTIDE 1386 1389
 FT PEPTIDE 1394 1397
 FT PEPTIDE 1402 1405
 FT PEPTIDE 1410 1413
 FT PEPTIDE 1418 1421
 FT PEPTIDE 1426 1429
 FT PEPTIDE 1434 1437
 FT PEPTIDE 1442 1445
 FT PEPTIDE 1450 1453
 FT PEPTIDE 1458 1461
 FT PEPTIDE 1466 1469
 FT PEPTIDE 1474 1477
 FT PEPTIDE 1482 1485
 FT PEPTIDE 1490 1493
 FT PEPTIDE 1498 1501
 FT PEPTIDE 1506 1509
 FT PEPTIDE 1514 1517
 FT PEPTIDE 1522 1525
 FT PEPTIDE 1530 1533
 FT PEPTIDE 1538 1541
 FT PEPTIDE 1546 1549
 FT PEPTIDE 1554 1557
 FT PEPTIDE 1562 1565
 FT PEPTIDE 1570 1573
 FT PEPTIDE 1578 1581
 FT PEPTIDE 1586 1589
 FT PEPTIDE 1594 1597
 FT PEPTIDE 1602 1605
 FT PEPTIDE 1610 1613
 FT PEPTIDE 1618 1621
 FT PEPTIDE 1626 1629
 FT PEPTIDE 1634 1637
 FT PEPTIDE 1642 1645
 FT PEPTIDE 1650 1653
 FT PEPTIDE 1658 1661
 FT PEPTIDE 1666 1669
 FT PEPTIDE 1674 1677
 FT PEPTIDE 1682 1685
 FT PEPTIDE 1690 1693
 FT PEPTIDE 1698 1701
 FT PEPTIDE 1706 1709
 FT PEPTIDE 1714 1717
 FT PEPTIDE 1722 1725
 FT PEPTIDE 1730 1733
 FT PEPTIDE 1738 1741
 FT PEPTIDE 1746 1749
 FT PEPTIDE 1754 1757
 FT PEPTIDE 1762 1765
 FT PEPTIDE 1770 1773
 FT PEPTIDE 1778 1781
 FT PEPTIDE 1786 1789
 FT PEPTIDE 1794 1797
 FT PEPTIDE 1802 1805
 FT PEPTIDE 1810 1813
 FT PEPTIDE 1818 1821
 FT PEPTIDE 1826 1829
 FT PEPTIDE 1834 1837
 FT PEPTIDE 1842 1845
 FT PEPTIDE 1850 1853
 FT PEPTIDE 1858 1861
 FT PEPTIDE 1866 1869
 FT PEPTIDE 1874 1877
 FT PEPTIDE 1882 1885
 FT PEPTIDE 1890 1893
 FT PEPTIDE 1898 1901
 FT PEPTIDE 1906 1909
 FT PEPTIDE 1914 1917
 FT PEPTIDE 1922 1925
 FT PEPTIDE 1930 1933
 FT PEPTIDE 1938 1941
 FT PEPTIDE 1946 1949
 FT PEPTIDE 1954 1957
 FT PEPTIDE 1962 1965
 FT PEPTIDE 1970 1973
 FT PEPTIDE 1978 1981
 FT PEPTIDE 1986 1989
 FT PEPTIDE 1994 1997
 FT PEPTIDE 2002 2005
 FT PEPTIDE 2010 2013
 FT PEPTIDE 2018 2021
 FT PEPTIDE 2026 2029
 FT PEPTIDE 2034 2037
 FT PEPTIDE 2042 2045
 FT PEPTIDE 2050 2053
 FT PEPTIDE 2058 2061
 FT PEPTIDE 2066 2069
 FT PEPTIDE 2074 2077
 FT PEPTIDE 2082 2085
 FT PEPTIDE 2090 2093
 FT PEPTIDE 2098 2101
 FT PEPTIDE 2106 2109
 FT PEPTIDE 2114 2117
 FT PEPTIDE 2122 2125
 FT PEPTIDE 2130 2133
 FT PEPTIDE 2138 2141
 FT PEPTIDE 2146 2149
 FT PEPTIDE 2154 2157
 FT PEPTIDE 2162 2165
 FT PEPTIDE 2170 2173
 FT PEPTIDE 2178 2181
 FT PEPTIDE 2186 2189
 FT PEPTIDE 2194 2197
 FT PEPTIDE 2202 2205
 FT PEPTIDE 2210 2213
 FT PEPTIDE 2218 2221
 FT PEPTIDE 2226 2229
 FT PEPTIDE 2234 2237
 FT PEPTIDE 2242 2245
 FT PEPTIDE 2250 2253
 FT PEPTIDE 2258 2261
 FT PEPTIDE 2266 2269
 FT PEPTIDE 2274 2277
 FT PEPTIDE 2282 2285
 FT PEPTIDE 2290 2293
 FT PEPTIDE 2298 2301
 FT PEPTIDE 2306 2309
 FT PEPTIDE 2314 2317
 FT PEPTIDE 2322 2325
 FT PEPTIDE 2330 2333
 FT PEPTIDE 2338 2341
 FT PEPTIDE 2346 2349
 FT PEPTIDE 2354 2357
 FT PEPTIDE 2362 2365
 FT PEPTIDE 2370 2373
 FT PEPTIDE 2378 2381
 FT PEPTIDE 2386 2389
 FT PEPTIDE 2394 2397
 FT PEPTIDE 2402 2405
 FT PEPTIDE 2410 2413
 FT PEPTIDE 2418 2421
 FT PEPTIDE 2426 2429
 FT PEPTIDE 2434 2437
 FT PEPTIDE 2442 2445
 FT PEPTIDE 2450 2453
 FT PEPTIDE 2458 2461
 FT PEPTIDE 2466 2469
 FT PEPTIDE 2474 2477
 FT PEPTIDE 2482 2485
 FT PEPTIDE 2490 2493
 FT PEPTIDE 2498 2501
 FT PEPTIDE 2506 2509
 FT PEPTIDE 2514 2517
 FT PEPTIDE 2522 2525
 FT PEPTIDE 2530 2533
 FT PEPTIDE 2538 2541
 FT PEPTIDE 2546 2549
 FT PEPTIDE 2554 2557
 FT PEPTIDE 2562 2565
 FT PEPTIDE 2570 2573
 FT PEPTIDE 2578 2581
 FT PEPTIDE 2586 2589
 FT PEPTIDE 2594 2597
 FT PEPTIDE 2602 2605
 FT PEPTIDE 2610 2613
 FT PEPTIDE 2618 2621
 FT PEPTIDE 2626 2629
 FT PEPTIDE 2634 2637
 FT PEPTIDE 2642 2645
 FT PEPTIDE 2650 2653
 FT PEPTIDE 2658 2661
 FT PEPTIDE 2666 2669
 FT PEPTIDE 2674 2677
 FT PEPTIDE 2682 2685
 FT PEPTIDE 2690 2693
 FT PEPTIDE 2698 2701
 FT PEPTIDE 2706 2709
 FT PEPTIDE 2714 2717
 FT PEPTIDE 2722 2725
 FT PEPTIDE 2730 2733
 FT PEPTIDE 2738 2741
 FT PEPTIDE 2746 2749
 FT PEPTIDE 2754 2757
 FT PEPTIDE 2762 2765
 FT PEPTIDE 2770 2773
 FT PEPTIDE 2778 2781
 FT PEPTIDE 2786 2789
 FT PEPTIDE 2794 2797
 FT PEPTIDE 2802 2805
 FT PEPTIDE 2810 2813
 FT PEPTIDE 2818 2821
 FT PEPTIDE 2826 2829
 FT PEPTIDE 2834 2837
 FT PEPTIDE 2842 2845
 FT PEPTIDE 2850 2853
 FT PEPTIDE 2858 2861
 FT PEPTIDE 2866 2869
 FT PEPTIDE 2874 2877
 FT PEPTIDE 2882 2885
 FT PEPTIDE 2890 2893
 FT PEPTIDE 2898 2901
 FT PEPTIDE 2906 2909
 FT PEPTIDE 2914 2917
 FT PEPTIDE 2922 2925
 FT PEPTIDE 2930 2933
 FT PEPTIDE 2938 2941
 FT PEPTIDE 2946 2949
 FT PEPTIDE 2954 2957
 FT PEPTIDE 2962 2965
 FT PEPTIDE 2970 2973
 FT PEPTIDE 2978 2981
 FT PEPTIDE 2986 2989
 FT PEPTIDE 2994 2997
 FT PEPTIDE 3002 3005
 FT PEPTIDE 3010 3013
 FT PEPTIDE 3018 3021
 FT PEPTIDE 3026 3029
 FT PEPTIDE 3034 3037
 FT PEPTIDE 3042 3045
 FT PEPTIDE 3050 3053
 FT PEPTIDE 3058 3061
 FT PEPTIDE 3066 3069
 FT PEPTIDE 3074 3077
 FT PEPTIDE 3082 3085
 FT PEPTIDE 3090 3093
 FT PEPTIDE 3098 3101
 FT PEPTIDE 3106 3109
 FT PEPTIDE 3114 3117
 FT PEPTIDE 3122 3125
 FT PEPTIDE 3130 3133
 FT PEPTIDE 3138 3141
 FT PEPTIDE 3146 3149
 FT PEPTIDE 3154 3157
 FT PEPTIDE 3162 3165
 FT PEPTIDE 3170 3173
 FT PEPTIDE 3178 3181
 FT PEPTIDE 3186 3189
 FT PEPTIDE 3194 3197
 FT PEPTIDE 3202 3205
 FT PEPTIDE 3210 3213
 FT PEPTIDE 3218 3221
 FT PEPTIDE 3226 3229
 FT PEPTIDE 3234 3237
 FT PEPTIDE 3242 3245
 FT PEPTIDE 3250 3253
 FT PEPTIDE 3258 3261
 FT PEPTIDE 3266 3269
 FT PEPTIDE 3274 3277
 FT PEPTIDE 3282 3285
 FT PEPTIDE 3290 3293
 FT PEPTIDE 3298 3301
 FT PEPTIDE 3306 3309
 FT PEPTIDE 3314 3317
 FT PEPTIDE 3322 3325
 FT PEPTIDE 3330 3333
 FT PEPTIDE 3338 3341
 FT PEPTIDE 3346 3349
 FT PEPTIDE 3354 3357
 FT PEPTIDE 3362 3365
 FT PEPTIDE 3370 3373
 FT PEPTIDE 3378 3381
 FT PEPTIDE 3386 3389
 FT PEPTIDE 3394 3397
 FT PEPTIDE 3402 3405
 FT PEPTIDE 3410 3413
 FT PEPTIDE 3418 3421
 FT PEPTIDE 3426 3429
 FT PEPTIDE 3434 3437
 FT PEPTIDE 3442 3445
 FT PEPTIDE 3450 3453
 FT PEPTIDE 3458 3461
 FT PEPTIDE 3466 3469
 FT PEPTIDE 3474 3477
 FT PEPTIDE 3482 3485
 FT PEPTIDE 3490 3493
 FT PEPTIDE 3498 3501
 FT PEPTIDE 3506 3509
 FT PEPTIDE 3514 3517
 FT PEPTIDE 3522 3525
 FT PEPTIDE 3530 3533
 FT PEPTIDE 3538 3541
 FT PEPTIDE 3546 3549
 FT PEPTIDE 3554 3557
 FT PEPTIDE 3562 3565
 FT PEPTIDE 3570 3573
 FT PEPTIDE 3578 3581
 FT PEPTIDE 3586 3589
 FT PEPTIDE 3594 3597
 FT PEPTIDE 3602 3605
 FT PEPTIDE 3610 3613
 FT PEPTIDE 3618 3621
 FT PEPTIDE 3626 3629
 FT PEPTIDE 3634 3637
 FT PEPTIDE 3642 3645
 FT PEPTIDE 3650 3653
 FT PEPTIDE 3658 3661
 FT PEPTIDE 3666 3669
 FT PEPTIDE 3674 3677
 FT PEPTIDE 3682 3685
 FT PEPTIDE 3690 3693
 FT PEPTIDE 3698 3701
 FT PEPTIDE 3706 3709
 FT PEPTIDE 3714 3717
 FT PEPTIDE 3722 3725
 FT PEPTIDE 3730 3733
 FT PEPTIDE 3738 3741
 FT PEPTIDE 3746 3749
 FT PEPTIDE 3754 3757
 FT PEPTIDE 3762 3765
 FT PEPTIDE 3770 3773
 FT PEPTIDE 3778 3781
 FT PEPTIDE 3786 3789
 FT PEPTIDE 3794 3797
 FT PEPTIDE 3802 3805
 FT PEPTIDE 3810 3813
 FT PEPTIDE 3818 3821
 FT PEPTIDE 3826 3829
 FT PEPTIDE 3834 3837
 FT PEPTIDE 3842 3845
 FT PEPTIDE 3850 3853
 FT PEPTIDE 3858 3861
 FT PEPTIDE 3866 3869
 FT PEPTIDE 3874 3877
 FT PEPTIDE 3882 3885
 FT PEPTIDE 3890 3893
 FT PEPTIDE 3898 3901
 FT PEPTIDE 3906 3909
 FT PEPTIDE 3914 3917
 FT PEPTIDE 3922 3925
 FT PEPTIDE 3930 3933
 FT PEPTIDE 3938 3941
 FT PEPTIDE 3946 3949
 FT PEPTIDE 3954 3957
 FT PEPTIDE 3962 3965
 FT PEPTIDE 3970 3973
 FT PEPTIDE 3978 3981
 FT PEPTIDE 3986 3989
 FT PEPTIDE 3994 3997
 FT PEPTIDE 4002 4005
 FT PEPTIDE 4010 4013
 FT PEPTIDE 4018 4021
 FT PEPTIDE 4026 4029
 FT PEPTIDE 4034 4037
 FT PEPTIDE 4042 4045
 FT PEPTIDE 4050 4053
 FT PEPTIDE 4058 4061
 FT PEPTIDE 4066 4069
 FT PEPTIDE 4074 4077
 FT PEPTIDE 4082 4085
 FT PEPTIDE 4090 4093
 FT PEPTIDE 4098 4101
 FT PEPTIDE 4106 4109
 FT PEPTIDE 4114 4117
 FT PEPTIDE 4122 4125
 FT PEPTIDE 4130 4133
 FT PEPTIDE 4138 4141
 FT PEPTIDE 4146 4149
 FT PEPTIDE 4154 4157
 FT PEPTIDE 4162 4165
 FT PEPTIDE 4170 4173
 FT PEPTIDE 4178 4181
 FT PEPTIDE 4186 4189
 FT PEPTIDE 4194 4197
 FT PEPTIDE 4202 4205
 FT PEPTIDE 4210 4213
 FT PEPTIDE 4218 4221
 FT PEPTIDE 4226 4229
 FT PEPTIDE 4234 4237
 FT PEPTIDE 4242 4245
 FT PEPTIDE 4250 4253
 FT PEPTIDE 4258 4261
 FT PEPTIDE 4266 4269
 FT PEPTIDE 4274 4277
 FT PEPTIDE 4282 4285
 FT PEPTIDE 4290 4293
 FT PEPTIDE 4298 4301
 FT PEPTIDE 4306 4309
 FT PEPTIDE 4314 4317
 FT PEPTIDE 4322 4325
 FT PEPTIDE 4330 4333
 FT PEPTIDE 4338 4341
 FT PEPTIDE 4346 4349
 FT PEPTIDE 4354 4357
 FT PEPTIDE 4362 4365
 FT PEPTIDE 4370 4373
 FT PEPTIDE 4378 4381
 FT PEPTIDE 4386 4389
 FT PEPTIDE 4394 4397
 FT PEPTIDE 4402 4405
 FT PEPTIDE 4410 4413
 FT PEPTIDE 4418 4421
 FT PEPTIDE 4426 4429
 FT PEPTIDE 4434 4437
 FT PEPTIDE 4442 4445
 FT PEPTIDE 4450 4453
 FT PEPTIDE 4458 4461
 FT PEPTIDE 4466 4469
 FT PEPTIDE 4474 4477
 FT PEPTIDE 4482 4485
 FT PEPTIDE 4490 4493
 FT PEPTIDE 4498 4501
 FT PEPTIDE 4506 4509
 FT PEPTIDE 4514 4517
 FT PEPTIDE 4522 4525
 FT PEPTIDE 4530 4533
 FT PEPTIDE 4538 4541
 FT PEPTIDE 4546 4549
 FT PEPTIDE 4554 4557
 FT PEPTIDE 4562 4565
 FT PEPTIDE 4570 4573
 FT PEPTIDE 4578 4581
 FT PEPTIDE 4586 4589
 FT PEPTIDE 4594 4597
 FT PEPTIDE 4602 4605
 FT PEPTIDE 4610 4613
 FT PEPTIDE 4618 4621
 FT PEPTIDE 4626 4629
 FT PEPTIDE 4634 4637
 FT PEPTIDE 4642 4645
 FT PEPTIDE 4650 4653
 FT PEPTIDE 4658 4661
 FT PEPTIDE 4666 4669
 FT PEPTIDE 4674 4677
 FT PEPTIDE 4682 4685
 FT PEPTIDE 4690 4693
 FT PEPTIDE 4698 4701
 FT PEPTIDE 4706 4709
 FT PEPTIDE 4714 4717
 FT PEPTIDE 4722 4725
 FT PEPTIDE 4730 4733
 FT PEPTIDE 4738 4741
 FT PEPTIDE 4746 4749
 FT PEPTIDE 4754 4757
 FT PEPTIDE 4762 4765
 FT PEPTIDE 4770 4773
 FT PEPTIDE 4778 4781
 FT PEPTIDE 4786 4789
 FT PEPTIDE 4794 4797
 FT PEPTIDE 4802 4805
 FT PEPTIDE 4810 4813
 FT PEPTIDE 4818 4821
 FT PEPTIDE 4826 4829
 FT PEPTIDE 4834 4837
 FT PEPTIDE 4842 4845
 FT PEPTIDE 4850 4853
 FT PEPTIDE 4858 4861
 FT PEPTIDE 4866 4869
 FT PEPTIDE 4874 4877
 FT PEPTIDE 4882 4885
 FT PEPTIDE 4890 4893
 FT PEPTIDE 4898 4901
 FT PEPTIDE 4906 4909
 FT PEPTIDE 4914 4917
 FT PEPTIDE 4922 4925
 FT PEPTIDE 4930 4933
 FT PEPTIDE 4938 4941
 FT PEPTIDE 4946 4949
 FT PEPTIDE 4954 4957
 FT PEPTIDE 4962 4965
 FT PEPTIDE 4970 4973
 FT PEPTIDE 4978 4981
 FT PEPTIDE 4986 4989
 FT PEPTIDE 4994 4997
 FT PEPTIDE 5002 5005
 FT PEPTIDE 5010 5013
 FT PEPTIDE 5018 5021
 FT PEPTIDE 5026 5029
 FT PEPTIDE 5034 5037
 FT PEPTIDE 5042 5045
 FT PEPTIDE 5050 5053
 FT PEPTIDE 5058 5061
 FT PEPTIDE 5066 5069
 FT PEPTIDE 5074 5077
 FT PEPTIDE 5082 5085
 FT PEPTIDE 5090 5093
 FT PEPTIDE 5098 5101
 FT PEPTIDE 5106 5109
 FT PEPTIDE 5114 5117
 FT PEPTIDE 5122 5125
 FT PEPTIDE 5130 5133
 FT PEPTIDE 5138 5141
 FT PEPTIDE 5146 5149
 FT PEPTIDE 5154 5157
 FT PEPTIDE 5162 5165
 FT PEPTIDE 5170 5173
 FT PEPTIDE 5178 5181
 FT PEPTIDE 5186 5189
 FT PEPTIDE 5194 5197
 FT PEPTIDE 5202 5205
 FT PEPTIDE 5210 5213
 FT PEPTIDE 5218 5221
 FT PEPTIDE 5226 5229
 FT PEPTIDE 5234 5237
 FT PEPTIDE 5242 5245
 FT PEPTIDE 5250 5253
 FT PEPTIDE 5258 5261
 FT PEPTIDE 5266 5269
 FT PEPTIDE 5274 5277
 FT PEPTIDE 5282 5285
 FT PEPTIDE 5290 5293
 FT PEPTIDE 5298 5301
 FT PEPTIDE 5306 5309
 FT PEPTIDE 5314 5317
 FT PEPTIDE 5322 5325
 FT PEPTIDE 5330 5333
 FT PEPTIDE

[Illegible text]

```

FN      (11)
DR      SEQUENCE FROM N.A.
RC      STRAIN-CV. 11-B;
RX      MEDLINE-99126449; PubMed-9927474;
RA      Putuganan M.D., Sudhiti J.T.;
RT      Molecular population genetics of floral homeotic loci. Departures
RT      from the floral homeotic gene model at the APETALAS and PISTILLATA
RT      genes of Arabidopsis thaliana.
RL      Genetics 151:839-848(1999).
CC      -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC      -1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR      EMBL: A015801; A051890.1;
DR      HSSP: P11746; 1MNN.
DR      InterPro: IPR002487; K-box.
DR      Pfam: PF00318; MADS_BOX_1.
DR      Pfam: PF00319; SERP_1.
DR      PRINTS: PR00404; MADSDOMAIN.
DR      SMART: SM00432; MADS; 1.
DR      PROSITE: PS00350; MADS_BOX_1; 1.
DR      PROSITE: PS50066; MADS_BOX_2; 1.
DR      DNA-binding: Nuclear protein; Transcription regulation.
SQ      SEQUENCE 232 AA: 27267 MW: 4248520697E22A65 CRC64;

Query Match      37 0%, Score 51; DB 10; Length 232;
Best local: Similarity 47.0%, Pctid No. 11;
Matches 12; Conservative 3; Mismatches 4; Indels 8; Gaps 1

Oy      6 ORG-----RELRAQMSDEFESGR 24
      |||:||||:||||:
Db      107 ORLSECLDELQELRLRDLDEMTENK 133

RESULT 6
OSQ21 095021 PRELIMINARY; PRT: 232 AA.
AC 095021:
DT 01-MAY-2000 (TREMBLE). 13. (Created)
DT 01-MAY-2000 (TREMBLE). 13. (Last sequence update)
DT 01-DEC-2001 (TREMBLE). 19. (Last annotation update)
DE 01. DEC-2001 (TREMBLE). 19. last annotation update)
GN FLORAL HOMEOTIC PROTEIN APF.
GS APETALA1.
OS Arabidopsis thaliana (mouse-ear cress).
GN EMBRYOFLAVINOLIPASE; STEPHOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OS Embryophyta; Streptophyta; Embryophyta; Tracheophyta;
OS eucolecids II; brassicales; brassicaceae; Arabidopsids.
RX NCBI_TaxId=3702;
RN (11)
RP STRAINE FROM N.A.
RC STRAIN-CV. KENT;
RX MEDLINE-99126449; PubMed-9927474;
RA Putuganan M.D., Sudhiti J.T.;
RT Molecular population genetics of floral homeotic loci. Departures
RT from the floral homeotic gene model at the APETALAS and PISTILLATA
RT genes of Arabidopsis thaliana.
RL Genetics 151:839-848(1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
DR EMBL: A015805; A051894.1;
DR HSSP: P11746; 1MNN.
DR InterPro: IPR002487; K-box.
DR InterPro: IPR002100; MADS-box.
DR Pfam: PF00318; MADS_BOX_1.
DR Pfam: PF00319; SERP_1.
DR PRINTS: PR00404; MADSDOMAIN.
DR SMART: SM00432; MADS; 1.
DR PROSITE: PS00350; MADS_BOX_1; 1.
DR PROSITE: PS50066; MADS_BOX_2; 1.
DR DNA-binding: Nuclear protein; Transcription regulation.
SQ SEQUENCE 232 AA: 27286 MW: 66976305B8806353 CRC64;

```

```

OY      6 ORG-----RELINDEFEENK 24
Db      107 CRIGCEUDELIOELRLRDEMENTK 133
111111
RESULT 7
09S030      PRELIMINARY:      PRF:      232 AA.
1D      09S020
2D      03-MAY-2000 (TREMBLEL 13. Created)
3D      01-MAY-2000 (TREMBLEL 13. Last sequence update)
4D      01-DEC-2001 (TREMBLEL 19. Last annotation update)
5D      DE FLORAL HOMEOTIC PROTEIN AP3.
6D      APEFLAL3.
7D      Arabidopsis thaliana (Mouse-ear cress).
8D      Eucalyptus vitiidplancae; Streptophyta; Embryophyta; Tracheophyta;
9D      Spermatophyta; Magnoliophyta; Eudicotyledons; Rosidae;
10D      Dipsacales; Fumariaceae; Brassicaceae; Arabidopsis.
11D      NCBI_TaxID=3702;
12D      [1]
13D      SEQUENCE FROM N.A.
14D      STRAIN-CV. CORSCAL3;
15D      MEDLINE=99126449; PubMed=9927474;
16D      PubMedGen N.B.; Suidth 1.1.;
17D      Arabidopsis thaliana (Mouse-ear cress) of floral homeotic loci. Departures
18D      from the separation general models at the APEFLAL3 and PISTILLATA
19D      genes of Arabidopsis thaliana.
20D      Genetics 151:839-848(1999).
21D      RL
22D      CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
23D      -1- SIMILARITY: TO THE VADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
24D      EMBL: AF158606; MAD51895.1; -.
25D      DR
26D      HSSP: P17746; MNK8;
27D      DR
28D      DR
29D      DR
30D      DR
31D      DR
32D      DR
33D      DR
34D      DR
35D      DR
36D      DR
37D      DR
38D      DR
39D      DR
40D      DR
41D      DR
42D      DR
43D      DR
44D      DR
45D      DR
46D      DR
47D      DR
48D      DR
49D      DR
50D      DR
51D      DR
52D      DR
53D      DR
54D      DR
55D      DR
56D      DR
57D      DR
58D      DR
59D      DR
60D      DR
61D      DR
62D      DR
63D      DR
64D      DR
65D      DR
66D      DR
67D      DR
68D      DR
69D      DR
70D      DR
71D      DR
72D      DR
73D      DR
74D      DR
75D      DR
76D      DR
77D      DR
78D      DR
79D      DR
80D      DR
81D      DR
82D      DR
83D      DR
84D      DR
85D      DR
86D      DR
87D      DR
88D      DR
89D      DR
90D      DR
91D      DR
92D      DR
93D      DR
94D      DR
95D      DR
96D      DR
97D      DR
98D      DR
99D      DR
100D      DR
101D      DR
102D      DR
103D      DR
104D      DR
105D      DR
106D      DR
107D      DR
108D      DR
109D      DR
110D      DR
111D      DR
112D      DR
113D      DR
114D      DR
115D      DR
116D      DR
117D      DR
118D      DR
119D      DR
120D      DR
121D      DR
122D      DR
123D      DR
124D      DR
125D      DR
126D      DR
127D      DR
128D      DR
129D      DR
130D      DR
131D      DR
132D      DR
133D      DR
134D      DR
135D      DR
136D      DR
137D      DR
138D      DR
139D      DR
140D      DR
141D      DR
142D      DR
143D      DR
144D      DR
145D      DR
146D      DR
147D      DR
148D      DR
149D      DR
150D      DR
151D      DR
152D      DR
153D      DR
154D      DR
155D      DR
156D      DR
157D      DR
158D      DR
159D      DR
160D      DR
161D      DR
162D      DR
163D      DR
164D      DR
165D      DR
166D      DR
167D      DR
168D      DR
169D      DR
170D      DR
171D      DR
172D      DR
173D      DR
174D      DR
175D      DR
176D      DR
177D      DR
178D      DR
179D      DR
180D      DR
181D      DR
182D      DR
183D      DR
184D      DR
185D      DR
186D      DR
187D      DR
188D      DR
189D      DR
190D      DR
191D      DR
192D      DR
193D      DR
194D      DR
195D      DR
196D      DR
197D      DR
198D      DR
199D      DR
200D      DR
201D      DR
202D      DR
203D      DR
204D      DR
205D      DR
206D      DR
207D      DR
208D      DR
209D      DR
210D      DR
211D      DR
212D      DR
213D      DR
214D      DR
215D      DR
216D      DR
217D      DR
218D      DR
219D      DR
220D      DR
221D      DR
222D      DR
223D      DR
224D      DR
225D      DR
226D      DR
227D      DR
228D      DR
229D      DR
230D      DR
231D      DR
232D      DR
233D      DR
234D      DR
235D      DR
236D      DR
237D      DR
238D      DR
239D      DR
240D      DR
241D      DR
242D      DR
243D      DR
244D      DR
245D      DR
246D      DR
247D      DR
248D      DR
249D      DR
250D      DR
251D      DR
252D      DR
253D      DR
254D      DR
255D      DR
256D      DR
257D      DR
258D      DR
259D      DR
260D      DR
261D      DR
262D      DR
263D      DR
264D      DR
265D      DR
266D      DR
267D      DR
268D      DR
269D      DR
270D      DR
271D      DR
272D      DR
273D      DR
274D      DR
275D      DR
276D      DR
277D      DR
278D      DR
279D      DR
280D      DR
281D      DR
282D      DR
283D      DR
284D      DR
285D      DR
286D      DR
287D      DR
288D      DR
289D      DR
290D      DR
291D      DR
292D      DR
293D      DR
294D      DR
295D      DR
296D      DR
297D      DR
298D      DR
299D      DR
300D      DR
301D      DR
302D      DR
303D      DR
304D      DR
305D      DR
306D      DR
307D      DR
308D      DR
309D      DR
310D      DR
311D      DR
312D      DR
313D      DR
314D      DR
315D      DR
316D      DR
317D      DR
318D      DR
319D      DR
320D      DR
321D      DR
322D      DR
323D      DR
324D      DR
325D      DR
326D      DR
327D      DR
328D      DR
329D      DR
330D      DR
331D      DR
332D      DR
333D      DR
334D      DR
335D      DR
336D      DR
337D      DR
338D      DR
339D      DR
340D      DR
341D      DR
342D      DR
343D      DR
344D      DR
345D      DR
346D      DR
347D      DR
348D      DR
349D      DR
350D      DR
351D      DR
352D      DR
353D      DR
354D      DR
355D      DR
356D      DR
357D      DR
358D      DR
359D      DR
360D      DR
361D      DR
362D      DR
363D      DR
364D      DR
365D      DR
366D      DR
367D      DR
368D      DR
369D      DR
370D      DR
371D      DR
372D      DR
373D      DR
374D      DR
375D      DR
376D      DR
377D      DR
378D      DR
379D      DR
380D      DR
381D      DR
382D      DR
383D      DR
384D      DR
385D      DR
386D      DR
387D      DR
388D      DR
389D      DR
390D      DR
391D      DR
392D      DR
393D      DR
394D      DR
395D      DR
396D      DR
397D      DR
398D      DR
399D      DR
400D      DR
401D      DR
402D      DR
403D      DR
404D      DR
405D      DR
406D      DR
407D      DR
408D      DR
409D      DR
410D      DR
411D      DR
412D      DR
413D      DR
414D      DR
415D      DR
416D      DR
417D      DR
418D      DR
419D      DR
420D      DR
421D      DR
422D      DR
423D      DR
424D      DR
425D      DR
426D      DR
427D      DR
428D      DR
429D      DR
430D      DR
431D      DR
432D      DR
433D      DR
434D      DR
435D      DR
436D      DR
437D      DR
438D      DR
439D      DR
440D      DR
441D      DR
442D      DR
443D      DR
444D      DR
445D      DR
446D      DR
447D      DR
448D      DR
449D      DR
450D      DR
451D      DR
452D      DR
453D      DR
454D      DR
455D      DR
456D      DR
457D      DR
458D      DR
459D      DR
460D      DR
461D      DR
462D      DR
463D      DR
464D      DR
465D      DR
466D      DR
467D      DR
468D      DR
469D      DR
470D      DR
471D      DR
472D      DR
473D      DR
474D      DR
475D      DR
476D      DR
477D      DR
478D      DR
479D      DR
480D      DR
481D      DR
482D      DR
483D      DR
484D      DR
485D      DR
486D      DR
487D      DR
488D      DR
489D      DR
490D      DR
491D      DR
492D      DR
493D      DR
494D      DR
495D      DR
496D      DR
497D      DR
498D      DR
499D      DR
500D      DR
501D      DR
502D      DR
503D      DR
504D      DR
505D      DR
506D      DR
507D      DR
508D      DR
509D      DR
510D      DR
511D      DR
512D      DR
513D      DR
514D      DR
515D      DR
516D      DR
517D      DR
518D      DR
519D      DR
520D      DR
521D      DR
522D      DR
523D      DR
524D      DR
525D      DR
526D      DR
527D      DR
528D      DR
529D      DR
530D      DR
531D      DR
532D      DR
533D      DR
534D      DR
535D      DR
536D      DR
537D      DR
538D      DR
539D
```



```

RESULT 15
C9H29 ID PRELIMINARY: PRT: 374 AA.
AC 09H29:
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-OCT-2001 (TREMblrel. 18, Last annotation update)
DE SPERMIDINE/PUTRESCINE ABC TRANSPORTER.
GN F07A2 OR VNG1871G.
CS Halobacterium sp. (strain NRC-1).
OS Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
OC Halobacterium.
OX 111-taxid=94091;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE-20504483; PubMed-11016950:
RA Ng W.V., Kennedy S.P., Mahairas G.G., Bergquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Shroya J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Weir R., Goo Y.A.,
RA Leithauer B., Keller K., Cruz R., Danon M.J., Hough D.W.,
RA Madocks D.G., Jablonski P.E., Krebs M.P., Angeles C.M., Dale H.,
RA Asenberger T.A., Beck R.F., Ponschroder M., Spudich J.L., Jung K.-H.,
RA Friedberg J.C., Hoshino T., Hoshino T., Hoshino T., Hoshino T.,
RA Bhargava H., Bhargava H., Bhargava H., Bhargava H., Bhargava H.,
RA Genome sequence of Halobacterium species NRC-1.
RT Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
CC -1- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
CC (ABC TRANSPORTERS).
CC EMBL: AE005086; ANGI20071.1; -.
DR InterPro: IPR001593; AAA.
DR InterPro: IPR001489; ABC_transport.
DR InterPro: IPR001667; KTY_GTP_A.
DR PIR: P00005; ABC1205.
DR SMART: SM00382; AAA: 1.
DR PROSITE: PS00211; ABC_TRANSPORTER: 1.
KW ATP-binding; Complete proteome; Transport.
SO SEQUENCE 374 AA; 39190 MW; 1442EF823037E16 CRC64;

```

Search completed: September 20, 2002, 11:03:36
Job time: 1653 sec

```

Query Match 36.2%; Score 50; DB 17; Length 374;
Best Local Similarity 76.9%; Pred. NO. 27;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 11 ELRMSDSEEGSF 23
Db 197 ELRLSDAVEGGSF 209

```

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2002, 10:35:58 : Search time 228.86 Seconds
(without alignments)
7.765 Million cell updates/sec

Title: US-09-544-664-29
Perfect score: 83
Sequence: 1 ORYGBREARMSDEEVD 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /SIDSI/gcgdata/hold-genseq/genseqp-emb1/AA1980.DAT.*
2: /SIDSI/gcgdata/hold-genseq/genseqp-emb1/AA1981.DAT.*
3: /SIDSI/gcgdata/hold-genseq/genseqp-emb1/AA1982.DAT.*
4: /SIDSI/gcgdata/hold-genseq/genseqp-emb1/AA1983.DAT.*
5: /SIDSI/gcgdata/hold-genseq/genseqp-emb1/AA1984.DAT.*
6: /SIDSI/gcgdata/hold-genseq/genseqp-emb1/AA1985.DAT.*
7: /SIDSI/gcgdata/hold-genseq/genseqp-emb1/AA1986.DAT.*
8: /SIDSI/gcgdata/hold-genseq/genseqp-emb1/AA1987.DAT.*
9: /SIDSI/gcgdata/hold-genseq/genseqp-emb1/AA1988.DAT.*
10: /SIDSI/gcgdata/hold-genseq/genseqp-emb1/AA1989.DAT.*
11: /SIDSI/gcgdata/hold-genseq/genseqp-emb1/AA1990.DAT.*
12: /SIDSI/gcgdata/hold-genseq/genseqp-emb1/AA1991.DAT.*
13: /SIDSI/gcgdata/hold-genseq/genseqp-emb1/AA1992.DAT.*
14: /SIDSI/gcgdata/hold-genseq/genseqp-emb1/AA1993.DAT.*
15: /SIDSI/gcgdata/hold-genseq/genseqp-emb1/AA1994.DAT.*
16: /SIDSI/gcgdata/hold-genseq/genseqp-emb1/AA1995.DAT.*
17: /SIDSI/gcgdata/hold-genseq/genseqp-emb1/AA1996.DAT.*
18: /SIDSI/gcgdata/hold-genseq/genseqp-emb1/AA1997.DAT.*
19: /SIDSI/gcgdata/hold-genseq/genseqp-emb1/AA1998.DAT.*
20: /SIDSI/gcgdata/hold-genseq/genseqp-emb1/AA1999.DAT.*
21: /SIDSI/gcgdata/hold-genseq/genseqp-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/hold-genseq/genseqp-emb1/AA2001.DAT.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	16	AAV05421	Human BAD BH3 doma
2	83	100.0	16	AAH37029	Bcl2 polypeptide B
3	83	100.0	26	AAV96321	Mammalian Bad Bcl-
4	83	100.0	26	AAH70371	BAD BH3 consensus
5	83	100.0	166	AAW32476	BBC6 protein for r
6	83	100.0	168	AAW55779	Human Bcl-XL/Bcl-2
7	83	100.0	168	AAH13512	Human cell prolif
8	83	100.0	168	AAH70368	Human BAD mutant a
9	83	100.0	168	AAH48287	Human BAD protein.
10	83	100.0	168	AAH67088	Mitotic acid sequen
11	73	50.4	18	AAH70379	Bad BH3 domain reg

12	75	50.4	20	22	AAH70380	BAD BH3 domain reg
13	75	88.0	16	20	AAV05432	Mouse BAD BH3 doma
14	73	88.0	16	21	AAH37028	Bcl2 polypeptide B
15	73	88.0	23	17	AAH95166	Bcl-XL/Bcl-2 ass
16	73	88.0	26	21	AAH37002	Bcl2 polypeptide B
17	73	88.0	26	21	AAH37002	Bcl2 polypeptide B
18	73	88.0	27	21	AAH37003	Bcl2 polypeptide B
19	73	88.0	27	21	AAH37056	Bcl2 polypeptide B
20	73	88.0	28	21	AAH37055	Bcl2 polypeptide B
21	73	88.0	59	19	AAH61319	Mutant BCL-XL/BCL-
22	73	88.0	59	19	AAH61320	Mutant BCL-XL/BCL-
23	73	88.0	59	19	AAH61321	Mutant BCL-XL/BCL-
24	73	88.0	59	19	AAH61322	Mutant BCL-XL/BCL-
25	73	88.0	162	22	AAH70370	Shorter murine BAD
26	73	88.0	204	17	AAH95168	Bcl-XL/Bcl-2 ass
27	73	88.0	204	17	AAH95169	Mutant BCL-XL/BCL-
28	73	88.0	204	19	AAH61317	Mutant BCL-XL/BCL-
29	73	88.0	204	19	AAH61318	Mutant BCL-XL/BCL-
30	73	88.0	204	19	AAH56832	Mutant BCL-XL/BCL-
31	73	88.0	204	19	AAH70359	Longer BAD protein
32	73	88.0	204	22	AAH70369	Longer murine BAD
33	73	88.0	567	22	AAU00250	Bcl-2/Bcl-2 ass
34	67	80.7	16	17	AAH95163	Bcl-XL/Bcl-2 ass
35	44	53.0	9	20	AAV05406	Human BAD BH3 doma
36	44	53.0	9	21	AAV70829	BH3 domain of huma
37	43	51.8	205	21	AAH59875	Arabidopsis thalia
38	42	50.6	110	20	AAH98154	Murine Bcl-2 inter
39	42	50.6	140	20	AAH98155	Murine Bim-L mutan
40	42	50.6	140	20	AAH98159	Murine Bim-L mutan
41	42	50.6	140	20	AAH98160	Murine Bim-L mutan
42	42	50.6	140	20	AAH98161	Murine Bim-L mutan
43	42	50.6	140	20	AAH98162	Murine Bim-L mutan
44	42	50.6	140	20	AAH98163	Murine Bim-L mutan
45	42	50.6	168	22	AAH13548	Novel human diagno

ALIGNMENTS

RESULT 1	
AAV05421	AAV05421 standard; peptide: 16 AA.
XX	
AC	AAV05421:
XX	
DT	02-JUL-1999 (first entry)
XX	
DE	Human BAD BH3 domain.
XX	
KW	BH3 domain; cell death agonist; bcl homology domain; BCL-2 family;
KW	apoptosis promoter; cancer cell; virus infected cell; inflammation;
KW	antibody producing cell; cancer; lymphoproliferative condition;
KW	arthritis; autoimmune disease; therapy.
XX	
OS	homo sapiens.
XX	
PK	MO916787-AL.
XX	
PD	08-APR-1999.
XX	
PF	22-SEP-1998; 98WO-US19765.
XX	
PR	07-OCT-1997; 97US-0946039.
XX	
FR	26-SEP-1997; 97US-0060133.
XX	
PA	(UNIV) UNIV WASHINGTON.
XX	
PT	Korsmeyer SJ;
XX	
DR	WPI; 1999-255058/21.
XX	
PT	Bcl homology domain 3 polypeptide
XX	

PS Example 1; Fig 4; 104pp; English.

XX This sequence represents the BH3 domain of human BAD.

CC The invention relates to a bcl homology domain 3 (BH3 domain),

CC derived from a proapoptotic member of the BCL-2 family. The

CC BH3 polypeptide can be used in a method for promoting apoptosis in a

CC target cell, especially where the cell is a cancer cell, a virus infected

CC cell or an autophagosome producing cell. The BH3 polypeptide can be used

CC in therapeutic compositions for treating disease including cancer, other

CC immunodeficiency syndromes (AIDS), stroke or myocardial infarction and

CC diseases which may result from the down regulation of cell death

CC regulation.

XX Sequence 16 AA:

50

Query Match 100.0%; Score 83; DB 20; Length 16;

Best Local Similarity 100.0%; Pred. No. 9.3e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QRYGRLRMSDEPVD 16

DB 1 qrygrelrmsdepv 16

|||||

RESULT 2

AAB37029 standard; peptide: 16 AA.

XX AAB37029:

AC

DE 28-FEB-2001 (first entry)

XX

DE Bcl2 polypeptide BH3 domain peptide #29.

XX

KW Cytosolic; neuroprotective; anti-HIV; virucide; cerebroprotective;

KW cardiac; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;

KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;

KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;

KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;

KW stroke; myocardial infarction.

OS Homo sapiens.

XX

XX MO2000059526-A1.

XX

PD 12-OCT-2000.

XX

PF 06-APR-2000: 2000MO-US09352.

XX

PR 07-APR-1999: 99US-0128202.

XX

PA (UYJE-) UNIV JEFFERSON THOMAS.

XX

PI Huang Z, Wang J, Zhang Z, Shan S, Lu Z;

XX

DR WPI: 2000-679325/66.

XX

PT New peptide conjugates for modulating apoptosis or for inhibiting B

PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for

PT treating neurodegenerative disorders, stroke, or cancer.

XX

PS Claim 18; Page 18; 74pp; English.

XX

CC The invention relates to a peptide conjugate having the formula:

CC (R-X)-peptide where n = 1-10; X = C=O. When the R-X group is attached

CC to the N-terminus of the peptide, or a side chain of the peptide where

CC the functional group of the side chain is NH₂ or OH; or X = O or NH.

CC When the R-X group is attached to the C-terminus of the peptide, or a

CC side chain of the peptide, where the side chain functional group is COOH

CC or a double bond, a Bcl-2 homology domain 3 (BH3 domain) containing one

CC or two double bonds, cysteine, serine, threonine, aspartate, glutamate,

CC monosubstituted with a 1-5C straight or branched chain alkyl group,

CC phenyl optionally monosubstituted with a 1-5C straight or branched chain

CC alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples

CC of the peptide portion of the conjugate. The peptides represent analogues

CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of

CC the BH3 domain of the cell death agonist bad. The peptide conjugate is

CC useful for modulating apoptosis in the cells of a subject, or for

CC reversing B cell lymphoma/leukemia 2 (bcl-2)-mediated blockage of

CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2

CC function. In particular, the peptide conjugates are useful in treating a

CC subject with B cell lymphoma/leukemia 2 (bcl-2)-mediated blockage of

CC apoptosis. The cancer includes prostate cancer, colorectal, gastric,

CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or

CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide

CC conjugate is also useful for treating disorders characterized by

CC increased apoptosis, e.g. neurodegenerative disorders, acquired

CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.

XX Sequence 16 AA:

50

Query Match 100.0%; Score 83; DB 21; Length 16;

Best Local Similarity 100.0%; Pred. No. 9.3e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QRYGRLRMSDEPVD 16

DB 1 qrygrelrmsdepv 16

|||||

RESULT 3

AAV96321 standard; Peptide: 26 AA.

XX AAV96321:

AC

DE 17-AUG-2000 (first entry)

XX

DE Mammalian Bad Bcl-2 homology domain 3 domain.

XX

DE Mammal; apoptosis; cell death; BRC3; apoptosis promotion; Bad;

XX

KW apoptosis inhibition; malignant cell; autoimmune disease.

KW

OS Mammalia.

XX

XX MO2000026228-A1.

XX

PD 11-MAY-2000.

XX

PF 28-OCT-1999: 99MO-US25285.

XX

PR 02-NOV-1998: 98US-0184168.

XX

PA (CLON-) CLONTECH LAB INC.

XX

PI Zhu L, Yin X, Chittenden T;

XX

DR WPI: 2000-365560/31.

XX

PT Novel polynucleotide encoding a BRC3 protein which is useful for

PT modulating apoptosis, especially in the treatment of cancer and

PT autoimmune diseases.

XX

PS Disclosure; Fig 4; 47pp; English.

XX

CC The present sequence is the mammalian Bad Bcl-2 homology domain 3

CC (BH3) domain, which was used in a sequence alignment with the same

CC domain of a putative version of the mammalian apoptosis

CC regulator BRC3, which was designated BRC3-ORF2. The BRC3 protein,

CC nucleic acids and antibodies are suitable for use in promoting cell

CC death or for preventing apoptosis in malignant cells and those causing

CC autoimmune diseases.

XX

SO Sequence 26 AA:


```

XX DE Human Bcl-XL/Bcl-2 associated death promoting polypeptide.
XX KM Human; Bcl-XL/Bcl-2 associated death promoting polypeptide; Bad:
XX KM Programmed cell death; apoptosis.
XX OS Homo sapiens.
XX PN WO9812328-A2.
XX PD 26-MAR-1998.
XX PF 18-SEP-1997; 97MO-US16991.
XX PR 20-SEP-1996; 96US-0717123.
XX PA (IDUN-) IDUN PHARM INC.
XX PI Horne WJ, Oltersdorf T;
XX DR MPI; 1998-217267/19.
XX DR N-PSDB: AMV25877.
XX PT Bad gene mediating apoptosis - used to develop products for treating
XX KM e.g., neurodegenerative disease, cancers or autoimmune disease
XX CS Claim 8; Fig 1; 41pp; English.
XX CC The present sequence is the human Bcl-XL/Bcl-2 associated
XX CC death promoting polypeptide. Bad: the binding of which to Bcl-XL
XX CC results in the induction of programmed cell death, i.e. apoptosis.
XX CC Bad can be used in screening assays for compounds to treat or
XX CC prevent diseases characterised by apoptotic cell death, such as
XX CC neurodegenerative disorders, e.g. Alzheimer's and Parkinson's
XX CC disease, amyotrophic lateral sclerosis, retinitis pigmentosa and
XX CC cerebellar degeneration, and myelodysplastic syndromes, e.g.
XX CC aplastic anaemia and ischemic injury including myocardial
XX CC infarction, stroke and reperfusion injury. Assays can also be
XX CC used to screen for compounds to treat, or prevent, as
XX CC diseases characterised by the induction of programmed cell death,
XX CC cancers, e.g. lymphoma and hormone dependent tumours, autoimmune
XX CC diseases, e.g. systemic lupus erythematosus and immune-mediated
XX CC glomerulonephritis and viral infections, e.g. herpesvirus,
XX CC poxvirus or adenovirus infection. Bad can also be used for
XX CC detection and diagnosis.
XX SO Sequence 168 AA:

Query Match 100.0%; Score 83; DB 19; Length 168;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ORYGRGLRMSDEFDV 16
DB 108 qrygrglrmsdefdv 123
|||||

```

```

PN US6080847-A.
XX PD 27-JUN-2000.
XX PF 04-DEC-1997; 97US-0985335.
XX PR 04-DEC-1997; 97US-0985335.
XX PA (INC-) INCYTE PHARM INC.
XX PI Corley NC, Hillman JL, Yue H, Lai P, Shah P;
XX DR MPI; 2000-451230/39.
XX DR N-PSDB: AAA63332.
XX PT Novel polynucleotide and polypeptide sequences of proteins associated
XX KM with cell proliferation for diagnosis, prevention and treatment of e.g.
XX KM cancer, acquired immunodeficiency syndrome, and Parkinson's disease -
XX CS Example 8; Fig 1; 58pp; English.
XX CC The present sequence is the human Apop-1 protein. This protein, which
XX CC shares structural and chemical homology with Bcl-2, is involved in cell
XX CC proliferation. Its coding sequence was isolated by screening a synovial
XX CC tissue cDNA library using a computer search for amino acid sequence
XX CC alignments. The gene and protein can be used in the treatment of various
XX CC cancers, disorders with associated inflammation such as Addison's
XX CC disease, adult respiratory distress syndrome, allergies, anemia, asthma,
XX CC arthritis, Sjogren's syndrome and autoimmune thyroiditis, complications
XX CC of myeloproliferative disorders, multiple sclerosis, myasthenia gravis,
XX CC emphysema, glomerulonephritis, rheumatoid arthritis, osteoporosis,
XX CC myocardial or pericardial inflammation, osteoporosis, rheumatoid
XX CC arthritis, Sjogren's syndrome and autoimmune thyroiditis, complications
XX CC of cancer, hemodialysis and extracorporeal circulation, infections,
XX CC leuemia, disorders with associated apoptosis including AIDS and other
XX CC infectious and genetic immunodeficiencies, neurodegenerative diseases
XX CC such as Alzheimer's disease and Parkinson's disease, ischemic injuries
XX CC such as myocardial infarction, and wasting diseases including cachexia.
XX SO Sequence 168 AA:

Query Match 100.0%; Score 83; DB 21; Length 168;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ORYGRGLRMSDEFDV 16
DB 108 qrygrglrmsdefdv 123
|||||

```

```

RESULT 7
AAB13512 AAB13512 standard; protein: 168 AA.
XX AAB13512:
XX 02-NOV-2000 (first entry)
XX Human cell proliferation protein Apop-1.
XX Human; cell proliferation; Apop-1; cancer; inflammation; infection;
XX trauma; neurodegenerative disease; ischemic injury; wasting disease.
XX Homo sapiens.
XX OS Homo sapiens.
XX PN WO200110888-A1.

```

```

RESULT 8
AAB70368 AAB70368 standard; protein: 168 AA.
XX AAB70368:
XX 02-MAY-2001 (first entry)
XX Human BAD mutant amino acid sequence SEQ ID NO:1.
XX Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
XX immunostimulant; neuroprotective; neurotrophic; antischismatic; vulnervary;
XX cytoskeletal; antiviral; antitachytic; antiinflammatory; wound healing;
XX immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;
XX immunoregulatory disease; neurodegenerative disease; viral infection;
XX immunoregulatory death; immunoregulatory; immunoregulatory;
XX lymphoproliferative condition; inflammation; autoimmune disease.
XX Homo sapiens.
XX OS Synthetic.
XX PN WO200110888-A1.

```



```

XX 30-SEP-1999: 99US-0410372.
XX
XX 04-DEC-1997: 97US-0985335.
XX
XX (JINCY-) INCYTE GENOMICS INC.
XX
XX
XX H11man JL, Yue H, Lal P, Shah P, Corley NC:
XX
XX WPI: 2001-569961/64.
XX
XX N-PSDB: AAH78430.
XX
XX New polypeptides associated with cell proliferation, useful for
XX preventing or treating cancer (e.g. brain cancer), a disorder
XX associated with an increase in apoptosis (e.g. Alzheimer's disease) or
XX inflammation (e.g. gout).
XX
XX Example: Fig 1A-C; 59pp; English.
XX
XX The present sequence represents a human protein which is associated
XX with cell proliferation, designated APO-1. The specification also
XX describes APO-1 and APO-3, the APO polypeptides are useful for
XX diagnosis and treatment of the diseases associated with abnormal
XX cell proliferation and apoptosis. The polypeptides can be used to
XX particularly useful for treating or preventing cancer (e.g. brain or
XX breast cancer), a disorder associated with an increase in apoptosis
XX (e.g. Alzheimer's disease or Parkinson's disease) or inflammation
XX (e.g. allergies, gout, osteoarthritis or bronchitis).
XX
XX Sequence 168 AA:

```

```

Query Match          100.0%; Score 83: DB 22: Length 168:
Best Local Similarity 100.0%; Pred. No. 1.2e-06:
Matches 16: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 1 QRYGRLRMSDEFPD 16
Db 108 qrygrelrmsdesvda 123

```

```

RESULT 11
AAB70379
ID AAB70379 standard; Peptide: 18 AA.
XX
XX AAB70379:
XX
XX 02-MAY-2001 (first entry)
XX
XX DE BAD BH3 domain region phosphopeptide SEQ ID NO:17.
XX
XX Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
XX immunostimulant; neuroprotective; nocrotropic; antischismatic; vulnery;
XX cytoskeletal; antiviral; antiarthritic; antiinflammatory; wound healing;
XX immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;
XX immunodeficiency disease; neurodegenerative disease; viral infection;
XX ischaemic cell death; reperfusion cell death; arthritis; infertility;
XX lymphoproliferative condition; inflammation; autoimmune disease.
XX
XX Homo sapiens.
XX
XX WO200110888-A1.
XX
XX 15-FEB-2001.
XX
XX 30-MAY-2000: 2000MC-US11864.
XX
XX 28-MAY-1999: 99US-0136783.
XX
XX (APO-) APOPTOSIS TECHNOLOGY INC.
XX
XX Zhou X:
XX

```

```

DR WPI: 2001-138734/14.
XX
XX New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,
XX useful for screening for candidate compounds which could inhibit
XX apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
XX Ser113.
XX
XX Example 9; Page 92; 157pp; English.
XX
XX The present invention describes an isolated or synthetic polypeptide
XX (I) comprising a less than full length amino acid sequence of a mutant
XX Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its
XX fragment, which contains amino acid substitutions at Ser118 of a human
XX BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine
XX BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective,
XX nocrotropic, antischismatic, vulnery, cytoskeletal, antiviral,
XX antiarthritic, antiinflammatory and immunosuppressive activities, and
XX can be used as an apoptosis inducer or inhibitor. BAD polypeptides and
XX polynucleotides can be used for screening candidate compounds and drugs
XX for activity that promote cell survival or apoptosis. Other uses include
XX inducing or inhibiting apoptosis in a cell. Candidate compounds
XX identified and (mutant) BAD polypeptides are useful in treating
XX immunodeficiency diseases, neurodegenerative diseases, ischaemic cell
XX death, reperfusion cell death, arthritis, infertility, inflammation,
XX lymphoproliferative condition, autoimmune disease, viral infection and
XX autoimmune diseases. The present sequence represents a BAD BH3 domain
XX region phosphopeptide which is used in an example from the present
XX invention.
XX
XX Sequence 18 AA:

```

```

Query Match          90.4%; Score 75: DB 22: Length 18:
Best Local Similarity 93.8%; Pred. No. 2.6e-06:
Matches 15: Conservative 0: Mismatches 1: Indels 0: Gaps 0:
QY 1 QRYGRLRMSDEFPD 16
Db 1 qrygrelrmsdesvda 16

```

```

RESULT 12
AAB70380
ID AAB70380 standard; Peptide: 20 AA.
XX
XX AAB70380:
XX
XX 02-MAY-2001 (first entry)
XX
XX DE BAD BH3 domain region related phosphopeptide SEQ ID NO:18.
XX
XX Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;
XX immunostimulant; neuroprotective; nocrotropic; antischismatic; vulnery;
XX cytoskeletal; antiviral; antiarthritic; antiinflammatory; wound healing;
XX immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;
XX immunodeficiency disease; neurodegenerative disease; viral infection;
XX ischaemic cell death; reperfusion cell death; arthritis; infertility;
XX lymphoproliferative condition; inflammation; autoimmune disease.
XX
XX Homo sapiens.
XX
XX WO200110888-A1.
XX
XX 15-FEB-2001.
XX
XX 30-MAY-2000: 2000MC-US11864.
XX
XX 28-MAY-1999: 99US-0136783.
XX
XX (APO-) APOPTOSIS TECHNOLOGY INC.
XX
XX Zhou X:
XX

```


DR WPI; 2001-138734/14.

XX New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,
PT useful for screening for candidate compounds which induce or inhibit
PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
PT Ser113 -

XX Example 9; Page 92; 157pp; English.

XX The present invention describes an isolated or synthetic polypeptide
XX (1) comprising less than full length amino acid sequence of mutant
XX Bcl-XL/Bcl-2-associated cell death-regulator polypeptide (BAD) or a
XX fragment, which contains amino acid substitutions at Ser118 of a human
XX BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine
XX BAD (shorter murine BAD). (1) has immunostimulant, neuroprotective,
XX neurotropic, antischismatic, vulnerary, cytoskeletal, antiviral,
XX antiarthritic, antiinflammatory and immunosuppressive activities, and
XX can be used as an apoptosis inducer or inhibitor. BAD polypeptides and
XX polynucleotides can be used for screening candidate compounds and drugs
XX for activity that promote cell survival or apoptosis. Other uses include
XX inducing or inhibiting apoptosis in a cell. Candidate compounds
XX identified and (mutant) BAD polypeptides are useful in treating
XX immunodeficiency diseases, neurodegenerative diseases, ischaemic cell
XX death, reperfusion cell death, wound healing, cancer, viral infections,
XX lymphoproliferative conditions, arthritis, infertility, inflammation and
XX autoimmune diseases. The present sequence represents a BAD BH3 domain
XX region related phosphopeptide which is used in an example from the
XX present invention.

CC Sequence 20 AA:

Query Match 90.4%; Score 75; DB 22; Length 20;
Best Local Similarity 93.8%; Pred. No. 2.9e-06;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ORYRELRMSDEPD 16
| | | | | | | | | | | | | | | | | |
Db 3 qyrgelrmedeavd 18

RESULT 13

AA054422 ID AAY05422 standard; peptide; 16 AA.

XX AAY05422:

DT 02-DUL-1999 (first entry)

XX Mouse BAD BH3 domain.

XX BH3 domain; cell death agonist; bcl homology domain; BCL-2 family;
XX apoptosis promoter; cancer cell; virus infected cell; inflammation;
XX autoantibody producing cell; cancer; lymphoproliferative condition;
XX arthritis; autoimmune disease; therapy.

XX Mus sp.

XX MO916787-A1.

XX 08-APR-1999.

XX 22-SEP-1998; 98MO-US19765.

XX 07-OCT-1997; 97US-0946039.

XX 26-SEP-1997; 97US-0060133.

XX (UNITV) UNIV WASHINGTON.

XX Korsmeyer SJ;

XX WPI; 1999-255058/21.

PT Bcl homology domain 3 polypeptide

XX Example 1; Fig 4; 104pp; English.

XX This sequence represents the BH3 domain of mouse BAD.
XX derived from a proapoptotic member of the BCL-2 family. The
XX BH3 polypeptide can be used in a method for promoting apoptosis in a
XX target cell, especially where the cell is a cancer cell. The
XX BH3 polypeptide can be used in a method for promoting apoptosis in a
XX cell or tissue, especially where the cell is a cancer cell. The
XX polypeptide can be used in a method for promoting apoptosis in a
XX lymphoproliferative conditions, including cancer, and autoimmune
XX diseases, which may result from the down regulation of cell death
XX regulation.

CC Sequence 16 AA:

Query Match 88.0%; Score 73; DB 20; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.1e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ORYRELRMSDEP 14
| | | | | | | | | | | | | | | |
Db 1 qyrgelrmedeav 14

RESULT 14

AA037028 ID AAB37028 standard; peptide; 16 AA.

XX AAB37028:

XX 28-FEB-2001 (first entry)

XX Bcl2 polypeptide BH3 domain peptide #28.

XX Cytostatic; neuroprotective; anti-HIV; vrinucide; cerebroprotective;
XX cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;
XX apoptosis modulator; B cell lymphoma/leukemia 2; cancer; prostate;
XX colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
XX melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
XX stroke; myocardial infarction.

XX Homo sapiens.

XX MO200059526-A1.

XX 12-OCT-2000.

XX 06-APR-2000; 2000MO-US09352.

XX 07-APR-1999; 9905-0128202.

XX (UYDE-) UNIV JEFFERSON THOMAS.

XX Huang Z, Wang J, Zhang Z, Shan S, Lu Z;

XX WPI; 2000-679325/66.

XX New peptide conjugates for modulating apoptosis or for inhibiting B
XX cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
XX treating neurodegenerative disorders, stroke, or cancer -

XX Claim 18; Page 18; 74pp; English.

XX The invention relates to a peptide conjugate having the formula:
XX (R-X)-peptide where n = 1-10; X = C=O, when the R-X group is attached
XX to the N-terminus of the peptide, or a side chain of the peptide where
XX the functional group of the side chain is NH2 or OH; or X = O or NH,
XX when the R-X group is attached to the C-terminus of the peptide, or a
XX side chain of the peptide, where the side chain functional group is COOH
XX or CONH2; and R = 2-Iso alkyl or alkoxy, 2-Iso alkyl containing one

or two double bonds, cyclohexyl, cyclopentyl, cyclohexyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, CC phenyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides AAR95166-817058 represent examples CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of CC the Bcl-2 domain of the cell death agonist Bad. The peptide conjugate is CC useful for modulating apoptosis in the cells of a subject, or for CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockade of CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2 CC function. In particular, the peptide conjugate is useful for treating a CC subject afflicted with a cancer characterized by cancer cells that CC express Bcl-2. The cancer includes prostate, colorectal, gastric, CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide CC conjugate is also useful for treating disorders characterized by CC increased apoptosis, e.g. neurodegenerative disorders, acquired CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.

Sequence 16 AA:
Query Match 88.0%; Score 73; DB 21; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.1e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ORGRELRRMSDEF 14
DB 1 qryrelrrmsdef 14

RESULT 15
AAR95166
ID AAR95166 standard; peptide: 23 AA.

AAR95166;
03-JAN-1997 (first entry)

bcl-x(L)/bcl-2 associated death promoter epitope, residues 138-160.

Epitope: murine; bcl-x(L)/bcl-2 associated death promoter; Bad; stroke;
polyepitope: bcl-x; cell death; regulate; BH1; BH2; apoptotic cell death;
cytokine deprivation; IL-3 dependent cell line; immunodeficiency; AIDS;
neurodegenerative disease; senescence; ischemia; neoplasia.

Mus musculus.

W06613614-A1.

09-MAY-1996.

31-OCT-1995; 95MO-US14246.

31-OCT-1994; 94US-033565.

(UNIT) UNIV WASHINGTON.

Korsmeyer SJ;

WPI: 1996-251465/25.

Polynucleotide encoding bcl-x(L)/bcl-2 associated death promoter -
useful to treat neoplasia and apoptosis and to identify agents
inhibiting its binding to bcl-2 or bcl-x(L) to form heteromultimers

Claim 2; Page 103; 130pp; English.

The sequences given in AAR95155-67 represent epitopes derived from the
murine bcl-x(L)/bcl-2 associated death promoter (Bad) polypeptide (see
also AAR95168). Bad is a 22.1 kD protein which interacts with bcl-2 and
bcl-x proteins and regulates cell death. It has homology to the bcl-2-
related family clustered in the BH1 and BH2 domain. Bad has been found

to hybridize to bcl-x(L) and bcl-2 in yeast two-hybrid assays and in
vivo in mammalian cells. Overexpressed Bad counters the death countering
inhibitory activity of bcl-x(L) and bcl-2 and accelerates
apoptotic cell death induced by cytokine deprivation in an IL-3 dependent
cell line expressing bcl-x(L). Bad competes with Bax for binding to bcl-x(L)
activity of bcl-x(L). Bad competes with Bax for binding to bcl-x(L)
or bcl-x(L) to form heterodimers. Such agents may be used to treat
neurodegenerative diseases, immunodeficiency diseases, e.g. AIDS,
senescence or ischemia.

Sequence 23 AA:
Query Match 88.0%; Score 73; DB 17; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ORGRELRRMSDEF 14
DB 8 qryrelrrmsdef 21

Search completed: September 20, 2002, 10:35:58
Job time: 426 sec

Gencore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2002, 10:37:20 : Search time 75.64 Seconds
(without alignments)
5.167 Million cell updates/sec

Title: US-09-544-664-29

Perfect score: 83

Sequence: 1 QRYGRLRRMSDEYD 16

Scoring table: GAPDP 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents, AA:*

1: /cgn2_6/p/ptodata/2/1aa/5A.COMB.pep:*

2: /cgn2_6/p/ptodata/2/1aa/5B.COMB.pep:*

3: /cgn2_6/p/ptodata/2/1aa/5A.COMB.pep:*

4: /cgn2_6/p/ptodata/2/1aa/5B.COMB.pep:*

5: /cgn2_6/p/ptodata/2/1aa/PCRDUS.COMB.pep:*

6: /cgn2_6/p/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	83	100.0	166	1	US-08-665-617-2	Sequence 2, Appl1
2	83	100.0	168	2	US-08-717-123-2	Sequence 2, Appl1
3	83	100.0	168	3	US-08-985-135-1	Sequence 1, Appl1
4	83	100.0	168	3	US-08-985-135-7	Sequence 7, Appl1
5	83	100.0	168	4	US-09-410-172-1	Sequence 1, Appl1
6	83	100.0	168	4	US-09-410-172-7	Sequence 7, Appl1
7	83	88.0	23	1	US-08-333-665-10	Sequence 10, Appl1
8	73	88.0	23	2	US-08-661-479-10	Sequence 10, Appl1
9	73	88.0	59	2	US-08-733-505A-55	Sequence 55, Appl1
10	73	88.0	59	2	US-08-733-505A-56	Sequence 56, Appl1
11	73	88.0	59	2	US-08-733-505A-57	Sequence 57, Appl1
12	73	88.0	59	2	US-08-733-505A-58	Sequence 58, Appl1
13	73	88.0	204	1	US-08-333-665-2	Sequence 2, Appl1
14	73	88.0	204	2	US-08-661-479-2	Sequence 2, Appl1
15	73	88.0	204	2	US-08-733-505A-1	Sequence 1, Appl1
16	73	88.0	204	2	US-08-733-505A-12	Sequence 12, Appl1
17	73	88.0	204	2	US-08-733-505A-13	Sequence 13, Appl1
18	73	88.0	204	2	US-08-733-505A-14	Sequence 14, Appl1
19	70	84.3	204	2	US-08-717-123-3	Sequence 3, Appl1
20	67	80.7	16	1	US-08-333-665-26	Sequence 26, Appl1
21	67	80.7	16	2	US-08-661-479-26	Sequence 26, Appl1
22	42	50.6	11	2	US-08-733-505A-34	Sequence 34, Appl1
23	42	50.6	11	2	US-08-706-741B-69	Sequence 69, Appl1
24	42	50.6	11	2	US-08-924-695A-69	Sequence 69, Appl1
25	42	50.6	876	1	US-08-985-135-2	Sequence 2, Appl1
26	42	50.6	876	3	US-08-985-135-1	Sequence 1, Appl1
27	38	45.8	432	3	US-09-075-087-2	Sequence 2, Appl1

28	38	45.8	432	4	US-09-472-971-1	Sequence 1, Appl1
29	38	45.8	575	3	US-08-913-805A-2	Sequence 2, Appl1
30	38	45.8	575	4	US-08-913-805A-10	Sequence 10, Appl1
31	38	45.8	575	4	US-09-442-629-2	Sequence 2, Appl1
32	38	45.8	575	4	US-09-442-629-10	Sequence 10, Appl1
33	36	43.4	173	3	US-08-669-408B-8	Sequence 8, Appl1
34	36	43.4	1093	5	PCT-US93-03077-1	Sequence 1, Appl1
35	35	42.2	108	2	US-08-160-524A-10	Sequence 10, Appl1
36	35	42.2	380	4	US-08-857-076-12	Sequence 12, Appl1
37	35	42.2	1724	4	US-08-857-076-12	Sequence 12, Appl1
38	34	41.0	66	2	US-08-667-087B-40	Sequence 40, Appl1
39	34	41.0	168	4	US-09-199-637A-425	Sequence 425, Appl1
40	34	41.0	339	3	US-08-758-280-1	Sequence 1, Appl1
41	34	41.0	339	3	US-08-758-280-2	Sequence 2, Appl1
42	34	41.0	339	3	US-08-964-614A-1	Sequence 1, Appl1
43	34	41.0	339	3	US-08-964-614A-2	Sequence 2, Appl1
44	34	41.0	355	4	US-09-194-905-10	Sequence 10, Appl1
45	34	41.0	476	1	US-08-216-276A-33	Sequence 33, Appl1

ALIGNMENTS

RESULT 1
US-08-665-617-2
Sequence 2, Application US/08665617
Patent No. 5663316
GENERAL INFORMATION:
APPLICANT: Xidong, Yin
TITLE OF INVENTION: Gene and protein for Regulation of Cell Death
NUMBER OF SEQUENCES: 2
ADDRESS: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,617
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: CL-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (352) 375-8100
TELEFAX: (352) 372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-665-617-2
Query Match 100.0%; Score 83; DB 1; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QRYGRLRRMSDEYD 16
DB 106 QRYGRLRRMSDEYD 121

```

RESULT 2
US-08-717-123-2
Sequence 2, Application US/08/717123
Patent No. 5965703
GENERAL INFORMATION:
APPLICANT: Horne, William A.
APPLICANT: Oltersdorf, Tilmann
TITLE OF INVENTION: Human BAC Polypeptides, Encoding Nucleic
NUMBER OF SEQUENCES: 15
TITLE OF INVENTION: Acids and Methods of Use
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,123
FILING DATE: 20-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ID 1929
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
TOPOLOGY: Linear
MOLECULE TYPE: protein
US-08-717-123-2

Query Match      100.0%: Score 83; DB 2; Length 168;
Best Local Similarity 100.0%: Pred. No. 1.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 1 ORGRELRLMSDEYVD 16
DB 108 ORGRELRLMSDEYVD 123

```

```

RESULT 3
US-08-985-335-1
Sequence 1, Application US/08/985335
Patent No. 6080847
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Lai, Preci
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
NUMBER OF SEQUENCES: 9
TITLE OF INVENTION: PROLIFERATION
CORRESPONDENCE ADDRESS:
ADDRESSEE: Inocyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Linear
IMMEDIATE SOURCE:
LIBRARY: SYNCRAD01
CLONE: 358673
US-08-985-335-1

Query Match      100.0%: Score 83; DB 3; Length 168;
Best Local Similarity 100.0%: Pred. No. 1.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 1 ORGRELRLMSDEYVD 16
DB 108 ORGRELRLMSDEYVD 123

```

```

RESULT 4
US-08-985-335-7
Sequence 7, Application US/08/985335
Patent No. 6080847
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Lai, Preci
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
NUMBER OF SEQUENCES: 9
TITLE OF INVENTION: PROLIFERATION
CORRESPONDENCE ADDRESS:
ADDRESSEE: Inocyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,335
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Linear
IMMEDIATE SOURCE:
LIBRARY: SYNCRAD01
CLONE: 358673
US-08-985-335-1

```

```

TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1683637
US-08-985-335-7

Query Match          100.0%; Score 83; DB 3; Length 168;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ORYGRELRMSDEPVD 16
DB 108 ORYGRELRMSDEPVD 123

RESULT 5
US-09-410-372-1
Sequence 1, Application US/09410372
Patent No. 6281334
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purni
APPLICANT: Corley, Neil C.
STRAND OF INVENTION: PROTEINS ASSOCIATED WITH CELL
NUMBER OF SEQUENCES: 9
TITLE OF INVENTION: PROLIFERATION
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 08/09/410.372
PRIORITY NUMBER:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985.335
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hillman, Lucy J.
REGISTRATION NUMBER: 36,749
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SYNORAB01
CLONE: 358673
US-09-410-372-1

```

```

Query Match          100.0%; Score 83; DB 4; Length 168;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ORYGRELRMSDEPVD 16
DB 108 ORYGRELRMSDEPVD 123

RESULT 6
US-09-410-372-7
Sequence 7, Application US/09410372
Patent No. 6281334
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purni
APPLICANT: Corley, Neil C.
STRAND OF INVENTION: PROTEINS ASSOCIATED WITH CELL
NUMBER OF SEQUENCES: 9
TITLE OF INVENTION: PROLIFERATION
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410.372
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985.335
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hillman, Lucy J.
REGISTRATION NUMBER: 36,749
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1683637
US-09-410-372-7

Query Match          100.0%; Score 83; DB 4; Length 168;
Best Local Similarity 100.0%; Pred. No. 1.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ORYGRELRMSDEPVD 16
DB 108 ORYGRELRMSDEPVD 123

RESULT 7
US-08-333-565-10
Sequence 10, Application US/08333565
Patent No. 562852
GENERAL INFORMATION:

```

```

? APPLICANT: KORSMEYER, Stanley J.
? TITLE OF INVENTION: BCL-X/BCL-2 ASSOCIATED CELL DEATH
? TITLE OF INVENTION: REGULATOR
? NUMBER OF SEQUENCES: 55
? CORRESPONDENCE ADDRESS:
? ADDRESS: 379 Lytton Avenue
? CITY: Palo Alto
? STATE: California
? COUNTRY: US
? ZIP: 94301
? COMPUTER READABLE FORM:
? MEDIUM TYPE: floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent In Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/333,565
? FILING DATE: 31-OCT-1994
? CLASSIFICATION: 435
? ATTORNEY/AGENT INFORMATION:
? NAME: Smith, William M.
? REGISTRATION NUMBER: 30,223
? REFERENCE/DOCKET NUMBER: 15726A-000700
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (415) 326-2400
? TELEFAX: (415) 326-2422
? INFORMATION FOR SEQ ID NO: 10:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 23 amino acids
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? US-08-333-565-10

Query Match      88.0%; Score 73; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ORYGRRLRMSEDF 14
DB 8 ORYGRRLRMSEDF 21

RESULT 8
US-08-661-479-10
? Sequence 10, Application US/08661479
? Patent No. 5834209
? GENERAL INFORMATION:
? APPLICANT: KORSMEYER, Stanley J.
? TITLE OF INVENTION: BCL-X/BCL-2 ASSOCIATED CELL DEATH
? TITLE OF INVENTION: REGULATOR
? NUMBER OF SEQUENCES: 55
? CORRESPONDENCE ADDRESS:
? ADDRESS: 379 Lytton Avenue
? CITY: Palo Alto
? STATE: California
? COUNTRY: US
? ZIP: 94301
? COMPUTER READABLE FORM:
? MEDIUM TYPE: floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent In Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/661,479
? FILING DATE: 11-JUN-1995
? CLASSIFICATION: 435
? INFORMATION FOR SEQ ID NO: 10:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 23 amino acids
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? US-08-661-479-10

```

```

? FILING DATE: 31-OCT-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: Smith, William M
? REGISTRATION NUMBER: 30,223
? REFERENCE/DOCKET NUMBER: 15726A-000700
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (415) 326-2400
? TELEFAX: (415) 326-2422
? INFORMATION FOR SEQ ID NO: 10:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 23 amino acids
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? US-08-661-479-10

Query Match      88.0%; Score 73; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ORYGRRLRMSEDF 14
DB 8 ORYGRRLRMSEDF 21

RESULT 9
US-08-733-505A-55
? Sequence 55, Application US/08733505A
? Patent No. 5834209
? GENERAL INFORMATION:
? APPLICANT: KORSMEYER, Stanley J.
? TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
? TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
? NUMBER OF SEQUENCES: 60
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: HOWELL & HAFERKAMP, L.C.
? STREET: 7733 FORSYTH BLVD., SUITE 1400
? CITY: SMITHFIELD
? STATE: MISSOURI
? COUNTRY: USA
? ZIP: 63105
? COMPUTER READABLE FORM:
? MEDIUM TYPE: floppy disk
? OPERATING SYSTEM: IBM PC compatible
? SOFTWARE: IBM PC-DOS/MS-DOS
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/733,505A
? FILING DATE:
? CLASSIFICATION: 530
? ATTORNEY/AGENT INFORMATION:
? NAME: HOLLAND, DONALD R.
? REGISTRATION NUMBER: 35,197
? REFERENCE/DOCKET NUMBER: 565458
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (314) 727-5180
? TELEFAX: (314) 727-6092
? INFORMATION FOR SEQ ID NO: 55:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 59 amino acids
? TYPE: amino acid
? STRANDEDNESS: linear
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? US-08-733-505A-55

Query Match      88.0%; Score 73; DB 2; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```


[illegible]

```

MEDION TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
FILING DATE NUMBER: 05/08/73.505A
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,147
REFERENCE/DOCKET NUMBER: 965458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 727-5188
TELEFAX: (314) 727-6092
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 amino acids
STRANDNESS:
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-733-505A-57

Query Match      88.0%; Score 73; DB 2; Length 59;
Best Local Similarity 100.0%; Pred. No. 2, 9e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 ORGTGRLRRNSDEP 14
        ||| ||| ||| ||| |||
Db      46 ORGTGRLRRNSDEP 59

RESULT 12
US-08-733-505A-58
; Sequence 58, Application US/08733505A
; Patent No. 5856445
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, STANLEY J.
; TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
; TITLE OF INVENTION: BCL-XL/BCL-2 ASSOCIATED CELL DEATH REGULATOR
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HARRKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: SPRINGFIELD
; STATE: MISSOURI
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733.505A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,147
; REFERENCE/DOCKET NUMBER: 965458
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 727-5188
; TELEFAX: (314) 727-6092
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 59 amino acids
; STRANDNESS:
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

```

US-08-733-505A-56

Query Match 88.0%: Score 73; DB 2; Length 59;
 Best Local Similarity 100.0%: Pred. No. 2,9e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 OYRGELRMSDEP 14
 DB 46 OYRGELRMSDEP 59

RESULT 13

US-08-333-565-2
 Sequence 1, Application US/0833565
 Sequence 2, Application US/0833565
 GENERAL INFORMATION:
 APPLICANT: KORSMEYER, Stanley J.
 TITLE OF INVENTION: BCL-X/BCL-2 ASSOCIATED CELL DEATH
 NUMBER OF SEQUENCES: 59
 CORRESPONDENCE ADDRESS:
 ADDRESS: Townsend and Townsend Kourile and Crew
 STREET: 379 Lytton Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: US
 ZIP: 94301
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 FILING DATE: 31-OCT-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M
 REGISTRATION NUMBER: 30,223
 TELEPHONE/DOCKET NUMBER: 15726A-000700
 TELEFAX: (415) 326-2422
 INFORMATION FOR SEQ ID NO: 2:
 LENGTH: 204 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..204
 OTHER INFORMATION: /note= "Deduced amino acid sequence
 OTHER INFORMATION: of mouse BAD."

US-08-333-565-2

Query Match 88.0%: Score 73; DB 1; Length 204;
 Best Local Similarity 100.0%: Pred. No. 1.1e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 OYRGELRMSDEP 14
 DB 145 OYRGELRMSDEP 158

RESULT 14

US-08-661-479-2
 Sequence 2, Application US/08661479
 Patient No 581209
 GENERAL INFORMATION:

APPLICANT: KORSMEYER, Stanley J.
 TITLE OF INVENTION: BCL-X/BCL-2 ASSOCIATED CELL DEATH
 NUMBER OF SEQUENCES: 59
 CORRESPONDENCE ADDRESS:
 ADDRESS: Townsend and Townsend Kourile and Crew
 STREET: 379 Lytton Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: US
 ZIP: 94301

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 FILING DATE: 31-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/333,565
 FILING DATE: 31-OCT-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M
 REGISTRATION NUMBER: 30,223
 TELEPHONE/DOCKET NUMBER: 15726A-000700
 TELEFAX: (415) 326-2400
 INFORMATION FOR SEQ ID NO: 2:
 LENGTH: 204 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..204
 OTHER INFORMATION: /note= "Deduced amino acid sequence
 OTHER INFORMATION: of mouse BAD."

US-08-661-479-2

Query Match 88.0%: Score 73; DB 2; Length 204;
 Best Local Similarity 100.0%: Pred. No. 1.1e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 OYRGELRMSDEP 14
 DB 145 OYRGELRMSDEP 158

RESULT 15

US-08-733-505A-1
 Sequence 1, Application US/08733505A
 Sequence 2, Application US/08733505A
 GENERAL INFORMATION:
 APPLICANT: KORSMEYER, STANLEY J.
 TITLE OF INVENTION: SERINE SUBSTITUTED MUTANTS OF
 NUMBER OF SEQUENCES: 60
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HOWELL & HAFERKAMP, L.C.
 STREET: 7733 FORSYTH BLVD., SUITE 1400
 CITY: ST. LOUIS
 STATE: MISSOURI
 COUNTRY: USA
 ZIP: 63105
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/733,505A
 FILING DATE:
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: HOLLAND, DONALD R.
 REGISTRATION NUMBER: 35,197
 TELEPHONE: (314) 727-6092
 TELEFAX: (314) 727-5188
 TELECOMMUNICATION INFORMATION:
 INFORMATION FOR SEQ. ID NO. 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 204 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-733-505A-1

Query Match 88.08; Score 73; DB 2; Length 204;
 Best Local Similarity 100.0%; Pred. NO. 1.1e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ORGRELRRMSDPF 14
 Db 145 ORGRELRRMSDPF 158

Search completed: September 20, 2002, 10:37:20
 Job time: 408 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2002, 10:35:07 ; Search time 95.59 seconds
(without alignments)

16.084 Million cell updates/sec

Title: US-09-544-664-29

Perfect score: 83

Sequence: 1 ORYGELRMSDEPVD 16

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR_71:*
2: PIR_71:*
3: PIR_71:*
4: PIR_71:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	73	85.0	2 A55671	bad protein - mouse
2	45	54.0	2 H75403	glycosyl hydrolase
3	44	53.0	2 G83278	cochlearli biosynth
4	42	50.0	2 E89949	valine-tRNA ligase
5	41.5	50.0	2 AD3414	hypothetical cyto
6	41	49.4	2 F83356	hypothetical prote
7	41	49.4	2 T40297	membrane transport
8	41	49.4	2 A44919	GCR3 protein - yea
9	40	48.2	2 F84388	conserved hypotet
10	40	48.2	2 B95043	conserved hypotet
11	40	48.2	2 D97913	hypothetical prote
12	40	48.2	2 A75088	probable enzyme (1
13	40	48.2	2 E9102	hypothetical prote
14	40	48.2	2 F85016	probable enzyme (1
15	40	48.2	2 F85016	probable enzyme (1
16	40	48.2	2 F85016	probable enzyme (1
17	40	48.2	2 F85016	probable enzyme (1
18	40	48.2	2 F85016	probable enzyme (1
19	40	48.2	2 F85016	probable enzyme (1
20	40	48.2	2 F85016	probable enzyme (1
21	40	48.2	2 F85016	probable enzyme (1
22	40	48.2	2 F85016	probable enzyme (1
23	39.5	47.6	2 B96695	hypothetical prote
24	39.5	47.6	2 B96695	hypothetical prote
25	39	47.0	2 AC3365	hypothetical prote
26	39	47.0	2 AC3365	hypothetical prote
27	39	47.0	2 AC3365	hypothetical prote
28	39	47.0	2 AC3365	hypothetical prote
29	39	47.0	2 AC3365	hypothetical prote

ALIGNMENTS

30	39	47.0	331	2 B90121	DNA repair protein
31	39	47.0	360	2 D86200	protein F12K11.20
32	39	47.0	365	2 S42107	RAD51 protein homo
33	39	47.0	380	2 T32163	hypothetical prote
34	39	47.0	383	2 T31136	hypothetical prote
35	39	47.0	383	2 T31136	hypothetical prote
36	39	47.0	418	2 FOXK12	sigma 2 protein -
37	39	47.0	432	2 ABO558	trigger factor (im
38	39	47.0	503	2 CYBPRH	site-specific DNA-
39	39	47.0	536	2 F90299	acylaminoacyl-pept
40	39	47.0	689	2 T29772	hypothetical prote
41	39	47.0	880	1 SYBVS	valine-tRNA ligase
42	39	47.0	959	1 B71405	probable kinesin -
43	39	47.0	965	2 AE2452	two-component hydr
44	39	47.0	1805	2 T02712	similar to late em
45	39	47.0	1967	2 S64604	hypothetical prote

RESULT 1
A55671
bad protein - mouse
C:Species: Mus musculus (house mouse)
C>Date: 03-Mar-1995 #sequence-revision 03-Mar-1995 #text-change 05-Nov-1999
C/Accession: A55671
R/Yang, E.; Zha, J.; Jockel, J.; Bojse, L.H.; Thompson, C.B.; Korsmeyer, S.J.
Cell 80, 285-291, 1995
A:Title: bad, a heterodimeric partner for Bcl-x-L and Bcl-2, displaces Bax and promotes
A:Reference number: A55671; MID:9516361
A:Accession: A55671
A:Species: Mus musculus (house mouse)
A:Molecular type: mRNA
A:Residues: 1-204 <YAN>
A:Cross-references: NID:9639778; PIDN:AM6465.1; PID:9639779
C:Keywords: heterodimer

Query Match 88.0%; Score 73; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 145 ORYGELRMSDEP 14
145 ORYGELRMSDEP 158
RESULT 2
H75403
glycosyl hydrolase, family 13 - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C>Date: 03-Dec-1999 #sequence-revision 03-Dec-1999 #text-change 17-Mar-2000
R/White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
S.; Smith, H.O.; Vamthavan, J.C.; Lam, P.; McDonald, L.; Ullrich, T.; Zalewski, C.
Science 286, 1571-1577, 1999
A:Reference number: A75250; MID:20056896
A:Accession: H75403
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-564 <WHI>
A:Cross-references: GB:AE001903; GB:AE000513; NID:96459123; PIDN:AMF10944.1; PID:9645
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR1375
A:Map position: 1
C:Superfamily: alpha-glucosidase; alpha-amylose core homology
Query Match 54.2%; Score 45; DB 2; Length 564;

```

Best Local Similarity 64.3%; Pred. No. 14;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
OY 3 YGRLRMDSDEVD 16
| | | | | | | | | |
Db 283 YVEMKRVVDEFD 296

RESULT 3
GB3278
cobalamin biosynthetic protein CbN PA2944 [Imported] - Pseudomonas aeruginosa (strain F
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 02-Mar-2001
R:Stoicescu, C. X. Pham, X. Q.; Erwin, A. L.; Mizoguchi, S. D.; Warringer, P.; Hickey, M. J.; B
adman, S.; Yun, Y.; Brody, L. L.; Collier, S. R.; Polgar, K. R.; Kas, A.; Latido, K.; Lim
Nure, A. G.; Olson, M. V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: AB2950; PMID:20437337
A:Accession: GB3278
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1248 <STO>
A:Cross-references: GB:AE004720; GB:AE004091; NID:99949032; PIDN:AA06332.1; GSPDB:GN001
C:Genetics:
A:Gene: cobV
C:Superfamily: Ribodibacter capsulatus magnesium-protoporphyrin O-methyltransferase

Query Match 53.0%; Score 44; DB 2; Length 1248;
Best Local Similarity 50.0%; Pred. No. 47;
Matches 9; Conservative 4; Mismatches 3; Indels 2; Gaps 1;
OY 1 OYRG-RELRMSDEVD 16
| | | | | | | | | |
Db 615 ESYGPRDLRLADEVD 632

RESULT 4
GB3299
cobalamin ligase [Imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
R:Kuroda, M.; Ohya, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogyu
ma, A.; Mizutani-Uli, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, R.; Hiramatsu, K.
Lancet 357, 1235-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: AB9758; PMID:11418146
A:Accession: E89949
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-876 <STO>
A:Cross-references: GB:BA000018; PID:913701460; PIDN:BA842754.1; GSPDB:GN00149
A:Experimental source: Strain N315
C:Genetics:
A:Gene: valS
C:Superfamily: valine--cRNA ligase

Query Match 50.6%; Score 42; DB 2; Length 876;
Best Local Similarity 61.5%; Pred. No. 70;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
OY 4 GRELRMSDEVD 16
| | | | | | | | | |
Db 251 GREPLADEVD 263

RESULT 5

```

```

AD3414
hypothetical cytosolic protein BME11298 [Imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C:Accession: AD3414
R:Dalyeochio, V. G.; Kaparaju, V.; Redkar, R. J.; Patra, G.; Mijer, C.; Los, T.; Ivanov
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella meli
A:Reference number: AD3252; PMID:11756688
A:Accession: AD3414
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-191 <NUR>
A:Cross-references: GB:AE008917; PIDN:AAL52479.1; PID:917983287; GSPDB:GN00190
A:Experimental source: Strain 16M
C:Genetics: BME11298
A:Gene: BME11298
A:Map position: 1

Query Match 50.0%; Score 41.5; DB 2; Length 191;
Best Local Similarity 33.3%; Pred. No. 18;
Matches 11; Conservative 2; Mismatches 3; Indels 17; Gaps 1;
OY 1 OYRG-----ELRMSDEVD 16
| | | | | | | | | |
Db 131 ORKGRVSVSTLTTPAMISDLRKQADPFD 163

RESULT 6
FB5356
hypothetical protein AT4g30490 [Imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
R:anonymous, The European Union Arabidopsis genome sequencing consortium, The Cold Sp
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: AB5001; PMID:20083488
A:Accession: FB5356
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-447 <STO>
A:Cross-references: GB:NC_001268; NID:97269950; PIDN:CAB79767.1; GSPDB:GN00140
C:Genetics: AT4g30490
A:Map position: 4

Query Match 49.4%; Score 41; DB 2; Length 447;
Best Local Similarity 66.7%; Pred. No. 52;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 5 RELRMSDEVD 16
| | | | | | | | | |
Db 84 RELRMLADEVD 95

RESULT 7
T40297
membrane transporter - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 18-Feb-2000
R:Lyme, M.; Wood, V.; Rajandream, M. A.; Barrell, B. G.; Hubbard, H.; Mosest, D.; Duest
submitted to the EMBL data library, May 1998
A:Reference number: Z21919
A:Accession: T40297
A:Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-577 <LYN>
A:Cross-references: EMBL:AL023589; PIDN:CA19050.1; GSPDB:GN00067; SPDB:SPPC36.02C

```

A:Experimental source: strain 972h; cosmid c36
 C:Genetics:
 A:Gene:SPB:SPB36.02c
 A:Map position: 2
 C:Superfamily: denomy/methotrexate resistance protein

Query Match 49.4%; Score 41; DB 2; Length 577;
 Best Local Similarity 57.1%; Pred. No. 67;
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 Oy 3 RYGRRLRMSDEPVD 16
 Db 563 RGRRLRMSMAVD 576

RESULT 8
 A44919
 GCR3 Protein - yeast (Saccharomyces cerevisiae)
 N:Alternate names: protein YN8564.07; protein YN9553.01; protein YMR125w
 C:Species: Saccharomyces cerevisiae
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 29-Oct-1999
 C:Accession: A44919; S53055; S54494
 R:Uemura, H.; Jigami, Y.
 J. Bacteriol. 174, 5536-5537, 1992
 A>Title: GCR3 encodes an acidic protein that is required for expression of glycolytic ge
 A:Reference number: A44919; M01D:92380925
 A:Accession: A44919
 A:Molecule type: DNA
 A:Residues: 1-858
 A:Cross-references: GB:010224; NID:9464221; P1DN:BA01076.1; P1D:d1001545; P1D:9464222
 A:Note: sequence extracted from NCBI backbone (NCBIN:112104, NCBI:P112106)
 R:Backoek, K.; Churcher, C.
 submitted to the EMBL Data Library, March 1995
 A:Reference number: S53055
 A:Accession: S53055
 A:Molecule type: DNA
 A:Residues: 315-458 <AND>
 R:Cross-references: EMBL:Z48622; NID:9728663; P1DN:CA08550.1; P1D:9728664; MIPS:YMR125w
 R:Churcher, C.W.
 submitted to the EMBL Data Library, May 1995
 A:Reference number: S54014
 A:Accession: S54014
 A:Molecule type: DNA
 A:Residues: 16NKRRC',6-489 <LYD>
 A:Cross-references: EMBL:Z49273; NID:9809577; P1DN:CA089274.1; P1D:9809584; MIPS:YMR125w
 C:Genetics:
 A:Gene: SGD:STO1; GCR3
 A:Cross-references: MIPS:YMR125w; SGD:S0004722
 A:Map position: 13R
 C:Keywords: DNA binding; nucleus

Query Match 49.4%; Score 41; DB 2; Length 858;
 Best Local Similarity 40.0%; Pred. No. 1e+02;
 Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 Oy 1 QRYGRRLRMSDEPVD 15
 Db 818 RRYSHRYRELADKFI 832

RESULT 9
 F84388
 hypothetical protein Yng2379h [imported] - Halobacterium sp. NRC-1
 C:Species: Halobacterium sp. NRC-1
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: F84388
 R:Ng, W.Y.; Kennedy, S.P.; Mahapatra, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasly, S.; Leibhuber, B.; Koller, K.; Koz, R.; Dawson, M.J.; Hough, D.W.; Maddocks, D.G.; Jindl, P.; Jung, N.; Alm, S.; U.S.A. 97, 12176-12181, 2000
 Proc Natl Acad Sci U S A 97, 12176-12181, 2000
 A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li

A>Title: Genome sequence of Halobacterium species NRC-1.
 A:Reference number: AB4160; M01D:20504483
 A:Accession: F84388
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-84 <STO>
 A:Cross-references: GB:AB004437; NID:910581786; P1DN:AMG20474.1; GSPDB:GN00138
 C:Genetics:
 A:Gene: YNG2379H

Query Match 48.2%; Score 40; DB 2; Length 84;
 Best Local Similarity 66.7%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Oy 2 RYGRRLRMSDE 13
 Db 66 RYGRRLRMSDE 77

RESULT 10
 B95043
 conserved hypothetical protein SP0372 [imported] - Streptococcus pneumoniae (strain T
 C:Species: Streptococcus pneumoniae
 C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
 C:Accession: B95043
 R:Petelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; H
 on, J.D.; Hickey, E.R.; Holt, I.E.
 Science 293, 498-506, 2001
 A:Authors: Lioris, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, R.A.; Morris
 A>Title: Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.
 A:Reference number: B95043
 A:Accession: B95043
 A:Molecule type: DNA
 A>Status: preliminary
 A:Residues: 1-109 <RUP>
 A:Cross-references: GB:AE005672; P1DN:AAK74539.1; P1D:914971841; GSPDB:GN00164; TIGR:
 A:Experimental source: strain TIGR4
 C:Genetics:
 A:Gene: SP0372

Query Match 48.2%; Score 40; DB 2; Length 109;
 Best Local Similarity 45.0%; Pred. No. 18;
 Matches 9; Conservative 4; Mismatches 3; Indels 4; Gaps 1;
 Oy 1 QRYGRRLRMS---DEPVD 16
 Db 14 QRYGRRLRMSDEPVD 33

RESULT 11
 D97913
 conserved hypothetical protein SP0332 [imported] - Streptococcus pneumoniae (strain
 C:Species: Streptococcus pneumoniae
 C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
 C:Accession: D97913
 R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.
 e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; Mahren, S.
 y, P.; Sun, P.M.; Winkler, M.E.
 J. Bacteriol. 183, 5709-5717, 2001
 A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.
 A>Title: Genome of the bacterium Streptococcus pneumoniae strain M6.
 A:Reference number: A97872; M01D:21423243; P1D:11543234
 C:Accession: D97913
 A>Status: preliminary
 A:Residues: 1-113 <RUP>
 A:Cross-references: GB:AE007317; P1DN:AAK99136.1; P1D:915457889; GSPDB:GN00174
 C:Genetics:
 A:Gene: SP0332

query Match	48.28;	Score 40;	DB 2;	length 113;
Best local Similarity	45.08;	Pred. No. 19;		
Matches	9;	Conservative	4;	Mismatches 3; Indels 4; Gaps 1

```

QY      1 ORYGRRLRMS---DEEVD 16
          1 : 1 1 1 : 1 1 1 : 1
Db      18 QEFGRVRCYNKVEVDFLD 37

```

hypothetical protein PAB1640 - Pyrococcus abyssi (strain Orsay)
Species: Pyrococcus abyssi
RESULT 12
A75088

C/Accession: AF2060
 R/anonymous: Genoscope
 submitted to the EMBL Data Library, July 1999
 Description: Pyrococcus abyssi genome sequence: inserts into archaeal chromosome structure

A; Experimental source: strain 0rsay
C; Genetics:
A; Cane: PAB1640

Query Match	48.46;	Score 40;	DB 4;	Length 219;
Best Local	47.18;	Pred. No. 37;		
Matches	8;	Conservative	4;	Mismatches 3;
				Indels 2;
				Gaps 1;

03	2	RYGNEFORVSP	120
Db	104	RYGNEFORVSP	120

C. Kawanishi: E3110
R. Hayashi, T.: Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.-G. gasevaya, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
GNA Res. 8, 11-22, 2001

A: Cross-references: GB:BA000007; PID:BA83/21.2.1; PID:G1363461; GSPDB:CN00254
A: Experimental source: strain 0157:H7, substrain RMD 0509952
C: Genetics:
C: Contact: EC93780

Query Match 48.2% Score 40: DB 2: Length 275:
c, superfamily: haptophyte synchroase, enoyl-coa hydratase homology

RESULT 14

hypothetical protein b2919 - Escherichia coli (strain K-12)

C;Species: *Escherichia coli*
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999

Science 277, 1453-1462, 1997
A/Title: The complete genome sequence of *Escherichia coli* K-12
A/Reference number: A64720; MUID:97426617

A: Experimental source: strain K-12, substrain MG1655
C: Superfamily: naphthoate synthase; enoyl-CoA hydratase homology
F: 40-192/Domain: enoyl-CoA hydratase homology <EC>

Query Match	48.28;	score 40;	DB 4;	lengthn 475;
Best Local	50.04;	Pred. No. 46;		
Matches	7;	Conservative	3;	Mismatches 4;
				Indels 0;
				Gaps 0;

Db 35 YGRKLNLSKVEID 48

Ripstein, N.T., Plunkett III, G., Burland, V., Mau, B., Glasser, L.J., Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Nature 409, 529-533, 2001

A:Experimental source: strain O157:H7, substrain ED1933
C:Genetics:
A:Gene: ynfG

QY 3 YGRETRRMSDFVD 16
111:1 :1 1:1
DB 35 YGRRKLNALSKVFID 48

Fri, Sep 20 11:03:10 2002

us-09-544-664-29.rpr

Page 5

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2002, 11:04:31 ; Search time 44.99 Seconds

(without alignments)
13.770 Million cell updates/sec

Title: us-09-544-664-29

Perfect score: 83

Sequence: 1 QRYGRELRLMSDFEVD 16

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	168	1	BAD_HUMAN
2	73	88.0	204	1	BAD_MOUSE
3	73	88.0	205	1	BAD_RAT
4	42	50.6	196	1	BIM_MOUSE
5	42	50.6	196	1	BIM_RAT
6	42	50.6	653	1	HT2A_HUMAN
7	41	49.4	370	1	AROC_CANAL
8	41	49.4	861	1	GCRA_YEAST
9	40	48.2	261	1	YGRG_YEAST
10	40	48.2	380	1	PHIC_ECOLI
11	40	48.2	429	1	MYA1_TYRCA
12	40	48.2	631	1	RPSD_HOBBU
13	39	47.0	220	1	6PCL_THYMA
14	39	47.0	365	1	RA51_SCHRO
15	39	47.0	418	1	VS12_ABOVD
16	39	47.0	503	1	MYR1_ABOVD
17	39	47.0	880	1	SVX1_BACST
18	39	47.0	880	1	SVX1_BACST
19	39	47.0	1967	1	YGRG_YEAST
20	38.5	46.4	468	1	SELA_FSEAE
21	38	45.8	87	1	T152_URENA
22	38	45.8	185	1	RRE_THYMA
23	38	45.8	128	1	BIM_HUMAN
24	38	45.8	251	1	KDRA_VIBOH
25	38	45.8	384	1	ODP2_MYCOE
26	38	45.8	402	1	ODP2_MYCIN
27	38	45.8	432	1	T16_ECOLI
28	38	45.8	1521	1	EMBL_CAEEL
29	38	45.8	1521	1	EMBL_CAEEL
30	37	44.6	375	1	DP3B_MYCOA
31	37	44.6	391	1	UB1E_ECOLI
32	37	44.6	398	1	PRSL_ARCFU
33	37	44.6	481	1	Y335_SYNY3

34	37	44.6	777	1	BAR1_HUMAN	099728 homo sapien
35	37	44.6	787	1	RELA_MYCLE	049640 mycobacteri
36	37	44.6	974	1	YMB4_CAEEL	003601 caenorhabdi
37	37	44.6	1513	1	STU1_YEAST	038198 saccharomyc
38	36.5	44.0	207	1	THIE_PYRAM	094205 pyrococcus
39	36.5	44.0	595	1	VO13-BPM2	064206 mycobacteri
40	36	43.4	113	1	GVK1_HAHLN	024375 halobacteri
41	36	43.4	143	1	YXAD_BACSU	042103 bacillus su
42	36	43.4	218	1	ESM1-DROME	097177 drosophila
43	36	43.4	218	1	PTH_SCHPO	074806 schizosacch
44	36	43.4	267	1	KD5A_AQUAE	066496 aquifex neo
45	36	43.4	373	1	RFL_AERPE	099411 aeropyrum p

ALIGNMENTS

RESULT	ID	STANDARD	PRT	168 AA.
BAD_HUMAN	092934; 014803;			
AC	01-NOV-1997 (Rel. 35, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	Bcl-2 antagonist of cell death (BAD) (Bcl-2 binding component			
DE	6) (Bcl-XL/Bcl-2 associated death promoter).			
GN	BAD OR BPC6 OR BCL2L6.			
OS	Homo sapiens (Human).			
OC	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN				
RP	SEQUENCE FROM N.A.			
RA	Yin D.X., Li Z., Huang B., Chen S., Zhou H.;			
RT	A human protein that interacts with Bcl-2 and have homology to mouse			
RT	BAD.;			
RL	Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.			
RN				
RP	SEQUENCE FROM N.A., AND PHOSPHORYLATION BY RAF-1.			
RA	MEDLINE=97083574; PubMed=8929532;			
RT	Wang H.-G., Hupp U.R., Reed J.C.;			
RT	Bcl-2 targets the protein kinase Raf-1 to mitochondria.*;			
RL	Cell 67:629-638(1996).			
RN				
RP	SEQUENCE FROM N.A.			
RA	Takeyama S., Reed J.C.;			
RT	Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.			
RN				
RP	SEQUENCE FROM N.A., AND DIMERIZATION.			
RC	TISSUE=Bone marrow;			
RX	MEDLINE=98049554; PubMed=9388232;			
RA	Ottlitz S., Diaz J.-L., Horne W., Chang J., Wang Y., Wilson G.,			
RA	Chang S., Weeks S., Fritz L.C., Oltersdorf T.;			
RT	"Dimerization properties of human BAD.*";			
RL	J. Biol. Chem. 272:30866-30872(1997).			
RN				
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lung;			
RA	Strausberg R.;			
RT	Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.			
RN				
RP	STRUCTURE BY NMR OF 103-127.			
RX	MEDLINE=21073561; PubMed=11206074;			
RA	Petros A.M., Nettesheim D.G., Wang Y., Olejniczak R.T., Meadows R.P.,			
RA	Mack J., Swift K., Matsuyoshi E.D., Zhang H., Thompson C.B.,			
RA	Fesik S.W.;			
RT	"Rationale for Bcl-XL/Bad peptide complex formation from structure,			
RT	mutagenesis, and biophysical studies.*";			
RL	Protein Sci. 9:2528-2534(2000).			
CC	-I- FUNCTION: Promotes cell death. Successfully competes for the			
CC	binding to Bcl-X(L). Bcl-2 and Bcl-X(L) thereby affecting the level			
CC	of heterodimerization of these proteins with BAX. Can reverse the			
CC	death repressor activity of Bcl-X(L), but not that of Bcl-2 (By			

CC similarity). Appears to act as a link between growth factor
CC receptor signaling and the apoptotic pathways.
CC -1 SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-
CC x(L), Bcl-2 and Bcl-w. Also binds protein S100A10 (by similarity).
CC The Ser-75/Ser-99 phosphorylated form binds 14-3-3 proteins (by
CC similarity).
CC -1 SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon
CC phosphorylation, locates to the cytoplasm.
CC -1 TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
CC -1 DOMAIN: Interact BH3 domain is required by BIK, BID, BAK AND
CC BAX for their pro-apoptotic activity and for their interaction
CC with anti-apoptotic members of the Bcl-2 family.
CC -1 PTM: Phosphorylated on Ser-75 in response to survival stimuli.
CC Subsequent phosphorylation on Ser-99 promotes heterodimerization
CC with 14-3-3 proteins. This interaction then facilitates the
CC phosphorylation at Ser-118, a site within the BH3 domain, leading
CC to the release of Bcl-x(L) and the promotion of cell survival.
CC Ser-99 is the major site of AKT/PKB phosphorylation. Ser-118 the
CC major site of protein kinase A (CAK) phosphorylation (by
CC similarity).
CC -1 SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -1 SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: 066879; AAB36516.1; -
CC EMBL: AF021792; AAB72092.1; -
CC EMBL: AF031523; AAB88124.1; -
CC EMBL: BC001901; AAB01901.1; -
CC PDB: 1CSJ; 07-FEB-01.
CC DR MIM: 603167; -
CC DR InterPro: IPR000712; Bcl-2.
CC DR PROSITE: PS01259; BH3; FALSE_NEG.
CC DR Apoptosis: Phosphorylation; 3d-structure.
CC FT DOMAIN 110 124 BH3.
CC FT MOD_RES 75 75 PHOSPHORYLATION (BY CAKP AND PKB) (BY -
CC SIMILARITY).
CC FT MOD_RES 99 99 PHOSPHORYLATION (BY CAKP AND PKB) (BY
CC SIMILARITY).
CC FT MOD_RES 118 118 PHOSPHORYLATION (BY CAKP AND PKB) (BY
CC SIMILARITY).
CC FT CONFLICT 64 91 ACVEATSRSSSYCAPGEGDEBGMSEPS -> RMCGGDPSPS
CC FT POLYPRDGSRRRDGGAG (IN REF. 1).
CC SO SEQUENCE 168 AA; 18392 MW; 69FDBD27DDEE3241 CRC64.
Query Match 100.0%; Score 83; DB 1; Length 168;
Best Local Similarity 100.0%; Pctid. No. 9;6e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Gy 1 GRYGRLRRMSDFVD 16
Db 108 GRYGRLRRMSDFVD 123
RESULT 2
BAD_MOUSE STANDARD: PRT: 204 AA.
AC 061337; -
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Bcl-2:antiapoptosis of cell death (BAD) (Bcl-2 binding component
DE 5) (Bcl-x(L)/Bcl-2 associated death promoter).
OS BAD OR BRC.
GN Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; -

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC NCBI_TaxID=10090;
CC RN [1]
CC SEQUENCE FROM N.A.
CC RC TISSUE=Brain, and Thymus;
CC RX MEDLINE=95136361; PubMed=7834748;
CC RA Yang E., Zhu J., Jockel J., Bolae L.R., Thompson C.B., Kormeyer S.J.;
CC "Bad, a heterodimeric partner for Bcl-XL and Bcl-2, displaces Bax and
CC promotes cell death.";
CC RL Cell 80:285-291(1995).
CC RN [2]
CC RP PHOSPHORYLATION, AND MUTAGENESIS OF SER-112 AND SER-136.
CC RX MEDLINE=9802283; PubMed=9381178;
CC RA Del Peso L., Gonzalez-Garcia M., Page C., Herrera R., Nunez G.;
CC "Interleukin-3-induced phosphorylation of BAD through the protein
CC kinase Akt.";
CC RL Science 278:687-689(1997).
CC RN [3]
CC RT MUTAGENESIS OF SERINE RESIDUES.
CC RP MEDLINE=70403302; PubMed=10949026;
CC RA Delta S.R., Katsiov A., Hu L., Petros A., Pesik S.W., Yaffe M.B.,
CC Greenberg M.E.;
CC "14-3-3 proteins and survival kinases cooperate to inactivate BAD by
CC BH3 domain phosphorylation.";
CC RL Mol. Cell 6:41-51(2000).
CC CC -1 FUNCTION: Promotes cell death. Successfully competes for the
CC binding to Bcl-x(L). Bcl-2 and Bcl-w, thereby affecting the level
CC of heterodimerization of these proteins with BAX. Can reverse the
CC death repressor activity of Bcl-x(L), but not that of Bcl-2.
CC Appears to act as a link between growth factor receptor signaling
CC and the apoptotic pathways.
CC -1 SUBUNIT: Forms heterodimers with the anti-apoptotic proteins, Bcl-
CC x(L), Bcl-2 and Bcl-w. Also binds protein S100A10 (by similarity).
CC The Ser-112/Ser-136 phosphorylated form binds 14-3-3 proteins.
CC -1 SUBCELLULAR LOCATION: Outer mitochondrial membrane. Upon
CC phosphorylation, locates to the cytoplasm.
CC -1 DOMAIN: Interact BH3 domain is required by BIK, BID, BAK, BAD AND
CC BAX for their pro-apoptotic activity and for their interaction
CC with anti-apoptotic members of the Bcl-2 family.
CC -1 PTM: Phosphorylated on Ser-112 in response to survival stimuli.
CC Subsequent phosphorylation on Ser-136 promotes heterodimerization
CC with 14-3-3 proteins. This interaction then facilitates the
CC phosphorylation at Ser-155, a site within the BH3 domain, leading
CC to the release of Bcl-x(L) and the promotion of cell survival.
CC Ser-136 is the major site of AKT/PKB phosphorylation. Ser-155 the
CC major site of protein kinase A (CAK) phosphorylation.
CC -1 SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -1 SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L37296; AAA64465.1; -
CC DR MGD: MGI:1096330; Bad.
CC DR InterPro: IPR000712; Bcl-2.
CC DR PROSITE: PS01259; BH3; FALSE_NEG.
CC KM Apoptosis: Phosphorylation.
CC FT DOMAIN 147 161 BH3.
CC FT MOD_RES 112 112 PHOSPHORYLATION (BY CAKP AND PKB).
CC FT MOD_RES 136 136 PHOSPHORYLATION (BY CAKP AND PKB).
CC FT MOD_RES 155 155 PHOSPHORYLATION (BY CAKP AND PKB).
CC FT MUTAGEN S->A: NO PHOSPHORYLATION.
CC FT MUTAGEN S->A: NO PHOSPHORYLATION.
CC FT MUTAGEN 155 155 BCL-x(L) NO PHOSPHORYLATION; INTERACTS WITH
CC BCL-x(L).
CC SO SEQUENCE 204 AA; 22080 MW; 6C2BA910205033E7 CRC64;

[illegible][illegible]

CC	-1	SUBUNIT: FORMS HETERODIMERS WITH A NUMBER OF ANTIAPOPTOTIC BCL-2 PROTEINS INCLUDING MCL-1, BCL-XL, BFL-1, AND BHRF-1. DOES NOT HETERODIMERIZE WITH PROAPOPTOTIC PROTEINS SUCH AS BAD, BOK, BAX OR BAK (BY SIMILARITY).
CC	-1	ALTERNATIVE PRODUCTS: 3 ISOFORMS: B1MEL (SHOWN HERE), B1ML AND B1MS; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC	-1	TISSUE SPECIFICITY: EXPRESSED IN A NUMBER OF B- AND T-LYMPHOID CELL LINES.
CC	-1	DOMAIN: THE BMS DOMAIN IS REQUIRED FOR BCL-2 BINDING AND CYTOTOXICITY.
CC	-1	SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BHS).
CC	-1	THIS SWISS-PROT ENTRY IS COPYRIGHT. IT IS PRODUCED THROUGH A COLLABORATION BETWEEN THE SWISS INSTITUTE OF BIOINFORMATICS AND THE EMBL OUTSTATION AT THE EUROPEAN BIOINFORMATICS INSTITUTE. THERE ARE NO RESTRICTIONS ON ITS USE BY NON-PROFIT INSTITUTIONS AS LONG AS ITS CONTENT IS IN NO WAY MODIFIED AND THIS STATEMENT IS NOT REMOVED. USAGE BY AND FOR COMMERCIAL ENTERPRISES REQUIRES A LICENSE AGREEMENT (SEE http://www.isb-sib.ch/announce/).
CC	-1	SEND AN EMAIL TO: contact@isb-sib.ch .
DR	EMBL	AF032460; AAC00029.1; -
DR	EMBL	AF032460; AAC00030.1; -
DR	MGI	AF032461; AAC00031.1; -
DR	MGI	MGI:1197519; Bcl2l11.
DR	INCEPTEP	IPRO00713; BCL2.
DR	PROSITE	PS01259; BHS; BCL2_NBC.
DR	PROSITE	PS01259; BHS; BCL2_NBC.
DR	DOMAIN	146 166 SPLICING MEMBRANE.
PT	VARSPIC	146 166 SPLICING MEMBRANE.
PT	VARSPIC	42 127 MISSING (IN ISOFORM B1ML).
PT	VARSPIC	42 127 MISSING (IN ISOFORM B1MS).
PT	SEQUENCE	196 AA; 22066 MW; 531C176551AC9AA CRC64;
Query Match	50.6%;	Score 42; DB 1; Length 196;
Matches	8; Conservatve	61.5%; Residues 5;
		2; Mismatches
		3; Indels
		0; Gaps
		0;
OY	2	RYGRELRLRMSDFE 14
DB	145	RIAGELRLRIDEF 157
		1: :111
RESULT	5	
ID	B1M.RAT	STANDARD; PRT: 196 AA.
AC	088499; OSN018; OS8497;	
DT	16-OCT-2001 (REL. 40; Created)	
DT	16-OCT-2001 (REL. 40; Last annotation update)	
DT	01-MAR-2002 (REL. 41; Last annotation update)	
DE	BCL-2 RELATED OVARIAN DEATH PROTECTIN.	
DE	(BCL-2 RELATED OVARIAN DEATH PROTECTIN).	
DE	BCL2L1 OR B1M OR BOD.	
OS	Rattus norvegicus (Rat).	
OS	Eutheria; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus;	
OX	NCBI-Taxid-101116;	
NC	SEQUENCE FROM N.A. FUNCTION, SUBUNIT, AND TISSUE SPECIFICITY	
NC	(ISOFORM BOD-L; BOD-M AND BOD-S).	
NC	TISSUE-Ovary;	
NC	MEDLINE-98400436; PubMed-9731710;	
NC	Hsu S.Y., Lin P., Hsueh A.J.W.;	
NC	"BOD (bcl-2-related ovarian death gene) is an ovarian BHS domain-	
NC	containing proapoptotic bcl-2 protein capable of dimerization with	
NC	diverse antiapoptotic bcl-2 members."	
NC	Proc Natl Acad Sci USA 98:13407-13410(1999).	
NC	[2]. Endocrinol. 12:1352-140(1995).	
NC	SEQUENCE FROM N.A. (ISOFORM B1ML).	
NC	Chen D., Simon R.P., Chen J.;	
NC	"Cloning of rat B1ML and B1ML, and their differential expression in	
NC	(asclema and normal) rat brain."	
NC	Submitted (MAR-1999) to the EMBL/GenBank/DBS databases.	

CC	-1- FUNCTION: INDUCES APOPTOSIS.
CC	-1- SUBUNIT: FORMS HETERODIMERS WITH A NUMBER OF ANTIAPOPTOTIC BCL-2
CC	PROTEINS INCLUDING BCL-XL, BCL-2, BCL-XS, BFL-1, AND BHRF-1. DOES
CC	NOT HOMODIMERIZE WITH PROAPOPTOTIC PROTEINS SUCH AS BAX, BOK,
CC	-1- SUBCELLULAR LOCATION: ASSOCIATED WITH INTRACYTOSOLASMIC MEMBRANES
CC	(BY SIMILARITY).
CC	-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: BOD-L (SHOWN HERE) AND BOD-S;
CC	ARE PRODUCED BY THE USE OF ALTERNATIVE INITIATION SITES. TWO-
CC	FURTHER ISOFORMS: B1M AND BOD-M; ARE PRODUCED BY ALTERNATIVE
CC	SPLICING OF BOD-L.
CC	-1- EXPRESSION: WIDELY EXPRESSED.
CC	-1- TISSUE SPECIFICITY: THE B1M DOMAIN IS REQUIRED FOR BCL-2 BINDING AND
CC	CYTOTOXICITY.
CC	-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC	- - - - -
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation at
CC	the European Bioinformatics Institute. There are no restrictions on usage
CC	of this information as long as you acknowledge its source. This entry has been
CC	modified and this statement is not removed, usage by and for commercial
CC	entities requires a license agreement (see http://www.ebi.ac.uk/announcement/)
CC	or send an email to license@ebi.sdb.ch).
DR	EMBL AF065433 AAC33595.1 ;
DR	EMBL AF065431 AAC33593.1 ;
DR	EMBL AF065427 AAC33594.1 ;
DR	InterPro: IPR000712; BCL-2.
DR	PROSITE: PS01359; BH3; FLICE_NG.
KW	Apoptosis; Alternative splicing; Membrane; Alternative Initiation.
FT	CHAIN 1 196
FT	GAIN 104 196
FT	INTR_MET 104 106
FT	INTR_MET 142 148
FT	VARIABLE 142 97
FT	VARSPHC 42 127
FT	VARSPHC 136 136
FT	CONFLICT 136 136 F -> D (IN REF. 1; AAC33594).
SE	SEQUENCE 196 AA; 22055 MW; BAD2146FC0B37A0 CREG4;
QY	2 RYGRRLRMSDGF 14
DY	1 : ::::: 11
DB	145 RIWDLRRIQDER 157
QUERY MATCH	50.6% Score 42 DB 1; Length 196;
Similarity	50.5%; Positives 14; Negatives 6
Matches	8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
RESULT 6	
ID	HTZA_HUMAN STANDARD; PRT; 653 AA.
AC	OJ3049;
DT	01-NOV-1997 (Ref. 35, Created)
DT	01-NOV-1997 (Ref. 35, Last annotation update)
DT	01-MAR-2002 (Ref. 41, Last annotation update)
GN	ZINC FINGER PROTEIN ZFP192 KIAA12 KDa TAC-interacting protein) (TFP192like
DN	TFRM12 OR HTZA
OS	Homo sapiens (human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
NCBI_TaxID=9606;	
RN	SEQUENCE FROM N.A.
RF	AB028456-45297135 PubMed67779266.
RA	Fidellai R-A., Harding L.S., Bogard H.P., Cullen P.R.;
RT	"Identification of a novel human zinc finger protein that
RT	specifically interacts with the activation domain of lentiviral Tat
RT	proteins."
RE	Virology 205:347-357(1995).
LC	-1- FUNCTION: MAY PLAY A SIGNIFICANT ROLE IN MEDIATING THE BIOLOGICAL

CC		ACTIVITY OF THE HIV-1 TAT PROTEIN IN VIVO. BINDS SPECIFICALLY TO
CC		THE ACTIVATION DOMAIN OF HIV-1 TAT AND CAN ALSO INTERACT WITH THE
CC		HIV-2 AND ELAV TAT PROTEINS IN VIVO.
CC	-1	SUBCELLULAR LOCATION: Nuclear.
CC	-1	TISSUE SPECIFICITY: SPLEEN, THYMUS, PROSTRATE, TESTIS, OVARY,
CC		INTERESTING AND COLORED. RING-TYPE ZINC FINGER.
CC	-1	FUNCTION: DNA-BINDING. CONTAINS 1 B BOX-TYPE ZINC FINGER.
CC		- SIMILARITY: CONTAINS 1 B BOX-TYPE ZINC FINGER.
CC		--
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration
CC		between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC		the European Bioinformatics Institute. There are no restrictions on its
CC		use by non-profit institutions as long as their content is in no way
CC		modified and this statement is not removed. Usage by for commercial
CC		entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC		or send an email to license@sib.slb.ch).
CC		--
DR	EMBL:	U18543; MAB6474.1; ?
DR	HSP:	P29590; IBOB.
DR	MIM:	602290.
DR	InterPro:	IPR001258; NHL.
DR	InterPro:	IPR000315; ZnF_Box.
DR	InterPro:	IPR001841; ZnF_Ting.
DR	Pfam:	PF01436; NHL_6.
DR	Pfam:	PF00659; ZF_Box_1.
DR	Pfam:	PF00659; ZF_Box_1.
DR	SMART:	SM00336; BROX_1.
DR	SMART:	SM00184; RING_1.
DR	PROSITE:	PS01119; ZF_BOX_1.
DR	PROSITE:	PS00518; ZF_RING_1;
DR	PROSITE:	PS00899; ZF_RING_2;
KV	Zinc-finger:	Nuclear protein.
KV	Domain:	2 POLY-ALA.
FT	ZN_FING	20 63
FT	ZN_FING	103 133
FT	SEQUENCE	653 AA; Y1934 WR; ZA003689D1D7390 CMC64;
QY		1 QRYGRLRMASDE 13
DB		186 QEYGEHRRVODE 198
RESIDU		
ID	APOC_CANAL	STANDARD: PRT: 370 AA.
PT9023:		
DY	01-NOV-1997	(Rel. 35, Created)
DY	01-NOV-1997	(Rel. 35, Last sequence update)
DY	16-OCT-2001	(Rel. 40, Last annotation update)
DE	Phospho-2-dehydro-3-deoxyheptanoate aldolase, cytosolic-inhibited	
DE	(EC 4.1.2.15) (phospho-2-keto-3-deoxyheptanoate aldolase) (DHAP	
GN	Alcohol dehydrogenase) (3-dehydro-D-arabino-heptulosonate 7-phosphate synthase).	
OS	Candida albicans (Yeast).	
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;	
OC	Fungi; Basidiomycetes; mitosporic saccharomycetales; Candida.	
NCBI_Xrefid=5476;		
BN		
RC	SEQUENCE FROM N.A.	
RC	STRAIN-ATCC 11651 / BY92.	
RA	Stouss S., Peters S.A., Daly G.P.	
RA	Submitted (Apr-1996) to the EMBL/GenBank/DBJ databases.	
RN	(12)	
RN	PARTIAL SEQUENCE FROM N.A.	
RN	MEDLINE-9607468; PubMed-8625423;	
RX	Petrella S.A., Daly G.P.;	
RT	*Aromatic amino-acid biosynthesis in candida albicans: Identification	
RT	*of the ARO4 gene encoding a second DHAP synthase.*	

RL Curr. Genet. 29:441-445(1996).
 CC -1- FUNCTION: STEREOSPECIFIC CONSDENSATION OF PHOSPHOENOLPYRUVATE (PEP)
 AND D-ERYTHROSE-4-PHOSPHATE (E4P) GIVING RISE TO 3-DEOXY-D-
 CC ARABINO-HEPTULOSUARE-7-PHOSPHATE (DHAP).
 CC -1- CATALYTIC ACTIVITY: 2-dehydro-3-deoxy-D-arabino-heptonoate 7-
 CC phosphate + H₂O = phosphate + phosphoenolpyruvate + D-erythrose 4-
 CC phosphate + H₂O
 CC -1- ENZYME REGULATION: INHIBITED BY TYROSINE (BY SIMILARITY).
 CC -1- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF CHROMISTATE WITHIN
 CC THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).
 CC -1- SIMILARITY: BELONGS TO CLASS-1 DHAP SYNTHETASE FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL database.
 CC use. No part of this publication may be reproduced, stored in a retrieval
 CC system, or transmitted, in any form or by any means, electronic, mechanical,
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: U53216; JAR4240.1; -
 DR HSSP: P00886; 10A7
 DR Interpro: IPR007B5; DAP synth.1.
 DR Pfam: PF00795; DAP synth.1.
 DR ProDom: PD0956; DAP synth.1.
 CC
 CC Aromatic amino acid biosynthesis; lyase; Multigene family.
 SO SEQUENCE 370 AA; 40291 MW; 1155324CDD7B5D8 C6C64;
 50
 60
 70
 80
 90
 100
 110
 120
 130
 140
 150
 160
 170
 180
 190
 200
 210
 220
 230
 240
 250
 260
 270
 280
 290
 300
 310
 320
 330
 340
 350
 360
 370
 380
 390
 400
 410
 420
 430
 440
 450
 460
 470
 480
 490
 500
 510
 520
 530
 540
 550
 560
 570
 580
 590
 600
 610
 620
 630
 640
 650
 660
 670
 680
 690
 700
 710
 720
 730
 740
 750
 760
 770
 780
 790
 800
 810
 820
 830
 840
 850
 860
 870
 880
 890
 900
 910
 920
 930
 940
 950
 960
 970
 980
 990
 1000
 1010
 1020
 1030
 1040
 1050
 1060
 1070
 1080
 1090
 1100
 1110
 1120
 1130
 1140
 1150
 1160
 1170
 1180
 1190
 1200
 1210
 1220
 1230
 1240
 1250
 1260
 1270
 1280
 1290
 1300
 1310
 1320
 1330
 1340
 1350
 1360
 1370
 1380
 1390
 1400
 1410
 1420
 1430
 1440
 1450
 1460
 1470
 1480
 1490
 1500
 1510
 1520
 1530
 1540
 1550
 1560
 1570
 1580
 1590
 1600
 1610
 1620
 1630
 1640
 1650
 1660
 1670
 1680
 1690
 1700
 1710
 1720
 1730
 1740
 1750
 1760
 1770
 1780
 1790
 1800
 1810
 1820
 1830
 1840
 1850
 1860
 1870
 1880
 1890
 1900
 1910
 1920
 1930
 1940
 1950
 1960
 1970
 1980
 1990
 2000
 2010
 2020
 2030
 2040
 2050
 2060
 2070
 2080
 2090
 2100
 2110
 2120
 2130
 2140
 2150
 2160
 2170
 2180
 2190
 2200
 2210
 2220
 2230
 2240
 2250
 2260
 2270
 2280
 2290
 2300
 2310
 2320
 2330
 2340
 2350
 2360
 2370
 2380
 2390
 2400
 2410
 2420
 2430
 2440
 2450
 2460
 2470
 2480
 2490
 2500
 2510
 2520
 2530
 2540
 2550
 2560
 2570
 2580
 2590
 2600
 2610
 2620
 2630
 2640
 2650
 2660
 2670
 2680
 2690
 2700
 2710
 2720
 2730
 2740
 2750
 2760
 2770
 2780
 2790
 2800
 2810
 2820
 2830
 2840
 2850
 2860
 2870
 2880
 2890
 2900
 2910
 2920
 2930
 2940
 2950
 2960
 2970
 2980
 2990
 3000
 3010
 3020
 3030
 3040
 3050
 3060
 3070
 3080
 3090
 3100
 3110
 3120
 3130
 3140
 3150
 3160
 3170
 3180
 3190
 3200
 3210
 3220
 3230
 3240
 3250
 3260
 3270
 3280
 3290
 3300
 3310
 3320
 3330
 3340
 3350
 3360
 3370
 3380
 3390
 3400
 3410
 3420
 3430
 3440
 3450
 3460
 3470
 3480
 3490
 3500
 3510
 3520
 3530
 3540
 3550
 3560
 3570
 3580
 3590
 3600
 3610
 3620
 3630
 3640
 3650
 3660
 3670
 3680
 3690
 3700
 3710
 3720
 3730
 3740
 3750
 3760
 3770
 3780
 3790
 3800
 3810
 3820
 3830
 3840
 3850
 3860
 3870
 3880
 3890
 3900
 3910
 3920
 3930
 3940

```

RC STRAIN=528BC / AB972;
RA Badcock K., Churcher C., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC
CC -1- FUNCTION: REQUIRED FOR EXPRESSION OF GLYCOLYTIC GENES. HAS
CC CERTAIN CHARACTERISTICS OF A TRANSCRIPTIONAL ACTIVATOR.
CC
CC -1- SUBCELLULAR LOCATION: Nuclear (probable).
CC
CC -1- SIMILARITY: SOME TO HUMAN CBR80.
CC
CC -1- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 708
CC ONWARDS AND IS SHORTER (725 AA) DUE TO A FRAMESHIFT.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: D10232; BAB01076.1; J01780.
CC EMBL: L07650; J01780.
CC EMBL: L27744; -. NOT-ANNOTATED_CDS.
CC EMBL: 249273; CAAB9274.1; -.
CC EMBL: 248622; CAAB8550.1; -.
CC PIR: A44919; A44919.
CC SCD: S0004732; ST01.
CC InterPro: IPR003890; EIP4G_cent.
CC Pfam: PF02854; MIF4G_1.
CC SMART: SM00543; MIF4G_1.
CC KEGG: DMAP-D1003; Nuclear protein.
CC FT DOMAIN 72 30 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
CC SCD: S0004732; ST01.
CC FT DOMAIN 164 164 ABC/lys-rich (basic).
CC FT CONFLICT 164 164 D -> V (IN REF. 3).
CC FT CONFLICT 633 633 R -> I (IN REF. 3).
CC FT CONFLICT 704 704 A -> R (IN REF. 3).
CC FT SEQUENCE 861 AA; 100017 MW; EDD04507BDC9207D CRC64;
CC
CC Query Match 49.48; Score 41; DB 1; Length 861;
CC Best Local Similarity 40.08; Pred. No. 43;
CC Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
CC
CC Oy 1 OYSGEIRMSDEPV 15
CC Db 821 RYSHREIADNRF 835
CC
CC RESULT 9
CC YGFG_ECOLI STANDARD: PRT; 261 AA.
CC ID YGFG_ECOLI
CC PS2045; P76643;
CC DT 01-OCT-1996 (Rel. 34, Created)
CC DT 15-OCT-2002 (Rel. 40, Last sequence update)
CC DT 15-OCT-2002 (Rel. 40, Last annotation update)
CC DE Hypothetical protein yfg6.
CC GN YGFG OR B2919.
CC OS Escherichia coli.
CC OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
CC Escherichia.
CC OX NCBI_TaxID=562;
CC OX NCBI_TaxID=562;
CC RN
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=K12 / MG1655;
CC RX MEDLINE=9742617; PubMed=9278503;
CC RA Blatner F.R., Plunkett G., III, Bloch C.A., Perna N.T., Burland V.,
CC RA Kelley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.P.,
CC RA Morgan J., Hayes W., Knapik B.A., Lapidus M.A., Lasker B.A.,
CC RA McInerney J., Miller N., Mortrud M.T., Orkin B.C., Peterson J.,
CC RA Rhee V., Shoemaker M.C., Smith T., Tabor C., Tabor T.,
CC RT "The complete genome sequence of Escherichia coli K-12."
CC CC -1- SIMILARITY: BELONGS TO THE ENOYL-COA HYDRASTASE/SOMEHASE FAMILY.
CC This SWISS-Prot entry is copyright. It is produced through a collaboration

```

```

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: U280325; AAA9086.1; A01_LNIT.
CC EMBL: U280325; AAA9086.1; A01_LNIT.
CC EMBL: U280325; AAA9086.1; A01_LNIT.
CC HSP: P16504; DDB.
CC Ecogene: Bg12972; YGFG.
CC InterPro: IPR001753; YGFG.
CC Pfam: PF00378; ECH_1.
CC PROSITE: PS00166; ENOYL_COA_HYDRASTASE; 1.
CC KW Hypothetical protein; Lyase; Complete proteome.
CC SEQUENCE 261 AA; 29172 MW; B6BA13BC2C2EB5D CRC64;
CC
CC Query Match 48.28; Score 40; DB 1; Length 261;
CC Best Local Similarity 50.08; Pred. No. 17;
CC Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
CC
CC Oy 3 YGRELIRMSDEPV 16
CC Db 21 YGRLNALSKVFD 34
CC
CC RESULT 10
CC PHLC_TRYCR STANDARD: PRT; 380 AA.
CC ID PHLC_TRYCR
CC DT 15-DEC-1998 (Rel. 37, Created)
CC DT 15-DEC-1998 (Rel. 37, Last sequence update)
CC DT 15-DEC-1998 (Rel. 37, Last annotation update)
CC DE Variant surface-glycoprotein phospholipase C (EC 3.1.4.47) (VSG
CC lipase) (Glycosylphosphatidylinositol-specific phospholipase C)
CC (GPI-PLC).
CC OS Trypanosoma cruzi.
CC BUkaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
CC NCBI_TaxID=5693;
CC RN
CC RP SEQUENCE FROM N.A.
CC RC Boppath M., Campbell N., Webb H., Courel M., Anclim A.,
CC RA Cardoso-da-Silva M.L., Carrington M.;
CC RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: BY HYDROLYSIS OF THE ATTACHED GLYCOLIPID, RELEASES
CC SOLUBLE VARIANT SURFACE GLYCOPROTEIN CONTAINING PHOSPHOINOSITOL.
CC FROM THE CELL WALL OF T. BRUCEI AFTER CELL LYSIS. IT ALSO CLEAVES
CC SIMILAR MEMBRANE ANCHORS ON SOME MAMMALIAN PROTEINS. VSG LIPASE
CC MAY PLAY A ROLE IN PROCESSES SUCH AS PARASITE DIFFERENTIATION OR
CC ANTIGENIC VARIATION (BY SIMILARITY).
CC -1- PHOSPHATIDYLINOSITOL (BY SIMILARITY).
CC -1- PHOSPHATIDYLINOSITOL + H(2)O -> 1,2-diacylglycerol + soluble
CC variant surface-glycoprotein (VSG).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Membrane-associated.
CC -1- SIMILARITY: DOMAIN X IS CONSERVED IN DIFFERENT FORMS OF PLC AND IS
CC ESSENTIAL FOR CATALYTIC ACTIVITY.
CC
CC This SWISS-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: A0000079; CA003904.1.
CC EMBL: A0000079; CA003904.1.
CC InterPro: IPR000909; PI-PLC_X.
CC Pfam: PF00388; PI-PLC_X; 1.
CC PROSITE: PS00167; VarsurfGlc_PLC; 1.
CC SMART: SM00148; PLCXc; 1.

```


OY 3 YGRELRRMSDEF 16
 1 111 111 111
 DB 279 YGRELRRMSDEF 292

RESULT 13
 6REL_THEMA STANDARD: PRT: 220 AA.
 AC 09Y0109
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 39, Last sequence update)
 DE 6-Phosphogluconolactonase (EC 3.1.1.31) (6PGL).
 GN PGL OR DBA9 OR TM1154.
 OS Thermotoga maritima.
 OC Bacteria; Thermotogales; Thermotoga.
 OK NCBI_TaxID=2336;
 (1)

SEQUENCE FROM N.A.
 RC STRAIN=MSB8 / DSM 3109;
 KC MEDLINE=99287316; PubMed=10360571;
 RA Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,
 RA Holt D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
 RA McDonald L., Utterback T.R., Malek J.A., Linher C.D., Garrett M.M.,
 RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
 RA Heidelberg J., Sutton G.G., Fleischman R.D., Eisen J.A., White O.,
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
 RT Evidence for lateral gene transfer between Archaea and Bacteria from
 RT genome sequence of *Thermotoga maritima*.;
 RL Nature 393:323-328(1999).
 CC -1- FUNCTION: HYDROLYTIC OF 6-PHOSPHOGLUCONOLACTONE TO 6-
 CC PHOSPHOGLUCONATE.
 CC -1- CATALYTIC ACTIVITY: 6-phospho-D-glucono-1,5-lactone + H(2)O = 6-
 CC phospho-D-gluconate.
 CC -1- PATHWAY: SECOND STEP IN PENTOSE PHOSPHATE PATHWAY.
 CC -1- SIMILARITY: BELONGS TO THE GLUCOSAMINE/GALACTOSAMINE-6-PHOSPHATE
 CC ISOMERASE FAMILY. 6-PHOSPHOGLUCONOLACTONASE SUBFAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: AE001772; RAD36230.1; -
 DR TIGR: TM1154; -
 DR InterPro: IPR000457; Glucosamine Iso.
 DR Pfam: PF01182; Glucosamine Iso. 1.
 DR HydroLase: Complete proteome.
 KW HydroLase: 220 AA; 25325 MW; 980FD07E01E60C3 CRC64;
 SO SEQUENCE

Query Match 47.0%; Score 39; DB 1; Length 220;
 Best Local Similarity 42.9%; Pred. No. 21;
 Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 1 OYRGELRRMSDEF 14
 1 111 111 111
 DB 113 EYEREIRSATQDF 126

RESULT 14
 RA51_SCHPO STANDARD: PRT: 365 AA.
 AC P36601;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE DNA repair protein Rhp51 (RAD51 homolog).
 GN RHP51 OR RAD51 OR SPAC644.14C.
 OS Schizosaccharomyces pombe (Fission yeast).
 SO SEQUENCE

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 OK NCBI_TaxID=4896;
 (1)

SEQUENCE FROM N.A.
 RA MEDLINE=94051565; PubMed=8233794;
 RX Muris D.F.R., Vreeken K., Carr A.M., Broughton B.C., Lehmann A.R.,
 RA Lohman P.H.M., Pastink A.;
 RT Cloning the RAD51 homologue of Schizosaccharomyces pombe.;;
 RL Nucleic Acids Res. 21:4586-4591(1993).
 (2)

SEQUENCE FROM N.A.
 RX MEDLINE=93364417; PubMed=8358431;
 RA Shinozuka A., Ogawa H., Matsuda Y., Ushio N., Ikey K., Ogawa T.;
 RT Cloning of human, mouse and fission yeast recombination genes
 RT homologous to RAD51 and recA.;;
 RL Nat. Genet. 4:239-243(1993).
 (3)

SEQUENCE FROM N.A.
 RA MEDLINE=94252568; PubMed=8194753;
 Jang Y.K., Jin Y.H., Kim E.M., Hong S.H., Fabre F., Park S.D.;
 RT Cloning and sequence analysis of rhp51+, a Schizosaccharomyces pombe
 RT homolog of the Saccharomyces cerevisiae RAD51 gene.;;
 RL Gene 142:207-211(1994).
 (4)

SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Lyne M.H., Rajandream M.A., Barrell B.G., Brown S., Harris D.;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: REQUIRED BOTH FOR RECOMBINATION AND FOR THE REPAIR OF
 CC DNA DAMAGE CAUSED BY X-RAYS.
 CC -1- SIMILARITY: STRONG TO OTHER EUKARYOTIC RECA-LIKE PROTEIN; SOME, TO
 CC PROKARYOTIC RECA PROTEIN.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: 222691; CAAB0399.1; -
 DR EMBL: D13805; BAA02963.1; -
 DR EMBL: 224756; CAAB0879.1; -
 DR EMBL: 224756; CAAB0879.1; M/LT_INT.
 DR EMBL: AL355012; CAP90141.1; -
 DR PIR: 533205; 533205.
 DR PIR: 534713; 534713.
 DR PIR: 542107; 542107.
 DR PIR: 537672; 537672.
 DR PIR: 536159; 536159.
 DR InterPro: IPR000445; HHH.
 DR InterPro: IPR001583; HHH.1.
 DR InterPro: IPR001553; RecA.
 DR Pfam: PF00653; HHH.1.
 DR SMART: SM00278; HHH.1.
 DR PROSITE: PS50162; RECA_2.1.
 DR PROSITE: PS50163; RECA_3.1.
 KW DNA damage; DNA repair; ATP-binding; DNA recombination.
 FT NP_BIND 149 156 ATP (POTENTIAL).
 FT CONFLICT 115 156 T -> H (1N REP. 2 AND 4).
 SO SEQUENCE 365 AA; 39823 MW; 9F26B9FA4F3C2BA CRC64;

Query Match 47.0%; Score 39; DB 1; Length 365;
 Best Local Similarity 53.8%; Pred. No. 37;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 2 YRGELRRMSDEF 14
 1 111 111 111
 DB 269 RFWRTQRLADEF 281

[illegible]

Query Match	53.0%	Score 44	DB 15	Length 1248
Best Local Similarity	50.0%	Pred No. 18		
Matches	7	Conservative	5	Mismatches
	1111	111111		
Oy	3 YG9RLRINSDSEYD 16			
Db	186 TQKQVGRADSEYD 199			
RESULT	4			
ID	COH003	PRELIMINARY	PRT: 1248 AA.	
AC	OGH003			
DT	01-MAR-2001 (FTEMBLrel. 16, Created)			
DR	01-MAR-2001 (FTEMBLrel. 16, Update)			
DE	COBALTIN BIOSYNTHETIC PROTEIN COBH.			
DE	PMH001 04244			
OS	Proteobacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;			
OC	Pseudomonas			
CC	111111Taxid=287.			
LN	SEQUENCE FROM N.A.			
RC	STRAIN=ATCC 15692 / PAOI.10984043			
RG	Stover C.C., Klotzel J., Pham X.O.,			
RA	Hickey N.J., Brittanham F.S.L., Hutnagle W.O., Kowalik D.J., Lagrou M.,			
RA	Garner R.L., Collier L., Tolentino E., Westbrock-Wadman S., Yuan Y.,			
RA	Smith K.A., Spencer D.H., Mong G.K., Ma Z., Paulsen O.,			
RA	Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V., an			
RT	Complete genome sequence of Pseudomonas aeruginosa PAOI. an			
RD	Complete genome sequence of Pseudomonas aeruginosa PAOI. an			
RL	Nature 400:959-964(2000).			
RM	EMBL: AF004720; AAC06332.1.			
DR	InterPro: IPR001406			
DR	InterPro: IPR001406			
DR	Pfam: PF02514; COB-NH-Site1; 1.			
DR	PROSITE: PS00626; RCD1.2; UNK0NN1.J.			
SO	SEQUENCE 1248 AA. 138499 MW. C3DBFE66736C7A CRC64;			
Query Match	53.0% <td>Score 44<td>DB 15<td>Length 1248</td></td></td>	Score 44 <td>DB 15<td>Length 1248</td></td>	DB 15 <td>Length 1248</td>	Length 1248
Best Local Similarity	50.0% <td>Pred No. 18<td><td></td></td></td>	Pred No. 18 <td><td></td></td>	<td></td>	
Matches	7 <td>Conservative</td> <td>4<td>Mismatches</td></td>	Conservative	4 <td>Mismatches</td>	Mismatches
	1111111111			
Oy	1 ORVQ-PELRMSDNYD 16			
Db	615 ESYGLRDLRLADEYD 632			
RESULT	5			
ID	OG96N1	PRELIMINARY	PRT: 5635 AA.	
AC	CG96N1			
DT	01-OCT-2000 (FTEMBLrel. 15, Created)			
DR	01-OCT-2000 (FTEMBLrel. 15, Last sequence update)			
DE	MYEIN HEAVY CHAIN, CYTOSOLIC.			
DE	LJ302.02.			
OS	Leishmania major			
OS	Leishmania major; Kinetoplastida; Trypanosomatidae; Leishmania.			
CC	NCBI_Taxid=5664			
LN	SEQUENCE FROM N.A.			
RG	Smith R.F., Wootler H., Wootler E., Duesterhoeft A., Lyons A.C.,			
RA	Quail M., Rajandream M.A., Barrell B.G.,			
RA	Summated (JUN-2000) to the EMBL/Genbank/DBD databases			
RT	Complete genome sequence of Leishmania major strain-FRIEDLIN			

RA MEDLINE:98146435; PubMed:9477341;
 RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
 RA Smith D.F.;
 RA "A physical map of the *Leishmania major* Fricidin genome.";
 RL Genome Res. 8:135-145(1998).
 DR EMBL: AL359781; CAB95305.1;
 DR InterPro: IPR000169; Thiolprot_act_site.
 DR PROSITE: PS00639; THIOL_PROTEASE_HIS; UNKNOWN.1.
 SO SEQUENCE 5635 AA; 62050 MW; 64A9EB81A9B1d641 CRC64;

Query Match 51.8%; Score 43; DB 5; Length 5635;
 Best Local Similarity 72.7%; Pred. No. 8,3e+02;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 ORYGRELRNMS 11
 11:11:11111
 DB 1535 ORGFRDLRMS 1545

RESULT 6 PRELIMINARY: PRT: 339 AA.
 ID 09F005
 AC 09F005
 DT 01-MAR-2001 (TRENBLrel. 16, Created)
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE ATTRANFLOZ PROTEIN (FRAGMENT).
 CN ATTRANFLOZ
 OS *Attrichum angustatum*.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 OC Polytichopsida; Polytichales; Polytichaceae; *Attrichum*.
 OX NCBI_TaxID=37310.
 RN [1]
 RX SEQUENCE FROM N.A.
 RX MEDLINE:20564611; PubMed=11110908;
 RA Frolich M.M., Estabrook G.F.;
 RA "Wilkinson Support Calculated with Exact Probabilities: An Example
 RA using Flortacalcaly Amino Acid Sequences that Compares three
 RA Hypotheses Involving Gene Involvement in Seed Plants.";
 RL Mol. Biol. Evol. 17:1984-1993(2000).
 DR EMBL: AF286055; AAC42893.1;
 DR InterPro: IPR002910; FLO_LF1.
 DR Pfam: PF01698; FLO_LF1; 2.
 RN NON_LIT
 SO SEQUENCE 339 AA; 38764 MW; A978P91EDBC912CA CRC64;

Query Match 50.6%; Score 42; DB 10; Length 339;
 Best Local Similarity 69.2%; Pred. No. 54;
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 GRELRNMSDEPV 16
 11:11:1111111
 DB 23 GRESRRNKLDFD 35

RESULT 7 PRELIMINARY: PRT: 415 AA.
 ID 09V7Y6
 AC 09V7Y6
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
 DE CG15612 PROTEIN.
 GN CG15612.
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; *Drosophila*.
 OX NCBI_TaxID=7227;
 RN [1]
 SO SEQUENCE FROM N.A.

RC STRAIN-BERKELEY;
 RX MEDLINE:20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Maanides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Morten J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.C., Helt G., Nelson C.R., Mills G.L.G.,
 RA Ballif J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Baerentzen D., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
 RA Borovaya D., Botchan M.R., Bouck J., Brooksstein P., Brotler P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra T.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieri W., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glisak A., Gong F., Gorrell J.R., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ibegam C.,
 RA Jalili M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.B., Kodira C.D., Kraft C., Kravitz S., Kolp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mervolov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Murray D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
 RA Palczolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Palmer K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Snyder E., Spradling A.C., Turner R., Venter Fong R., Sun E.,
 RA Sytkas R., Tector C., Turner R., Venter Fong R., Sun E.,
 RA Wang Z.-Y., Wasserman D.A., Weissstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeat T., Yeat T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Zheng Y., Zhong F.N., Zhong Y., Zhou K., Zhou S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.N., Rubin G.M., Venter J.C.;
 RL Science 297:2185-2195(2002).
 DR EMBL: AB038604; AA576988.1;
 DR FlyBase: FBgn001419; CG15612.
 DR InterPro: IPR001849; RH.
 DR InterPro: IPR000219; KNOGEF.
 DR Pfam: PF00621; KNOGEF; 1.
 DR SMART: SM00233; FH; 1.
 DR SKART: SM00123; KNOGEF; 1.
 SO SEQUENCE 415 AA; 49479 MW; C3B0574DB56DF20A CRC64;

Query Match 50.6%; Score 42; DB 5; Length 415;
 Best Local Similarity 53.3%; Pred. No. 66;
 Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 ORYGRELRNMSDEPV 15
 11:11:1111111
 DB 121 ORNRDLRLDFDPL 135

RESULT 8 PRELIMINARY: PRT: 457 AA.
 ID 0983U4
 AC 0983U4
 DT 01-OCT-2001 (TRENBLrel. 18, Created)
 DT 01-OCT-2001 (TRENBLrel. 18, Last sequence update)
 DT 01-OCT-2001 (TRENBLrel. 18, Last annotation update)
 DE HOMOGENTISATE 1,2-DIOXYGENASE.
 GN MUR8303.
 OS *Rhizobium loti* (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Pseudomonadaceae; Mesorhizobium.
 OX NCBI_TaxID=381;
 RN [1]

RP SEQUENCE FROM N.A.
STRAIN-MAFF303099;
RX MEDLINE-1082930; PubMed-11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Ideawaga K., Ishikawa A., Kawashima K., Kikuno T.,
RA Kistida Y., Kiyosawa C., Kohara M., Matsuno M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takuchi C., Yamada M., Tabata S.
RT *Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.*
RL DNA Res. 7:331-338(2000).
RD EMBL: AP003013; BABS387.1; -;
KW Divergences: Complete proteome.
SQ SEQUENCE 457 AA; 5106 MW; 6A20B6959A2B2BD1 CRC64;

Query Match	50.6%	Score 42	DB 16	Length 457
Best Local Similarity	45.7%	Pred. No. 75		
Matches	7	Conservative	2	Mismatches 6
				Indels 0
				Gaps 0
QY	2	RYGHELRKNSDEYVD	16	
DB	425	RYGAELETRKQDYTD	439	

RESULT	9	
P71029	PRELIMINARY;	PRT; 548 AA.
AC	P71029;	
DT	01-FEB-1997 (TRIMBLREI. 02, Created)	
DT	01-FEB-1997 (TRIMBLREI. 02, Last sequence update)	
DT	01-DEC-2001 (TRIMBLREI. 19, Last annotation update)	
DE	4-METHYL-5-NITROCATHECOL OXYGENASE.	
GN	DNTB.	
OS	Burkholderia sp. (strain RASC).	
OC	Bacteria; Proteobacteria; beta subdivision; Burkholderia group;	
CC	Burkholderia.	
CC	NCBI_TaxID=69003;	
RN	[1]	
RP	SOURCE FROM N. A.	
RC	STRAIN-DNT:	
RC	MEDLINE=66427337; PubMed=8830701;	
RA	Halzler B.E., Suen W.C., Spain J.C.;	
RT	"Purification and sequence analysis of 4-methyl-5-nitrocatechol	
RT	oxygenase from Burkholderia sp. strain DNT."	
RL	J. Bacteriol. 178:6019-6024 (1996).	
RL	EMBL: U68411; AAC44479.1;	
DR	InterPro: IPR001033; 11avo_monoxygenase.	
DR	InterPro: IPR029382; Moxy_FAD_binding.	
DR	InterPro: IPR003042; Nmg_moxoygenase.	
DR	Pfam: PF01494; FAD_binding_3; 1.	
DR	Pfam: PF01360; Monoxygenase; 1.	
DR	PRINTS: PR00420; RNMNOXNASE.	
SO	SOURCE: 548 AA; 59166 MW; A1B508A7413BC5E CRC64;	

Query Match	50.6%	Score 42	DB 2	Length 548
Best Local Similarity	43.8%	Pred. No. 92		
Matches	7	Conservative	5	Mismatches
			4	Indels
				Gaps
OY	1	ORXGRLRKMSDEYD	16	
Db	371	QAFSRYTRRLAPELD	386	

DE	SD09786p.	
DT	01-DEC-'001	(TREMBAIrel, 19, last annotation update).
DT	01-DEC-'000	(TREMBAIrel, 19, last sequence update).
DT	01-DEC-'001	(TREMBAIrel, 19, Created).
ID	Q960B3	
AC	Q960B3	
0960B3		
RESULT	10	

GN CG15612
 ON *Drosophila melanogaster* (Fruit fly).
 SC *Eukaryota*: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta:
 OC *Eukaryota*: Neoptera, Endopterygota, Diptera; Brachycera, Muscomorpha:
 OX *Ephyridae*: *Drosophilidae*: *Drosophila*.
 RX NCBI_TaxID:727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stapleton M., Brokstein P., Hong L., Aghayani A., Carlson J.,
 RA Champagne M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall G.T.,
 RA Numan J., Pacelz J.F., Pargacs V., Park S., Phouathavong S., Wan K.,
 RA Yu C., Lewis S.R., Rubin G.M., Celisner S.
 DO Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
 EMBL: AY052140; AAK3564.1; --
 DO SEQUENCE 592 AA; 64357 MW; C5FD5724559E2A83 CRR64;

```

Query Match      50.6%; Score 42; DB 5; Length 592;
Best Local Similarity 53.3%; Pred. No. 1e+02;
Matches      8; Conservative      4; Mismatches      3; Indels      0; Gaps      0
OY      1 ORGRELRRMSDEY 15
      11 +:::1::111:
DB      298 ORNRDRKRLFDEFL 312

```

RESULT	11	
09NOP8	PRELIMINARY;	PT; 653 AA.
AC	09NOP8;	
DT	01-OCT-2000 (TREMBLel.15, Created)	
DT	01-OCT-2000 (TREMBLel.15, Last sequence update)	
DT	01-DEC-2001 (TREMBLel.19, Last annotation update)	
DE	Ba67K19.2 (ZINC-FINGER PROTEIN HR2A 772 KDA TAT-INTERACTING PROTEIN)	
DE	(TAT-INTERACTING PROTEIN, 72-KD).	
GN	Ba67K19.2	
OS	Human splicins (Human);	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Homalia; Euteheria; Primates; Catarrhini; Hominoidei; Homo.	
OX	NCBI_TaxID=9606;	
RM	[1]	
RP	SEQUENCE FROM N.A.	
RA	Sehra H.;	
RA	Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=SKIN, AND MELANOMA.	
RA	Straussberg R.;	
RL	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.	
CC	-1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.	
DR	EMBL; BC003154; CAB92773.1; -	
DR	EMBL; BC003154; AAH03154.1; -	
DR	HSSP; P29590; IBOR.	
DR	InterPro; IPR000345; CytoC_heme_bind.	
DR	InterPro; IPR001258; NHL.	
DR	InterPro; IPR000822; Znf_C242.	
DR	InterPro; IPR000315; Znf_Box.	
DR	InterPro; IPR001841; Znf_Fing.	
DR	Pfam; PF01436; NHL; 6.	
DR	Pfam; PF00643; Zf-B_box; 1.	
DR	Pfam; PF00097; Zf-C3HC4; 1.	
DR	SMART; SMO0184; RING; 1.	
DR	PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.	
DR	PROSITE; PS00028; ZINC_FINGER_C242_1; 1.	
DR	PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.	
DR	DNA-binding; Metal-binding; Zinc; Zinc-finger.	
SW	SEQUENCE 653 AA: D83B1595CA8378BD CRC64:	

Query Match	50.68;	Score 42;	DB 4;	Length 653;
Best Local Similarity	61.58;	Pred. No. 1.1e+02;		

Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 ORYGRELRMSDE 13
DB 186 OYCHERRVODE 198

RESULT 12

O99J78

ID O99J78; PRELIMINARY; PRT; 876 AA.

DT 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE VALINE-TRNA LIGASE.

GN VALS OR SNA148.

OS Staphylococcus aureus (strain N315).

OC Bacteria; Firmicutes; Bacillus/Clostridium group;

OC Bacillus/Staphylococcus group; Staphylococcus.

OX NCBI_TaxID=158879;

RM [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=21311952; PubMed=11418146;

RA Kuroda M., Ouchi T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

RA Cui L., Oguchi A., Aoki K.I., Nagai Y., Lian J., Ito T., Kanamori M.,

RA Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y.,

RA Kikushima N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,

RA Hiramatsu A., Kohara S., Goto S., Yabuzaki J., Kanehisa M.,

RA Ogasawara N., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,

RA Whole genome sequencing of methicillin-resistant Staphylococcus

RT aureus 37:1225-1240(2001).

RL Lancet 357:1225-1240(2001).

RM BSR: AP003463; BAB57825.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

DR HSP: P90142; CXP842754.1; -.

RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.I., Kaito C.,
RA Sekimizu K., Hiramatsu A., Kohara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus";
RL Lancet 357:1225-1240(2001).
DR EMBL: AP003463; BAB57825.1; -.
KW Ligase; Complete proteome.
SQ SEQUENCE 876 AA; 101772 MW; F76294F4D0C2055D CRC64;

Query Match 50.6%; Score 42; DB 16; Length 876;

Best Local Similarity 61.5%; Pred. No. 1.5e+02;

Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 4 GRELRMSDEYD 16
DB 251 GREPLRLADEYD 263

RESULT 14

O9KZC5; PRELIMINARY; PRT; 216 AA.

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE HYPOPHETICAL 23.8 KDA PROTEIN.

GN SC67.17C.

OS Streptomyces coelicolor.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Streptomycetaceae; Streptomycetaceae; Streptomycetes.

OX NCBI_TaxID=1502;

RM [1]

RP SEQUENCE FROM N.A.

RC SRAIN-A3(2);

RA Saunders D.C., Harris D.;

RA Submitted (Apr-2000) to the EMBL/Genbank/DBJ databases.

RM [2]

RP SEQUENCE FROM N.A.

RC SRAIN-A3(2);

RA Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;

RA Submitted (Apr-2000) to the EMBL/Genbank/DBJ databases.

RM [3]

RP SEQUENCE FROM N.A.

RC SRAIN-A3(2);

RA Redenbach M., Kleser H.M., Denapalre D., Eichner A., Cullum J.,

RA Kanehisa M., Hopwood D.A.;

RA "A set of ordered cosmids and a detailed genetic and physical map for

RT the 8 Mb streptomycetes coelicolor A3(2) chromosome.";

RL Mol. Microbiol. 21:77-96(1996).

DR EMBL: AL353870; CAB89025.1; -.

DR InterPro: IPR003265; Endo_3c.

DR SMART: SM00478; EMD03c; 1.

DR Hypothetical protein.

RM [4]

RP SEQUENCE 216 AA; 23810 MW; DDD7C717D60F7AA7 CRC64;

Query Match 49.4%; Score 41; DB 2; Length 216;

Best Local Similarity 53.8%; Pred. No. 48;

Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 OYGRELRMSDE 13
DB 109 ERMGDLRLRIDE 121

RESULT 15

O9M0B1; PRELIMINARY; PRT; 447 AA.

AC 09MOB1:
 DT 01-OCT-2000 (Tremblrel. 15, created)
 DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, last annotation update)
 DE HYPOTHETICAL 50.8 KDA PROTEIN.
 GN AT4G30490.
 OS Arabidopsis thaliana (mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosidae ii; Brassicales; Brassicaceae; Arabidopsi.
 OC NCBI_TaxID=3702;
 OX 11
 RN
 RP SEQUENCE FROM N.A.
 RA Lamar B., Stoneking T., Stumpf J., Neves H.W., Lemcke K.,
 RA Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN 12
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL161577; CAB79767.1;
 KW Hypothetical protein.
 SO SEQUENCE 447 AA: 50837 MW: CB24C84F167CE3AF CRC64;

Query Match 49.48; Score 41; DB 10; Length 447;
 Best Local Similarity 66.78; Pred. NO. 1.1e+02;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 RETLRMSDEYD 16
 |||:|:|
 DB 84 RELQRLYDELVD 95

Search completed: September 20, 2002, 11:03:44
 Job time: 1661 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2002, 10:35:58 (Search time 228.86 Seconds
(Without alignments)
7.765 Million cell updates/sec

Title: US-09-544-664-30
Perfect score: 80
Sequence: 1 GCGVROLAIGSDINR 16

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 11073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Listing first 45 summaries

1: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:*
4: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT:*
5: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1984.DAT:*
6: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1985.DAT:*
7: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1986.DAT:*
8: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1987.DAT:*
9: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1988.DAT:*
10: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1989.DAT:*
11: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1990.DAT:*
12: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1991.DAT:*
13: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1992.DAT:*
14: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1993.DAT:*
15: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1994.DAT:*
16: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1995.DAT:*
17: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1996.DAT:*
18: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1997.DAT:*
19: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT:*
20: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT:*
21: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:*
22: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	80	100.0	16	20	AAV05423 Human BAK BH3 doma
2	80	100.0	16	21	AAV05423 Bcl2 polypeptide B
3	80	100.0	16	22	AAV05423 Bcl2 polypeptide B
4	80	100.0	17	21	AAV05423 Bcl2 polypeptide B
5	80	100.0	26	21	AAV05423 Bcl2 polypeptide B
6	80	100.0	26	22	AAV05423 Bcl2 polypeptide B
7	80	100.0	27	21	AAV05423 Bcl2 polypeptide B
8	80	100.0	28	17	AAV05423 Bcl2 polypeptide B
9	80	100.0	117	19	AAV05423 Bcl2 polypeptide B
10	80	100.0	141	16	AAV05423 Bcl2 polypeptide B
11	80	100.0	152	16	AAV05423 Bcl2 polypeptide B

12	80	100.0	211	15	AAV05423 Human BAK BH3 doma
13	80	100.0	211	16	AAV05423 Bcl2 polypeptide B
14	80	100.0	211	17	AAV05423 Bcl2 polypeptide B
15	80	100.0	211	17	AAV05423 Bcl2 polypeptide B
16	80	100.0	211	17	AAV05423 Bcl2 polypeptide B
17	80	100.0	211	19	AAV05423 Bcl2 polypeptide B
18	80	100.0	211	20	AAV05423 Bcl2 polypeptide B
19	78	97.5	16	20	AAV05423 Bcl2 polypeptide B
20	78	97.5	16	21	AAV05423 Bcl2 polypeptide B
21	78	97.5	16	21	AAV05423 Bcl2 polypeptide B
22	78	97.5	16	21	AAV05423 Bcl2 polypeptide B
23	75	93.8	16	21	AAV05423 Bcl2 polypeptide B
24	74	92.5	16	21	AAV05423 Bcl2 polypeptide B
25	69	86.2	15	17	AAV05423 Bcl2 polypeptide B
26	69	86.2	15	17	AAV05423 Bcl2 polypeptide B
27	47	58.8	15	22	AAV05423 Bcl2 polypeptide B
28	47	58.8	15	22	AAV05423 Bcl2 polypeptide B
29	47	58.8	15	22	AAV05423 Bcl2 polypeptide B
30	46.5	58.1	175	21	AAV05423 Bcl2 polypeptide B
31	46.5	58.1	175	21	AAV05423 Bcl2 polypeptide B
32	46.5	58.1	175	21	AAV05423 Bcl2 polypeptide B
33	46.5	58.1	175	21	AAV05423 Bcl2 polypeptide B
34	46.5	58.1	175	21	AAV05423 Bcl2 polypeptide B
35	46.5	58.1	175	21	AAV05423 Bcl2 polypeptide B
36	46.5	58.1	175	21	AAV05423 Bcl2 polypeptide B
37	46.5	58.1	175	21	AAV05423 Bcl2 polypeptide B
38	46.5	58.1	175	21	AAV05423 Bcl2 polypeptide B
39	46.5	58.1	175	21	AAV05423 Bcl2 polypeptide B
40	46.5	58.1	175	21	AAV05423 Bcl2 polypeptide B
41	46.5	58.1	175	21	AAV05423 Bcl2 polypeptide B
42	46.5	58.1	175	21	AAV05423 Bcl2 polypeptide B
43	46.5	58.1	175	21	AAV05423 Bcl2 polypeptide B
44	46.5	58.1	175	21	AAV05423 Bcl2 polypeptide B
45	46.5	58.1	175	21	AAV05423 Bcl2 polypeptide B

ALIGNMENTS

RESULT 1	AAV05423	standard; peptide: 16 AA.
ID	AAV05423	standard; peptide: 16 AA.
AC	AAV05423	standard; peptide: 16 AA.
DT	02-JUL-1999	(first entry)
XX	Human BAK BH3 domain.	
DE	Human BAK BH3 domain.	
XX	BH3 domain; cell death agonist; bcl homology domain; BCL-2 family;	
KW	apoptosis promoter; cancer cell; virus infected cell; inflammation;	
KW	antitumor; antitumor producing cell; cancer; lymphoproliferative condition;	
KW	arthritis; autoimmune disease; therapy.	
XX	Human sapiens.	
OS	Human sapiens.	
XX	MO9916787-A1.	
FN	MO9916787-A1.	
XX	08-APR-1999.	
PD	08-APR-1999.	
XX	22-SEP-1996.	98AC-US19765.
XX	07-OCT-1997.	97US-0946039.
PR	26-SEP-1997.	97US-0060133.
XX	(UNIT) UNIV WASHINGTON.	
PA	Korsmeyer SJ.	
PI	Korsmeyer SJ.	
XX	WPI; 1999-255058/21.	
DR	Bcl homology domain 3 polypeptide	
XX	Bcl homology domain 3 polypeptide	

PS Example 1: Fig 4; 104pp; English.

CC This sequence represents the BH3 domain of human BAX.
 CC The invention relates to a bcl2 homology domain 3 (BH3 domain).
 CC derived from a proapoptotic member of the Bcl-2 family. The
 CC BH3 polypeptide can be used in a method for promoting apoptosis in a
 CC target cell, especially where the cell is a cancer cell, a virus infected
 CC cell or an autacell body producing cell. The BH3 polypeptide can be used
 CC in therapeutic compositions for treating disease including cancer, other
 CC lymphoproliferative conditions, arthritis, inflammation, and autoimmune
 CC diseases, which may result from the down regulation of cell death
 CC regulation.

CC Sequence 16 AA:

Query Match 100.0%; Score 80; DB 20; Length 16;
 Best Local Similarity 100.0%; Pred. NO. 1.2e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGVGRQLAIIIGDINR 16
 |||
 DB 1 ggvgrqaligddlnr 16

RESULT 2

AB87030 standard; peptide; 16 AA.

AB87030:

28-FEB-2001 (first entry)

Bcl2 polypeptide BH3 domain peptide #30.

CC Cytostatic; neuroprotective; anti-HIV; vituicide; Cerebroprotective;
 CC cardiant; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;
 CC apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;
 CC colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
 CC melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
 CC stroke; myocardial infarction.

OS Homo sapiens.

PN MO200059526-A1.

PD 12-OCT-2000.

PF 06-APR-2000; 2000MO-US09352.

PR 07-APR-1999; 99US-0128202.

XX (UYJE-) UNIV JEFFERSON THOMAS.

PI Huang Z, Wang J, Zhang Z, Shan S, Lu Z;

DR WPI: 2000-679325/66.

PT New peptide conjugates for modulating apoptosis or for inhibiting B
 cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
 PT treating neurodegenerative disorders, stroke, or cancer.

XX Claim 18; Page 18; 74pp; English.

CC The invention relates to a peptide conjugate having the formula:
 CC (R-X)-peptide where n = 1-10; X = C=O, when the R-X group is attached
 CC to the N-terminus of the peptide, or a side chain of the peptide where
 CC the functional group of the side chain is NH2 or OH; or X = O or NH,
 CC when the R-X group is attached to the C-terminus of the peptide, or a
 CC side chain of the peptide, where the side chain functional group is COOH
 CC or CONH2, and R is 2-18C alkyl or alkoxy, 2-14C alkenyl containing one
 CC or two double bonds, cycloalkyl, cyclopentenyl, cyclohexyl optionally
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,

CC phenyl optionally monosubstituted with a 1-5C straight or branched chain
 CC alkyl group or benzyl. The peptides AB87001-871058 represent examples
 CC of the peptide portion of the conjugate. The peptides represent analogues
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
 CC the BH3 domain of the cell death agonist Bad. The peptide conjugate is
 CC useful for modulating apoptosis in the cells of a subject, or for
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
 CC function. In particular, the peptide conjugate is useful for treating a
 CC subject afflicted with a cancer characterized by cancer cells that
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
 CC conjugate is also useful for treating disorders characterized by
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.

CC Sequence 16 AA:

Query Match 100.0%; Score 80; DB 21; Length 16;
 Best Local Similarity 100.0%; Pred. NO. 1.2e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGVGRQLAIIIGDINR 16
 |||
 DB 1 ggvgrqaligddlnr 16

RESULT 3

AB871977 standard; peptide; 16 AA.

AB871977:

11-MAY-2001 (first entry)

Bak BH3 peptide.

CC Bak; BH3 domain; antiapoptotic; cytostatic; antimycin; apoptosis;
 CC Bcl-2; neoplasia; cancer.

OS Mammalia.

PN WO200114365-A1.

PD 01-MAR-2001.

PF 18-AUG-2000; 2000MO-US22891.

PR 20-AUG-1999; 99US-0149968.

XX (HUTC-) HUTCHINSON CANCER RES CENT FRED.

PI Hockenbery DM, Simon JA, Tzung S;

DR WPI: 2001-244291/25.

PT Novel antimycin derivatives that bind to antiapoptotic Bcl-2 family
 PT protein, useful for modulating the apoptotic state of a cell.

XX Example 6; Page 41; 60pp; English.

CC The present sequence was used in an example 11 illustrating an invention
 CC relating to an antimycin derivative which modulates apoptosis by
 CC binding to a Bcl-2 family protein and preferentially induces apoptosis
 CC in a cell which over-expresses the Bcl-2 family protein. The antimycin
 CC derivative is used in treating an apoptosis-associated disease and for
 CC inducing apoptosis. It is also useful for treating neoplasia and drug
 CC resistance. The present sequence binds to the hydrophobic pocket of
 CC Bcl-2. A competitive binding assay was used to determine if the site of
 CC antimycin A3 interaction was the hydrophobic pocket of Bcl-2.

SQ Sequence 16 AA:
 Query Match 100.0%; Score 80; DB 22; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.2e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGVGROLATIGDDINR 16
 DB 1 gvgvrglatigddinr 16

RESULT 4
 AAB37057 standard; peptide: 17 AA.
 ID AAB37057
 AC AAB37057;
 DT 28-FEB-2001 (first entry)
 XX
 XX Bcl2 polypeptide Bcl-2 domain peptide #57.
 XX
 XX Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective;
 KW cardiatic; Bcl-2 superfamily; Bcl-2 domain; cell death agonist; Bcl-2
 KW apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;
 KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
 KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
 KW stroke; myocardial infarction.
 XX
 OS Homo sapiens.
 XX
 XX W0200059526-A1.
 XX
 XX 12-OCT-2000.
 XX
 XX 06-APR-2000; 2000MO-US09352.
 XX
 XX 07-APR-1999; 990US-0128302.
 XX
 XX (UYJE-) UNIV JEFFERSON TROMAS.
 XX
 XX Huang Z, Zhang Z, Shan S, Lu Z;
 PI WPI: 2000-679325/66.
 DR
 XX
 XX New peptide conjugates for modulating apoptosis or for inhibiting B
 PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
 PT treating neurodegenerative disorders, stroke, or cancer
 XX
 XX Claim 18; Page 20; 74pp; English.

CC The invention relates to a peptide conjugate having the formula:
 CC (R-X)_n-peptide where n = 1-10; X = C=O, when the R-X group is attached
 CC to the N-terminus of the peptide, or a side chain of the peptide where
 CC the functional group of the side chain is NH2 or OH; or X = O or NH,
 CC when the R-X group is attached to the C-terminus of the peptide, or a
 CC side chain of the peptide, where the side chain functional group is COOH
 CC or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkenyl, optionally
 CC or two double bonds, cycloalkyl, cycloalkenyl, cycloalkenyl optionally
 CC phenyl, optionally substituted with a 1-6C straight or branched chain
 CC phenyl, optionally substituted with a 1-6C straight or branched chain
 CC alkyl group or benzyl. The peptides AAB37001-B37058 represent examples
 CC of the peptide portion of the conjugate. The peptides represent analogues
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
 CC the Bcl-2 domain of the cell death agonist Bcl-2. The peptide conjugate is
 CC useful for modulating apoptosis in the cells of a subject, or for
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
 CC function. In particular, the peptide conjugate is useful for treating a
 CC subject afflicted with a cancer characterized by cancer cells that
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric, or
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide

CC conjugate is also useful for treating disorders characterized by
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.

SQ Sequence 17 AA:
 Query Match 100.0%; Score 80; DB 21; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.3e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGVGROLATIGDDINR 16
 DB 2 gvgvrglatigddinr 17

RESULT 5
 AAY96322 standard; Peptide: 26 AA.
 ID AAY96322
 AC AAY96322;
 DT 17-AUG-2000 (first entry)
 XX
 XX Mammalian Bcl-2 homology domain 3 domain.
 DE
 XX Mammal; apoptosis; cell death; BRC3; apoptosis promotion; Bak;
 KW apoptosis inhibition; malignant cell; autoimmune disease.
 XX
 OS Mammalia.
 XX
 XX W0200026228-A1.
 XX
 XX 11-MAY-2000.
 XX
 XX 28-OCT-1999; 99WC-US25285.
 XX
 XX 02-NOV-1998; 98US-0184168.
 XX
 XX (CION-) CIONTECH LAB INC.
 PA
 PA Zhu L, Yin X, Chittenden T;
 PI WPI: 2000-365560/31.
 DR
 XX
 XX Novel polynucleotide encoding a BRC3 protein which is useful for
 PT modulating apoptosis, especially in the treatment of cancer and
 PT autoimmune diseases.
 XX
 XX Disclosure; Fig 4; 47pp; English.

CC The present sequence is the mammalian Bak Bcl-2 homology domain 3
 CC (BHC3) domain, which was used in a sequence alignment with the same
 CC regulator BRC3, which was designated BRC3-ORF2. The BRC3 protein,
 CC nucleic acids and antibodies are suitable for use in promoting cell
 CC death or for preventing apoptosis in malignant cells and those causing
 CC autoimmune diseases.

SQ Sequence 26 AA:
 Query Match 100.0%; Score 80; DB 21; Length 26;
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGVGROLATIGDDINR 16
 DB 3 gvgvrglatigddinr 18

RESULT 6
 AAB70372

ID	AA870372 standard; Peptide: 26 AA.
AC	AAB70372;
XX	
DT	02-MAY-2001 (first entry)
XX	
XX	BAM BH3 consensus peptide sequence SEQ ID NO:5.
KM	Bcl-XL/Bcl-2 associated cell death regulator; BCL: mutant; apoptosis:
KM	immunostimulant; neuroprotective; neotropic; antileukemic; viroinhibitory;
KM	cyclostatic; antiviral; antitubercle; antiinflammatory; wound healing;
KM	immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;
KM	immunodeficiency disease; neurodegenerative disease; viral infection;
KM	ischemic cell death; reperfusion cell death; arthritis; intertality;
KW	lymphoproliferative condition; inflammation; autoimmune disease.
OS	unidentified.
XX	
XX	WO200110888-A1.
XX	
PD	15-FEB-2001.
PE	
PE	30-MAY-2000; 2000MO-US11864.
PR	
PR	28-MAY-1999; 98US-0136783.
PA	(APOF-) APOPTOSIS TECHNOLOGY INC.
PI	
PI	Zhou X;
DR	
WP1	2001-13B734/14.
PT	New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,
PT	described for screening of candidate compounds which induce or inhibit
PT	apoptosis, comprises amino acid substitutions at Ser18, Ser15 or
PT	Ser113 -
XX	
PS	
PS	Example 2; Fig 3a; 157pp; English.
CC	The present invention describes an isolated or synthetic polypeptide
CC	(1) comprising a less than full length amino acid sequence of a mutant
CC	Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its
CC	fragment, which contains amino acid substitutions at Ser18 of a human
CC	BAD. Ser15 of a murine BAD (longer murine BAD) or Ser13 of a murine
CC	BAD (shorter murine BAD). (1) has immunostimulant, neuroprotective,
CC	anti-leukemic, cyclostatic, antiviral, anti-tubercle, anti-inflamma-
CC	tory, wound healing, immunosuppressive, apoptosis inducing, and
CC	can be used as an apoptosis inducer or inhibitor. BAD polypeptides and
CC	polynucleotides can be used for screening candidate compounds and drugs
CC	for activity that promote cell survival or apoptosis. Other uses include
CC	inducing or inhibiting apoptosis in a cell. Candidate compounds
CC	identified and (mutant) BAD polypeptides are useful in treating
CC	immunodeficiency diseases, neurodegenerative diseases, ischemic cell
CC	death, reperfusion cell death, wound healing, cancer, viral infections,
CC	lymphoproliferative conditions, arthritis, intertality, inflammation and
CC	autoimmune diseases. The present sequence represents a Bcl-family member
CC	BH3 domain consensus sequence which is used in an example from the
CC	present invention.
XX	
XX	
SO	Sequence 26 AA:
Query Match	100.0%; Score 80; DB 22; Length 26;
Best Local Similarity	100.0%; Pred. No. 2,je-07;
Matches 16; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 GGAGGRLATIGDGINR 16
Ob	
	3 ggagrglaigddlar 18

RESULT
AAB37004

ID	AAB37004 standard; peptide: 27 AA.
XX	
AC	AAB37004;
XX	
DY	28-FEB-2001 (first entry)
DD	
XX	Bcl2 polypeptide Bhl domain peptide #4.
XX	Cytostatic; neuroprotective; anti-HIV; virucide; cerebroprotective; KM cardian; Bcl-2 superfamily; htl domain; cell death agonist; Bad; KM apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate; KM colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma; KM melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS; KM stroke; myocardial infarction.
KM	
XX	Homo sapiens.
XX	
PX	M0200059526-AI.
PN	12-OCT-2000.
PD	
PE	06-APR-2000; 2000MO-US09352.
PF	
PR	07-APR-1999; 99US-0128202.
PR	(UYJE-) UNIT JEFFERSON THOMAS.
PT	
PT	Huang Z., Wang J., Zhang Z., Shan S., Lu Z:
PI	WPI: 2000-679325/66.
DR	
XX	New peptide conjugates for modulating apoptosis or for inhibiting B cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer -
XX	Claim 18: Page 17: 74pp: English.
XX	The invention relates to a peptide conjugate having the formula: CC (R-X)n-peptide where n = 1-10; X = C=O, When the R-X group is attached CC to the N-terminus of the peptide, or a side chain of the peptide where CC the functional group of the side chain is NH2 or OH; or X = O or NH, CC When the R-X group is attached to the C-terminus of the peptide, or a CC side chain of the peptide, where the side chain functional group is COH CC or CONH2; and R = 2-10C alkyl or alkoxy, 2-14C alkenyl containing one CC or two double bonds; cyclohexyl, cyclopentyl, cyclobutyl, optionally CC substituted with a hydroxyl group; 2-10C aryl, optionally substituted CC phenyl optionally monosubstituted with a 1-5C straight or branched chain CC alkyl group, or benzyl. The peptides AAB37001-337058 represent analogues CC of the peptide portion of the conjugate. The peptides represent analogues CC of the Bhl domain of the cell death agonist Bad. The peptide conjugate is CC useful for modulating apoptosis in the cells of a subject, or for CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2 CC mediated inhibition of apoptosis in cells dependent upon Bcl-2 for CC survival. The peptide conjugate may be used in treating a CC subject afflicted with a cancer characterized by cancer cells that CC express Bcl-2. The cancer includes prostate, colorectal, gastric, CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide CC conjugate is also useful for treating disorders characterized by CC increased apoptosis, e.g., neurodegenerative disorders, acquired CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
XX	
XX	Sequence 27 AA:
XX	
XX	Query Match 100.0%; Score 80; DB 21; Length 27;
XX	Best Local Similarity 100.0%; Prid. No. 2.2e-07;
XX	Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
XX	
XX	I GVGGRALATIGCDINR 16
XX	
XX	6 gvgvgralaligddinr 21

```

RESULT 8
AA06294 ID AA06294 standard; Peptide: 28 AA.
XX
XX
AC AA06294:
XX
XX 29-JUL-1997 (first entry)
XX
XX GD domain region for Bak amino acid residues 67-94.
XX
XX Apoptosis; follicular lymphoma; tumour; p53; antibody.
XX
XX OS Synthetic.
XX
XX PN W09635951-A1.
XX
XX 14-NOV-1996.
XX
XX PF 06-MAY-1996; 96WO-US06122.
XX
XX PR 12-MAY-1995; 95US-0440391.
XX
XX PA (IMMU-) IMMUNOGEN INC.
XX
XX PI Chittenden TP, Lutz RJ;
XX
XX WPI: 1996-518805/51.
XX
XX DR N-PSDB: AAT42428.
XX
XX Peptide(s) comprising GD domains - have similar activities to wild
XX
XX PT type Bak, and cause cellular apoptosis for treatment of viral
XX
XX PT infection
XX
XX PS Claim 2; Page 52; 69pp; English.
XX
XX CC The term GD domain refers to a protein domain first identified in
XX
XX CC Bak and shown to be essential for the interaction of Bak with Bcl-X(L)
XX
XX CC and for Bak's cell killing function; and to peptides and/or molecules
XX
XX CC capable of mimicking its structure and/or function. The present sequence
XX
XX CC represents a GD domain corresponding to amino acid residues 67-94 of
XX
XX CC Bak. An antibody raised against a GD domain may be used to screen a
XX
XX CC cDNA expression library for clones comprising cDNA inserts encoding
XX
XX CC immunoreactive proteins. Truncated GD domain peptides have been
XX
XX CC shown to maintain the protein binding and cell killing function
XX
XX CC exhibited by wild type Bak. These molecules may induce apoptosis in
XX
XX CC tumour cells. These peptides act independently of p53 status. Bak or
XX
XX CC GD domain mimetics that inhibit Bcl-2 may be selectively toxic to
XX
XX CC certain tumours, e.g. follicular lymphoma, which depend on high levels
XX
XX CC of Bcl-2 for their continued growth and survival. GD domain mimetics
XX
XX CC may also be used for combating viral infections by causing apoptosis
XX
XX CC of infected cells.
XX
XX CC
XX
XX SQ Sequence 28 AA:

```

```

Query Match 100.0%; Score 80; DB 17; Length 28;
Best Local Similarity 100.0%; Pred. No. 2,2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GQVGRQLATIGDDINR 16
   |||||
Db 6 gvgvgrqlaligddinr 21

```

```

RESULT 9
AA079535 ID AA079535 standard; Protein: 117 AA.
XX
XX AC AA079535;
XX
XX 11-JAN-1999 (first entry)

```

```

XX
XX Truncated Bak polypeptide Bak-delta2-TM.
XX
XX DE
XX
XX KW Bak; bak binding protein; BBP; bbbpd-1; bbbpd-2; Bcl-2; apoptosis;
XX
XX KW cell death; cancer; lymphoma; neurodegeneration; heart disease;
XX
XX KW cell proliferation; infection; human; therapy; diagnosis.
XX
XX OS Homo sapiens.
XX
XX PN W09841626-A1.
XX
XX PD 24-SEP-1998.
XX
XX PF 03-MAR-1998; 98WO-US04079.
XX
XX PR 09-JAN-1998; 98US-0071097.
XX
XX PR 20-MAR-1997; 97US-0041328.
XX
XX PA (LXRB-) LXR BIOTECHNOLOGY INC.
XX
XX PI Barr PJ, Fitzpatrick PA, Gibson HL, Kiefer MC;
XX
XX WPI: 1998-521220/44.
XX
XX PT New Bak-binding protein and related nucleic acid, vectors,
XX
XX PT transformed cells and antibodies - are useful for modulation of
XX
XX PT apoptosis in cancer, neuro-degeneration etc., also peptide fragments
XX
XX PT of Bak that interact with the protein
XX
XX PS Example 1; Page 53; 77pp; English.
XX
XX CC This is the amino acid sequence of Bak-delta2-TM, a truncated
XX
XX CC polypeptide comprising amino acids 71-187 of Bak (see AA079533).
XX
XX CC A nucleotide sequence encoding Bak-delta2-TM was obtained from
XX
XX CC cDNA by PCR and cloned as an in-frame fusion to the GAL4 DNA
XX
XX CC binding domain in vector pAS2-1. The construct was used in a
XX
XX CC two-hybrid screen of human heart cDNA for the identification of
XX
XX CC clones encoding Bak binding proteins. The invention relates to a
XX
XX CC novel Bak binding protein (BBP, see AA079537), the gene encoding BBP
XX
XX CC (see AA061499), methods for detecting substances that alter the
XX
XX CC specific binding between Bak and BBP, as well as diagnostic and
XX
XX CC therapeutic methods utilizing BBP.
XX
XX SQ Sequence 117 AA:

```

```

Query Match 100.0%; Score 80; DB 19; Length 117;
Best Local Similarity 100.0%; Pred. No. 1,1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GQVGRQLATIGDDINR 16
   |||||
Db 2 gvgvgrqlaligddinr 17

```

```

RESULT 10
AA077880 ID AA077880 standard; Protein: 141 AA.
XX
XX AC AA077880;
XX
XX 21-NOV-1995 (first entry)
XX
XX DE Human Cdn-1(71-211).
XX
XX KW Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
XX
XX KW autoimmune disease; reperfusion injury; hepatitis; osteoporosis;
XX
XX KW shock; lymphoma; eczema.
XX
XX OS Homo sapiens.
XX
XX PN W09515084-A.

```

PD 08-JUN-1995.
 XX
 XX 30-NOV-1994; 94WO-US13930.
 XX
 XX 07-OCT-1994; 94US-0320157.
 PR 30-NOV-1993; 93US-0160067.
 PA (LXRB-) LXR BIOTECHNOLOGY INC.
 XX
 XX Barr PJ, Kiefer MC;
 DR WPI: 1995-215106/28.
 XX
 XX New nucleic acid sequences encoding Cdn apoptosis modulators - and
 PR related vectors, transformed cells, proteins and antibodies, useful
 PT or diagnosis and treatment e.g. of HIV infection, reperfusion injury
 PT etc.
 XX
 XX Disclosure: Fig.11; 66pp; English.
 XX
 XX Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in
 CC increased cell survival in response to anti-Fas-mediated apoptosis.
 CC Deletion of the N-terminal 70 amino acids of Cdn-1 improved this
 CC activity, suggesting that small, truncated Cdn-1 molecules may be
 CC potent therapeutics.
 CC
 XX Sequence 141 AA:

Query Match 100.0%; Score 80; DB 16; Length 141;
 Best Local Similarity 100.0%; Pred. No. 1.3e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCGGQALAIIGDDINR 16
 DB 2 gqvgqraligddlnr 17

RESULT 11

AA77879 standard; Protein; 152 AA.

XX
 XX AA77879;
 AC
 XX 21-NOV-1995 (first entry)
 DT
 XX Human Cdn-1(60-211).
 DE
 XX Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
 KW autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
 KW shock; lymphoma; eczema.
 XX
 XX Homo sapiens.
 OS
 XX MO9515084-A.
 PN
 XX 08-JUN-1995.
 PD
 XX 30-NOV-1994; 94WO-US13930.
 PF
 XX 07-OCT-1994; 94US-0320157.
 PR 30-NOV-1993; 93US-0160067.
 XX
 XX (LXRB-) LXR BIOTECHNOLOGY INC.
 PA
 XX Barr PJ, Kiefer MC;
 PI
 XX WPI: 1995-215106/28.
 DR
 XX New nucleic acid sequences encoding Cdn apoptosis modulators - and
 PR related vectors, transformed cells, proteins and antibodies, useful
 PT or diagnosis and treatment e.g. of HIV infection, reperfusion injury
 PT etc.

XX
 XX Disclosure: Fig.11; 66pp; English.
 PS
 XX Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in
 CC increased cell survival in response to anti-Fas-mediated apoptosis.
 CC Deletion of the N-terminal 59 amino acids of Cdn-1 only slightly
 CC decreased this activity, suggesting that small, truncated Cdn-1
 CC molecules may be potent therapeutics.
 CC
 XX Sequence 152 AA:

Query Match 100.0%; Score 80; DB 16; Length 152;
 Best Local Similarity 100.0%; Pred. No. 1.5e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GCGGQALAIIGDDINR 16
 DB 13 gqvgqraligddlnr 28

RESULT 12

AA77876 standard; Protein; 211 AA.

XX
 XX AA77876;
 AC
 XX 21-NOV-1995 (first entry)
 DT
 XX Human Cdn-1.
 DE
 XX Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
 KW autoimmune disease; reperfusion injury; hepatitis, osteoporosis;
 KW shock; lymphoma; eczema.
 XX
 XX Homo sapiens.
 OS
 XX MO9515084-A.
 PN
 XX 08-JUN-1995.
 PD
 XX 30-NOV-1994; 94WO-US13930.
 PF
 XX 07-OCT-1994; 94US-0320157.
 PR 30-NOV-1993; 93US-0160067.
 XX
 XX (LXRB-) LXR BIOTECHNOLOGY INC.
 PA
 XX Barr PJ, Kiefer MC;
 PI
 XX WPI: 1995-215106/28.
 DR N-PSDB; AA095492.
 XX
 XX New nucleic acid sequences encoding Cdn apoptosis modulators - and
 PR related vectors, transformed cells, proteins and antibodies, useful
 PT or diagnosis and treatment e.g. of HIV infection, reperfusion injury
 PT etc.
 XX
 XX Disclosure: Fig.3A-B; 66pp; English.
 PS
 XX Cdn-1 cDNA was isolated from a human heart cDNA library using a
 CC previously isolated clone as probe. Recombinant Cdn-1 was produced
 CC in Sf9 and human colon adenocarcinoma HT29 cells. Expression of
 CC Cdn-1 in WI-L2 lymphoblastoid cells resulted in increased cell
 CC survival in response to anti-Fas-mediated apoptosis.
 CC
 XX Sequence 211 AA:

Query Match 100.0%; Score 80; DB 16; Length 211;
 Best Local Similarity 100.0%; Pred. No. 2.1e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 G0VGR0LAIIGDDINR 16
 DB 72 gqvgrrqaligddlnr 87

RESULT 13

AA077877
 ID AAR77877 standard; Protein: 211 AA.

AA077877;

AC 21-NOV-1995 (first entry)

DT Human Cdn-2.

XX Cdn-2; apoptosis modulator; adoptive immunotherapy; therapy; HIV;

XX autoimmune disease; reperfusion injury; hepatitis; osteoporosis;

XX shock; lymphoma; eczema.

XX Homo sapiens.

XX W09515084-A.

XX 08-JUN-1995.

XX 30-NOV-1994; 94MO-US13930.

XX 07-OCT-1994; 94US-0320157.

XX 30-NOV-1993; 93US-0160067.

XX (LXRB-) LXR BIOTECHNOLOGY INC.

XX Barr PJ, Kiefer MC;

XX WPI: 1995-215106/28.

XX N-PSDB; AA093493.

XX New nucleic acid sequences encoding Cdn apoptosis modulators - and

XX related vectors; transformed cells; proteins and antibodies; useful

XX or diagnosis and treatment e.g. of HIV infection; reperfusion injury

XX etc.

XX Disclosure: Fig 5D-E; 66pp; English.

XX Sequence 211 AA;

Query Match 100.0%; Score 80; DB 16; Length 211;

Best Local Similarity 100.0%; Pred. No. 2,1e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 G0VGR0LAIIGDDINR 16
 DB 72 gqvgrrqaligddlnr 87

RESULT 14

AA003668
 ID AA003668 standard; Protein: 211 AA.

AA003668;

XX 22-FEB-1997 (first entry)

XX Bak protein.

XX Human; Bak; apoptosis; latency; virus replication;

KW Epstein-Barr virus; BHRF1; fusion protein; epitope tag;

KW drug screening; co-precipitation; ELISA; immunoassay; antibody;

XX protein interaction; trapping; virucide; antitumour; diagnostic.

XX Homo sapiens.

XX W09633416-A1.

XX 24-OCT-1996.

XX 19-APR-1996; 96MO-US05639.

XX 20-APR-1995; 95US-0426529.

XX (LXRB-) LXR BIOTECHNOLOGY INC.

XX Barr PJ, Kiefer MC;

XX WPI: 1996-48586/48.

XX N-PSDB; AAT42138.

XX Screening for anti-viral agents - by detecting the ability of an

XX agent to disrupt the interaction of a Bak protein and a viral

XX protein

XX Disclosure; Fig 1; 24pp; English.

XX This Bak protein sequence represents a bcl-1 homologue which

XX interacts with Epstein-Barr virus (EBV) early lytic cycle BHRF1

XX protein, and is capable of modulating apoptosis. The protein may

XX be used in complete or partial form, or as an epitope tag fusion

XX protein, in a new virucide drug screening method, which involves

XX combination of Bak protein and a viral protein (e.g. EBV BHRF1),

XX exposure to a test compound, and monitoring for disruption of the

XX interaction, e.g. by co-precipitation, protein interaction trapping

XX or ELISA. Interaction of Bak and viral proteins allows viral

XX replication or latency in the absence of apoptosis. Compounds which

XX inhibit the interaction may be used as virucide, antitumour or

XX diagnostic agents.

XX Sequence 211 AA;

Query Match 100.0%; Score 80; DB 17; Length 211;

Best Local Similarity 100.0%; Pred. No. 2,1e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 G0VGR0LAIIGDDINR 16
 DB 72 gqvgrrqaligddlnr 87

RESULT 15

AA003669
 ID AA003669 standard; Protein: 211 AA.

AA003669;

XX 22-FEB-1997 (first entry)

XX Bak-2 protein.

XX Human; Bak-2; apoptosis; latency; virus replication;

XX Epstein-Barr virus; BHRF1; fusion protein; epitope tag;

XX drug screening; co-precipitation; ELISA; immunoassay; antibody;

XX protein interaction; trapping; virucide; antitumour; diagnostic.

XX Homo sapiens.

XX W09633416-A1.

XX 24-OCT-1996.

PF 19-APR-1996; 96WO-US05639.
 XX
 PR 20-APR-1995; 95US-0426529.
 XX
 PA (LXRB-) LXR BIOTECHNOLOGY INC.
 XX
 PI Barr PJ, Kiefer MC;
 XX
 XX WPI: 1996-48586/48.
 DR N-PSDB; AA742139.
 XX
 PT Screening for anti-viral agents - by detecting the ability of an
 PT agent to disrupt the interaction of a Bak protein and a viral
 PT protein
 PS Disclosure: Fig 2: 24pp; English.
 XX
 CC This Bak-2 protein sequence represents a bcl-1 homologue which
 CC interacts with Epstein-Barr virus (EBV) early lytic cycle BHRT
 CC protein, and is capable of modulating peptidase. The protein may
 CC be used in complete or partial form as a screening method which involves
 CC protein in complete or partial form as a screening method which involves
 CC comparison of Bak-2 protein and a viral protein (e.g. EBV BHRT),
 CC exposure to a test compound, and monitoring for disruption of the
 CC interaction, e.g. by co-precipitation, protein interaction trapping
 CC or ELISA. Interaction of Bak-2 and viral proteins allows viral
 CC replication or latency in the absence of apoptosis. Compounds which
 CC inhibit the interaction may be used as virucide, antitumor or
 CC diagnostic agents.
 XX
 SQ Sequence 211 AA:

Query Match 100.0%; Score 80; DB 17; Length 211;
 Best Local Similarity 100.0%; Pred. No. 2, 1e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GOVGRQATIGDDINR 16
 ||||||||||||
 DB 72 GGVGRQATIGDDINR 87

Search completed: September 20, 2002, 10:35:58
 Job time: 426 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Comugen Ltd.

OM protein - protein search, using SW model

Run on: September 20, 2002, 10:37:20 : Search time 75.64 seconds
(without alignments)
5.167 Million cell updates/sec

Title: US-09-544-664-30

Sequence: 1 GOVROLATIGDDINR 16

Scoring table: BLOSUM62

Gapop 10.0 , Capext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued-Patents_AA:*
1: /cgn2.6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2.6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2.6/ptodata/2/1aa/5A.COMB.pep:*
4: /cgn2.6/ptodata/2/1aa/5B.COMB.pep:*
5: /cgn2.6/ptodata/2/1aa/PCOTUS.COMB.pep:*
6: /cgn2.6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	80	100.0	19	4	US-09-236-385A-35
2	80	100.0	20	4	US-09-236-385A-36
3	80	100.0	28	1	US-08-440-391-2
4	80	100.0	28	1	US-08-440-391-18
5	80	100.0	28	2	US-08-908-597A-2
6	80	100.0	28	2	US-08-908-597A-18
7	80	100.0	28	4	US-09-236-385A-2
8	80	100.0	28	4	US-09-236-385A-18
9	80	100.0	28	5	PCT-US96-06122-2
10	80	100.0	28	5	PCT-US96-06122-18
11	80	100.0	36	1	US-08-440-391-14
12	80	100.0	36	2	US-08-908-597A-14
13	80	100.0	36	4	US-09-236-385A-14
14	80	100.0	36	5	PCT-US96-06122-14
15	80	100.0	141	1	US-08-471-058-23
16	80	100.0	152	1	US-08-471-058-22
17	80	100.0	210	3	US-08-471-057-22
18	80	100.0	211	1	US-08-321-071A-16
19	80	100.0	211	1	US-08-471-058-7
20	80	100.0	211	1	US-08-471-058-9
21	80	100.0	211	1	US-08-471-058-10
22	80	100.0	211	1	US-08-471-058-11
23	80	100.0	211	2	US-08-944-530-4
24	80	100.0	211	2	US-08-944-530-2
25	80	100.0	211	3	US-08-471-057-9
26	80	100.0	211	3	US-08-471-057-7
27	80	100.0	211	3	US-08-471-057-10

28	80	100.0	211	3	US-08-471-057-11	Sequence 11, Appl
29	74	92.5	15	4	US-09-236-385A-37	Sequence 37, Appl
30	74	92.5	31	1	US-08-440-391-3	Sequence 3, Appl
31	74	92.5	31	1	US-08-440-391-16	Sequence 16, Appl
32	74	92.5	31	2	US-08-908-597A-3	Sequence 3, Appl
33	74	92.5	31	2	US-08-908-597A-16	Sequence 16, Appl
34	74	92.5	31	4	US-09-236-385A-16	Sequence 16, Appl
35	74	92.5	31	4	US-09-236-385A-38	Sequence 38, Appl
36	74	92.5	31	5	PCT-US96-06122-3	Sequence 3, Appl
37	74	92.5	31	5	PCT-US96-06122-16	Sequence 16, Appl
38	69	86.2	15	1	US-08-440-391-10	Sequence 10, Appl
39	69	86.2	15	2	US-08-908-597A-10	Sequence 10, Appl
40	69	86.2	15	2	US-08-908-597A-20	Sequence 20, Appl
41	69	86.2	15	4	US-09-236-385A-10	Sequence 10, Appl
42	69	86.2	15	4	US-09-236-385A-20	Sequence 20, Appl
43	69	86.2	15	4	US-09-236-385A-38	Sequence 38, Appl
44	69	86.2	15	4	US-09-236-385A-30	Sequence 30, Appl
45	69	86.2	15	5	PCT-US96-06122-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-236-385A-35
Sequence 35, Appl location US/09236385A
Patent No. 6221615
GENERAL INFORMATION:
APPLICANT: CHITENDEN, Thomas D.; and
LUTE, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESS: Pale and Dorr
Street 1455 Pennsylvania Avenue, N.M.
City: Albuquerque
State: N.M.
ZIP: 87104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/236,385A
FILING DATE: 25-Jan-1999
CLASSIFICATION: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
TELECOMMUNICATION INFORMATION:
(C) ATTORNEY DOCKERY NO. 104322.147CIP
TELEPHONE: 202-942-8400
FAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-236-385A-35
Query Match 100.0%; Score 80; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 3; be-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
OY 1 GOVROLATIGDDINR 16
DB 2 GOVROLATIGDDINR 17

RESULT 2
US-09-236-385A-36
Sequence 36, Application US/09236385A
Patent No. 6221615
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
LUTZ, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/236.385A
FILING DATE: 25-Jan-1999
CLASSIFICATION: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: MAXON, HENRY N.
REGISTRATION NUMBER: 32.073
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 36
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: Linear
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 36
US-09-236-385A-36

Query Match 100.0%; Score 80; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCGGROLAITGDDINR 16
|||||

DB 3 GCGGROLAITGDDINR 18

RESULT 3
US-08-440-391-2
Sequence 2, Application US/08440391
Patent No. 5656725
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
LUTZ, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

US-08-440-391-2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440.391
FILING DATE: 12-MAY-1999
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32.073
REFERENCE/DOCKET NUMBER: 104322.147
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acid
TYPE: amino acid
TOPOLOGY: Linear
MOLECULE TYPE: Peptide
US-08-440-391-2

Query Match 100.0%; Score 80; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.7e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCGGROLAITGDDINR 16
|||||

DB 6 GCGGROLAITGDDINR 21

RESULT 4
US-08-440-391-18
Sequence 18, Application US/08440391
Patent No. 5656725
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
LUTZ, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440.391
FILING DATE: 12-MAY-1999
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32.073
REFERENCE/DOCKET NUMBER: 104322.147
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: Linear
MOLECULE TYPE: Peptide
US-08-440-391-18

Query Match 100.0%; Score 80; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.7e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

LENGTH: 28 amino acid
 TYPE: AMINO ACID
 TOPOLOGY: 1 linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-236-385A-2

Query Match 100.0%; Score 80; DB 4; Length 28;
 Best Local Similarity 100.0%; Pred. No. 5.7e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCGVQALATIGDDINR 16
 DB 6 GCGVQALATIGDDINR 21

RESULT 8
 US-09-236-385A-18
 Sequence 18, Application US/09236385A
 Patent No. 6221615

GENERAL INFORMATION:

APPLICANT: CUYER, THOMAS D.; and
 LITZ, ROBERT J.

TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
 MODULATE APOPTOSIS

NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hale and Dorr
 STREET: 1455 Pennsylvania Avenue, N.W.
 CITY: Washington
 STATE: D.C.
 ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/236.385A
 FILING DATE: 25-Jan-1999

CLASSIFICATION: <UNKNOWN>

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 32,073

TELECOMMUNICATION INFORMATION: (C) ATTORNEY DOCKET NO. 104322.147CIP

TELEPHONE: 202-942-8400

TELEFAX: 202-942-8484

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 28 amino acids

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Query Match 100.0%; Score 80; DB 4; Length 28;
 Best Local Similarity 100.0%; Pred. No. 5.7e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCGVQALATIGDDINR 16
 DB 6 GCGVQALATIGDDINR 21

RESULT 9
 PCT-US96-06122-2
 Sequence 2, Application PC/TUS9606122
 GENERAL INFORMATION:
 APPLICANT: IMMUNOGEN, INC.

TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS
 WHICH MODULATE APOPTOSIS

ADDRESSEE: Hale and Dorr
 STREET: 1455 Pennsylvania Avenue, N.W.
 CITY: Washington
 STATE: D.C.
 ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/06122

FILING DATE: HEREWITH

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/440,391

FILING DATE: 12-MAY-1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 32,073

REFERENCE/DOCKET NUMBER: 104322.147PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-942-8484

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 28 amino acid

MOLECULE TYPE: peptide

PCT-US96-06122-2

Query Match 100.0%; Score 80; DB 5; Length 28;
 Best Local Similarity 100.0%; Pred. No. 5.7e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCGVQALATIGDDINR 16
 DB 6 GCGVQALATIGDDINR 21

RESULT 10
 PCT-US96-06122-18
 Sequence 18, Application PC/TUS9606122

GENERAL INFORMATION:

APPLICANT: IMMUNOGEN, INC.

TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS
 WHICH MODULATE APOPTOSIS

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hale and Dorr
 STREET: 1455 Pennsylvania Avenue, N.W.
 CITY: Washington
 STATE: D.C.
 ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/06122

FILING DATE: HEREWITH

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/440,391

FILING DATE: 12-MAY-1995

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.147PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US96-06122-18

Query Match 100.0%; Score 80; DB 5; Length 28;
Best Local Similarity 100.0%; Pred. No. 5,7e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 G0VGR0LATIIGDDINR 16
DB 6 G0VGR0LATIIGDDINR 21

RESULT 11
US-08-440-391-14
Sequence 14, Application US/08440391
Patent No. 5656725
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
APPLICANT: LUTZ, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,391
FILING DATE: 12-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.147
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-440-391-14

Query Match 100.0%; Score 80; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 7,6e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 G0VGR0LATIIGDDINR 16
DB 6 G0VGR0LATIIGDDINR 21

DB 8 G0VGR0LATIIGDDINR 23

RESULT 12
US-08-908-597A-14
Sequence 14, Application US/08908597A
Patent No. 5653795
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
APPLICANT: LUTZ, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/908,597A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/440,391
FILING DATE: 12-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.147
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 36
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-908-597A-14

Query Match 100.0%; Score 80; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 7,6e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 G0VGR0LATIIGDDINR 16
DB 8 G0VGR0LATIIGDDINR 23

RESULT 13
US-09-236-385A-14
Sequence 14, Application US/09236385A
Patent No. 6221615
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
APPLICANT: LUTZ, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/236,385A
FILING DATE: 25-Jan-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
(C) ATTORNEY DOCKET NO. 104322.147CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-236-385A-14

Query Match 100.0%; Score 80; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 7.6e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GOVROLATIGDDINR 16
|||||
DB 8 GOVROLATIGDDINR 23

RESULT 14
PCT-US96-06122-14
Sequence 14, Application PC/TUS9606122
GENERAL INFORMATION:
APPLICANT: IMMUNOGEN, INC.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS
TITLE OF INVENTION: WHICH MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06122
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/440,391
FILING DATE: 12-MAY-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.147PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide
PCT-US96-06122-14

Query Match 100.0%; Score 80; DB 5; Length 36;
Best Local Similarity 100.0%; Pred. No. 7.6e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GOVROLATIGDDINR 16
|||||
DB 8 GOVROLATIGDDINR 23

RESULT 15
US-08-471-058-23
Sequence 23, Application US/08471058
Patent No. 5770443
GENERAL INFORMATION:
APPLICANT: Kiefer, Michael C.
APPLICANT: Barr, Philip J.
TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING
TITLE OF INVENTION: PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,058
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/220,157
FILING DATE: 07-SEP-1994
APPLICATION NUMBER: 08/160,067
FILING DATE: 30-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lehmardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20007.12
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-471-058-23

Query Match 100.0%; Score 80; DB 1; Length 141;
Best Local Similarity 100.0%; Pred. No. 3.8e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GOVROLATIGDDINR 16
|||||
DB 2 GOVROLATIGDDINR 17

Search completed: September 20, 2002, 10:37:21

Job time: 409 sec

us-09-544-664-30.ra1

A:Residues: 1-834 <HAV>
 A:Cross-references: GB:BA000007; PTD:BA033960.1; PTD:G1335994; GSPDB:GN00154
 A:Experimental source: strain 0157:H7, substrain RMD 050952
 C:Genetics:
 A:Gene: EC05057
 C:Superfamily: Bacillus probable copper-transporting ATPase yv9X; ATPase nucleotide-bind

Query Match 57.5%; Score 46; DB 2; Length 834;
 Best Local Similarity 66.7%; Pred. No. 11;
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 4 GROLAIGDDIN 15
 |||:::|||||
 Db 712 GROVAVMGDGIN 723

RESULT 7

probable ATPase ybar [imported] - Escherichia coli (strain 0157:H7, substrain EDL933)
 C:Species: Escherichia coli
 C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
 C:Accession: B85546
 R:Perlmutter, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 Miller, L.; Grochbeck, E.J.; Davis, N.W.; Linn, A.; Dimmlante, E.; Potamowski, K.; Apodaca,
 Nature 409 529-533, 2001
 A>Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
 A:Reference number: AB54460; MUID:21074935; PMID:11206551
 A:Accession: B85546
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-834 <GNG>
 A:Cross-references: GB:AE0005174; NID:G12513357; PTD:AA054833.1; GSPDB:GN00145; UWGP:206
 A:Experimental source: strain 0157:H7, substrain EDL933
 C:Genetics:
 A:Gene: ybar
 C:Superfamily: Bacillus probable copper-transporting ATPase yv9X; ATPase nucleotide-bind

Query Match 57.5%; Score 46; DB 2; Length 834;
 Best Local Similarity 66.7%; Pred. No. 11;
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 4 GROLAIGDDIN 15
 |||:::|||||
 Db 712 GROVAVMGDGIN 723

RESULT 8

cation transport ATPase, E1-E2 family VC2215 [imported] - Vibrio cholerae (strain N16961)
 C:Species: Vibrio cholerae
 C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
 C:Accession: H82104
 R:Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gilm, M.L.; Dodson, R.J.;
 Charlson, D.; Ermolenko, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoti, I.; Sellers, F.
 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A>Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A:Reference number: AB2035; MUID:20406833
 A:Accession: H82104
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-915 <HEIR>
 A:Cross-references: GB:AF004293; GB:AE003852; NID:G9656766; PTD:AAF95359.1; GSPDB:GN001
 A:Experimental source: serogroup O1, strain N16961; biotype El Tor
 C:Genetics:
 A:Gene: VC2215
 A:Map position: 1
 C:Superfamily: Bacillus probable copper-transporting ATPase yv9X; ATPase nucleotide-bind

Query Match 57.5%; Score 46; DB 2; Length 915;

Best Local Similarity 64.3%; Pred. No. 12;
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 OY 2 OVRGOLAIIGDDIN 15
 |||:::|||||
 Db 786 OQGRKAVMIGDGIN 799

RESULT 9

S44824
 F54F2.1 protein - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 23-Mar-2001
 C:Accession: S44824
 R:Anderson, K.
 submitted to the EMBL Data Library, September 1993
 A:Description: Sequence of the C. elegans cosmid F54F2.
 A:Reference number: S44817
 A:Accession: S44824
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1226 <AND>
 A:Cross-references: EMBL:L23645; NID:G388603; PTD:G388605
 C:Genetics:
 A:Insertions: 58/2; 137/3; 179/1; 316/2; 393/1; 551/3; 597/2; 662/2; 899/3; 1178/3
 C:Keywords: cytoskeleton; transmembrane protein

Query Match 57.5%; Score 46; DB 2; Length 1226;
 Best Local Similarity 53.8%; Pred. No. 17;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 GOVRGOLAIIGDDIN 13
 |||:::|||||
 Db 359 GVRGKQAVMGDGD 371

RESULT 10

S58684
 phosphopyruvate hydratase (EC 4.2.1.11) - Helicobacter pylori (strains 26695 and other
 N:Alternative names: enolase
 C:Species: Helicobacter pylori
 C>Date: 29-Nov-1995 #sequence_revision 17-Sep-1997 #text_change 22-Jun-1999
 C:Accession: B64539; S58684
 R:Tom, J.F.; White, O.; Kerlavage, A.R.; Sutton, R.A.; Gilm, G.G.; Fleischmann, R.
 Peterson, S.; Loftus, B.; Richardson, P.; Dodson, R.; Khakhria, H.G.; Glodek, A.; McKe
 son, J.D.; Kelley, J.M.; Cotton, M.D.; Weisman, J.M.; Fujii, C.; Bowman, C.; Wathey,
 Nature 388, 539-547, 1997
 A:Authors: Wallin, E.; Hayes, W.S.; Bordovsky, M.; Karik, P.D.; Smith, H.O.; Fraser,
 A>Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
 A:Reference number: B64520; MUID:97394467
 A:Accession: B64539
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-426 <GNG>
 A:Cross-references: GB:AE000536; GB:AE000511; NID:G2313330; PTD:AA007219.1; PTD:G231
 A:Experimental source: strain 26695
 R:Schmitt, W.; Odenbreit, S.; Heuvelink, D.; Haas, R.
 Mol. Gen. Genet. 248, 563-572, 1995
 A>Title: Cloning of the Helicobacter pylori recA gene and functional characterization
 A:Reference number: S58683; MUID:9602928
 A:Accession: S58684
 A:Molecule type: DNA
 A:Residues: 1-25, 1, 27-68 <SGCH>
 A:Cross-references: EMBL:Z35478
 C:Genetics:
 A:Gene: HP0154
 A:Function:
 A:Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to P
 A:Pathway: glycolysis
 C:Superfamily: enolase
 C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; magnesium
 F.42/Binding site: magnesium 2 (ser) #status predicted

F:205,338/Active site: Glu, Lys #status predicted
F:242,286,313/Binding site: magnesium 1 (asp, Glu, Asp) #status predicted

Query Match 56.2%; Score 45; DB 2; Length 426;
Best Local Similarity 46.2%; Pred. No. 7.9;
Matches 6; Conservative 1; Indels 0; Gaps 0;

OY 2 OVGROLAITGDDINR 14
DB 303 ELGROQLATGVDL 315

RESULT 11
H71967
enolase - Helicobacter pylori (strain 399)

C:Species: Helicobacter pylori
A:Variety: strain 399
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 22-Jun-1999
C:Accession: H71967
R:Alm, R.A.; Ling, L.S.L.; Molr, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Miller, S.D.; Jiang, O.; Taylor, D.E.; Voyts, G.F.; Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; MUID:99120557
A:Accession: H71967
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-426 <RAN>
A:Cross-references: GB:AE001453; GB:AE001439; NID:94154651; PIDN:RAD05723.1; PID:9415465
A:Experimental source: strain 399
C:Genetics:
A:Gene: eno
C:Superfamily: enolase

Query Match 56.2%; Score 45; DB 2; Length 426;
Best Local Similarity 46.2%; Pred. No. 7.9;
Matches 6; Conservative 1; Indels 0; Gaps 0;

OY 2 OVGROLAITGDDINR 14
DB 303 ELGROQLATGVDL 315

RESULT 12

H75027
ay v-epsase proteolipid PAB1189 - Pyrococcus abyssi (strain Orsay)

C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C:Accession: H75027
R:anonymous, Genoscope

A:Description: Pyrococcus abyssi genome sequence: Insights into archaeal chromosome stru

A:Reference number: A75001
A:Accession: H75027
A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-258 <RAN>
A:Cross-references: GB:AJ248288; GB:AL096836; NID:94545960; PIDN:CAD50662.1; PID:9451656

A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB1189

Query Match 55.0%; Score 44; DB 2; Length 258;
Best Local Similarity 43.8%; Pred. No. 6.7;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 1 GOVGROLATIGDDINR 16
DB 122 GEAGRGFAVADDIR 137

RESULT 13
B71213
probable chemoreceptor protein - Pyrococcus horikoshii

C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1999 #sequence_revision 14-Aug-1999 #text_change 21-Jul-2000
C:Accession: B71213
R:Kawarayashi, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Se
M.; Ohfuku, Y.; Punahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kusida, N.; Ogu
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophil
A:Reference number: A71000; MUID:98344137
A:Accession: B71213
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-261 <RAN>
A:Cross-references: GB:AP000007; NID:93236134; PIDN:BAA31097.1; PID:93258414
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by Genba
C:Genetics:
A:Gene: PH1970

Query Match 55.0%; Score 44; DB 2; Length 261;
Best Local Similarity 43.8%; Pred. No. 6.8;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 1 GOVGROLATIGDDINR 16
DB 125 GEAGRGFAVADDIR 140

RESULT 14

S75352
ABC-type transport protein sir2019 - Synechocystis sp. (strain PCC 6803)

C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 02-Feb-2001

C:Accession: S75352
R:Raneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asanizu, E.; Nakamura, Y.; Miyajima,

O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys

S.
A:Reference number: S74322; MUID:97061201
A:Accession: S75352

A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

A:Residues: 1-593 <RAN>
A:Cross-references: EMBL:090904; GB:AB001339; NID:91652225; PIDN:BAA17266.1; PID:9165

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Genetics:
A:Start codon: GTG

A:Superfamily: Escherichia coli ABC transporter mdaA; ATP-binding cassette homology

C:Reference: ATP, nucleotide binding P-loop, transport protein
F:16560/Domain: ATP-binding cassette homology (ABC)

F:83-390/Region: nucleotide-binding motif A (P-loop)

Query Match 55.0%; Score 44; DB 2; Length 593;
Best Local Similarity 61.5%; Pred. No. 17;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 4 GROLATIGDDINR 16
DB 128 GRUMLNDNDINQ 140

RESULT 15

G82618
plus biogenesis protein xrl953 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd

OM protein - protein search, using sw model

Run on: September 20, 2002, 11:04:32 ; Search time 44.99 Seconds

Title: US-09-544-664-30

Sequence: 1 GQVGRQLAIGDDINR 16

Scoring table: BLOSUM62

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
84

1. The first step is to identify the problem or question that needs to be answered. This involves understanding the context and the specific requirements of the task.

1. *Chlorophyll a* (Chl *a*)

Maximum DB seq length: 200000000000

Post-processing: Minimum Match 0%

Listing first 45

Database : SwissProt_40:*

Pred. No. is the number of

and is derived by analysis

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Query Match	Length	DB	ID	Description
1	80	100.0	211	1	BK2_HUMAN	Q0104 home sapien
1	80	100.0	211	1	BK2_HUMAN	Q0611 home sapien
2	78	97.5	208	1	BK1_MOUSE	Q08734 mus musculu
3	46	57.5	834	1	ATCCU_ECOLI	O59985 escherichia
4	46	57.5	1226	1	PAT2_CAEEL	P4446 caenorhabdit
5	46	56.2	426	1	ENO_HELPJ	O92946 helicobacter
6	45	56.2	426	1	ENO_HELPJ	P48285 helicobacter
7	44	55.0	803	1	ATCCU_BCG50	Q03220 bacillus su
8	44	55.0	803	1	ATCCU_BCG50	P41134 sphingomonas
9	43.5	54.4	512	1	CERT_LAFER	Q04282 lycopodium
10	43	53.8	444	1	ENO2_HAZE	P42895 lycopodium
11	43	53.8	446	1	ENO_ORSEA	Q042871 oryza sativa
12	43	53.8	770	1	YRNG_CAEEL	O06069 caenorhabdit
13	43	53.8	827	1	ATCC2_RHIME	P68342 rhabdolum n
14	43	53.8	827	1	ATCC2_RHIME	P68343 rhabdolum n
15	43	53.8	827	1	ATC1_RHIME	P68344 rhabdolum n
16	42	52.5	826	1	YX55_THERA	O08354 treponema f
17	41	51.2	761	1	CER1_MESNU	P56520 mesocricetu
18	41	51.2	659	1	ENO1_PERSU	P42357 pseudomona
19	41	51.2	582	1	PILI1_PERSU	O54478 caulobacter
20	41	51.2	759	1	PARG_CADUR	Q92444 staphylococ
21	41	51.2	263	1	YLMO_STAVU	O59605 pyrococcus
22	40	50.0	446	1	ENO_PYHMO	P26501 zea mays (t
23	40	50.0	446	1	ENO1_MAZE	P45544 ementiaella
24	40	50.0	4344	1	DYHC_EMBNT	P47816 fusicarin so
25	40	50.0	4349	1	DYHC_EMBNT	P47816 fusicarin so
26	39	48.8	4124	1	VAF2_CHOMP	O06141 dirosophila
27	39	48.8	211	1	CRB3_CHICK	P55165 gallus gallu
28	39	48.8	351	1	ICDP_CACOR	O59260 caulobacter
29	39	48.8	428	1	ENO_PYABA	O92420 pyrococcus
30	39	48.8	429	1	ENO_PYABA	P42848 thermotoga
31	39	48.8	433	1	ENO_THICH	O63655 vibrio chro

ALIGNMENTS

RESULT	1	STANDARD:	FRY: 211 AA.
ID	BAK2_HUMAN		
AC	015014		
DT	01-NOV-1997 (REL 35, Created)		
DR	01-NOV-1997 (REL 35, last sequence update)		
DE	16-OCT-2001 (REL 40, last annotation update)		
DT	Bcl-2 homologous antiapoptosis/xliller 2 (Apoptosis regulator BAK-2).		
GN	BCL2L2P1 OR BAK2.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OX	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
NC	NCBI_Taxid=9606;		
LN	SEQUENCE FROM N. A.		
FX	Medline=95231654; Pubmed=7715731;		
RA	Kiefer M.C., Brauer M.J., Powers V.C., Wu J.J., Unanue S.R.,		
RT	Toncl L.D., Barr P.J.;		
FT	"Modulation of apoptosis by the widely distributed Bcl-2 homologue		
RT	BAK-1."		
RL	Nature 374:736-739(1995).		
RE	-1- FUNCTION: IN THE PRESENCE OF AN APPROPRIATE STIMULUS, ACCELERATES		
CC	THE RATE OF CELL DEATH BY INDUCING TO UNWINDING AND DISINTEGRATING THE A		
CC	REPRESSOR BCL-2 OR ITS ANOGENOUS HOMOLOG ELB 19K PROTEIN.		
CC	-1- SUBUNIT: FORMS HETERODIMERS WITH BCL-2, ELB 19K PROTEIN, AND BCL-		
CC	XL1).		
CC	-1- SUBCELLULAR LOCATION: Membrane-associated (potential).		
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES, WITH		
CC	HIGHEST LEVELS IN THE HEART AND SKELETAL MUSCLE.		
CC	-1- DOMAIN: IMPACT BHO-ADAPTOIC ACTIVITY AND FOR THEIR INTERACTION		
CC	BAK FOR THEIR BHO-ADAPTOIC ACTIVITY AND FOR THEIR INTERACTION		
CC	ADAPTOIC MEMBERS OF THE BCL-2 FAMILY.		
CC	-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).		
CC	-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).		
CC	-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).		
CC	-1- CAUTION: THIS COULD BE THE PRODUCT OF A PSEDOGENE.		
CC	-1- THIS SWISS-PROT entry is copied from the EMBL database through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation.		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (See http://www.isb-sib.ch/announcements ,		
CC	or send an email to license@isb-sib.ch).		
CC	EMBL: U16012; AAA44467.1; -		
DR	ENSEMBL: ENSB01IP0001245; BCL2 family.		
DR	Interpro: ipr0001712; BCL-2.		
DR	Pfam: PF00453; Bcl-2; 1.		
DR	SMART: SM00337; BCL-1.		
DR	PROSITE: PS01080; BH1; 1.		
DR	PROSITE: PS01258; BH2; 1.		
DR	PROSITE: PS01259; BH3; 1.		

```

DR PROSITE: P550062; NC12 FAMILY; 1.
KW Apoptosis: Transmembrane.
FT DOMAIN 74 88 BH3.
FT DOMAIN 117 136 BH1.
FT DOMAIN 169 184 BH2.
FT TRANSMEM 188 205
SO SEQUENCE 211 AA; 23411 MW; 7038756CDCCCD3 CRC64;

Query Match 100.0%; Score 80; DB 1; Length 211;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGVQGLATIGDDINR 16
DB 72 GCGVQGLATIGDDINR 87

RESULT 2
BAK_HUMAN STANDARD: PRT; 211 AA.
AC Q16611; 092533;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Bcl-2 homologous antagonist/killer (Apoptosis regulator BAK).
CN BAK1 OR BAK2
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
CX NCBI_ProtID=9506;
NM 11
NM SEQUENCE FROM N.A.
NM MEDLINE:95231652;
RX FARROW S.N., WHITE J.H.M., MORTILLO I., RAYEN T., PUN K.-T.,
RA GRUBMAN C.J., MARLINO J.C., BROWN R.;
RT "Cloning of a Bcl-2 homologue by interaction with adenovirus E1B
RT 19K."
RL Nature 374:731-733(1995).
RM 21
RM SEQUENCE FROM N.A.
RM MEDLINE:95231653;
RX CHILTINGER T., HARRINGTON E.A., O'CONNOR R., FLEMINGTON C., LUTZ R.J.,
RA EVAN G.I., GUILD B.C.;
RT "Induction of apoptosis by the Bcl-2 homologue BAK."
RL Nature 374:733-736(1995).
RM 31
RM SEQUENCE FROM N.A.
RM MEDLINE:95231654;
RX TONER J.D., CHAIKIN K.J., FOWERS V.C., WU J.J., UMANSKY S.R.,
RA TONER J.D., BART P.J.;
RT "Modulation of apoptosis by the widely distributed Bcl-2 homologue
RT BAK."
RL Nature 374:736-739(1995).
RM 41
RM SEQUENCE FROM N.A.
RM WILLIAMS S.;
RM Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RM 15
RM SEQUENCE OF 96-206 FROM N.A.
RM Eguich J.H., HAYASHI S.;
RM Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RM 61
RM MUTAGENESIS, AND FUNCTION OF BH3 DOMAIN.
RM MEDLINE:96091131; PubMed=8521816;
RX CHILTINGER T., FLEMINGTON C., Houghton A.B., EBB R.G., GALLO G.J.,
RA Houghton A.B., CHILTINGER C., LUTZ R.J.;
RT "Analysis of the BH3 domain of BAK, a distinct Bcl-2 family
RT death and protein binding functions."
RL EMBO J. 14:5589-5596(1995).
RM 17
RM STRUCTURE BY NMR OF 72-87.

```

```

RX MEDLINE:97172567; PubMed=9020082;
RA Sattler M., Liang H., Nettlesheim D., Meadows R.P., Harlan J.E.,
RA Ersfeld M., Yoon H.S., Shaker S.B., Chang B.S., Munn A.J.;
RA Thompson C.B., Feak S.W.;
RT "Structure of Bcl-xL-bak peptide complex: recognition between
RT regulators of apoptosis."
RL Science 275:963-966(1997).
RM 11
RM PROGRAM: CELL DEATH BY BINDING TO AND ANTAGONIZING THE
CC REPRESSOR BCL-2 OR ITS ADENOVIRUS HOMOLOG E1B 19K PROTEIN.
CC -1- SUBUNIT: FORMS HETERODIMERS WITH BCL-2, E1B 19K PROTEIN, AND BCL-
CC X(L).
CC -1- SUBCELLULAR LOCATION: Membrane-bound (potential).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES, WITH
CC HIGHEST LEVELS IN THE HEART AND SKELETAL MUSCLE.
CC -1- DOMAIN: INTRIC BH3 DOMAIN IS REQUIRED IN BCL, BID, BAX, BAD AND
CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC -1- APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 1 (BH1).
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 2 (BH2).
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC THIS SMIS-PRO entry is copyright. It is produced through collaboration
CC with the National Cancer Institute and the European Bioinformatics
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: A64213; CAA3997.1;
DR EMBL: A64213; CAA3997.1;
DR EMBL: U16811; AA174466.1;
DR EMBL: 293017; CAA65526.1;
DR EMBL: D88397; BAA13606.1;
DR EMBL: D88396; BAA13606.1; JOINED.
DR PDB: 1BX1; 29-OCT-97.
DR MTM: 600516;
DR InterPro: IPR007475; BCL2_Family.
DR Pfam: PF00452; BCL2.
DR SMART: SMR0337; BCL2.1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: P550062; BCL2_FAMILY; 1.
KW Apoptosis; Transmembrane; 3D-structure.
FT DOMAIN 114 88 BH1.
FT DOMAIN 117 136 BH2.
FT DOMAIN 169 184 BH3.
FT TRANSMEM 188 205
SO SEQUENCE 211 AA; 23409 MW; A220DFE72A6D04E CRC64;

Query Match 100.0%; Score 80; DB 1; Length 211;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGVQGLATIGDDINR 16
DB 72 GCGVQGLATIGDDINR 87

RESULT 3
BAK_MOUSE STANDARD: PRT; 208 AA.
AC BAK_MOUSE
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Bcl-2 homologous antagonist/killer (Apoptosis regulator BAK)

```

GN BAK1 OR BAK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 RX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SWISS; TISSUE=Liver;
 RX MEDLINE=9744618; PubMed=9299236;
 RA Ullrich E., Kaufman-Zeh A., Hueber A.O., Williamson J.,
 RA Chittenden T., Ma A., Evan G.I.;
 RT 'Gene structure, cDNA sequence, and expression of murine Bak, a
 RT proapoptotic Bcl-2 family member.';
 RL Genomics 44:195-200(1997).
 CC -1- FUNCTION: IN THE PRESENCE OF AN APPROPRIATE STIMULUS, ACCELERATES
 CC PROGRAMED CELL DEATH BY BINDING TO, AND ANTAGONIZING THE A
 CC REPRESSOR BCL-2 OR ITS ADENOVIRUS HOMOLOG E1B 19K PROTEIN (BY
 CC SIMILARITY).
 CC -1- SUBUNIT: FORMS HETERODIMERS WITH BCL-2, E1B 19K PROTEIN, AND BCL-
 CC X(1) (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Membrane-associated (Potential).
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
 CC -1- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
 CC BAX FOR THEIR PRO-APOTOTIC ACTIVITY AND FOR THEIR INTERACTION
 CC WITH ANTI-APOTOTIC MEMBERS OF THE BCL-2 FAMILY.
 CC -1- APOTOTIC MEMBERS OF THE BCL-2 FAMILY (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 1 (BH1).
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 2 (BH2).
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 3 (BH3).
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: Y13331; CNA73684.1; -.
 DR HSP: 016611; 1BK1.
 DR MGI: 1097161; Bak1.
 DR InterPro: IPR002175; BCL2_family.
 DR InterPro: IPR007412; BCL_2.
 DR Pfam: PF00452; BCL-2_1.
 DR SMART: SM00337; BCL: 1.
 DR PROSITE: PS01060; BH1; 1.
 DR PROSITE: PS01258; BH2; 1.
 DR PROSITE: PS01259; BH3; 1.
 DR PROSITE: PS50062; BCL2_FAMILY; 1.
 KW Apoptosis; Transmembrane.
 FT DOMAIN 1 71 85 BH3.
 FT DOMAIN 2 114 133 BH1.
 FT DOMAIN 3 166 181 BH2.
 FT TRANSMEM 185 202 POTENTIAL.
 SQ SEQUENCE 208 AA; 23300 MW; DAFCLIB160C523C9 CRC64;

Query Match 97.5% Score 78; DB 1; Length 208;
 Best Local Similarity 93.8%; Pred. No. 8, 2e-06;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GOVGR0LATIGDDINR 16
 DB 69 GOVGR0LATIGDDINR 84

RESULT 4
 ID ATCU_ECOLI STANDARD; PRT; 834 AA.
 AC 059385; P78245;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Probable copper-transporting ATPase (EC 3.6.3.4).
 OS YAKR OR B0484.
 OC Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 RX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RA Das S., Chuang E., Vulpe C., Goldman J., Gitschler J.;
 RA Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=9742617; PubMed=9278503;
 RA Blattner F.R., Plunkett G., III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 CC [3]
 CC SEQUENCE FROM N.A.
 RA Roberts D., Allen E., Araujo R., Aparicio A., Chung E., Davis K.,
 RA Duncan M., Federapfel N., Hyman R., Kalman S., Komp C., Kurdi O.,
 RA Lew H., Lin D., Narmath A., Oefner P., Schramm S., Davis R.W.;
 RA Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: INVOLVED IN COPPER TRANSPORT.
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + OXYPHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
 CC (P1-P2 ATPASES). SUPERFAMILY ID:
 CC -1- SIMILARITY: CONTAINS 2 HMA DOMAINS.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U58330; AAB02268.1; -.
 DR EMBL: AE00154; AAC73586.1; -.
 DR HSP: U82664; AAB40238.1; -.
 DR HSP: P04129; IAF1.
 DR Ecodgene: EGI3246; ybar.
 DR InterPro: IPR001757; E1-E2_ATPase.
 DR InterPro: IPR001934; HMA.
 DR Pfam: PF00122; E1-E2_ATPase; 1.
 DR Pfam: PF00403; HMA; 2.
 DR Pfam: PF00702; Hydrolase; 1.
 DR PRINTS: PF00119; CATAPASE.
 DR PROSITE: PS00154; ATPASE_E1_E2; 1.
 DR PROSITE: PS01047; HMA_1; 1.
 DR PROSITE: PS50846; HMA_2; 2.
 KW Hydrolyase; Transmembrane; Phosphorylation; ATP-Binding; Copper;
 KW Metal-binding; Repeat; Complete proteome.
 FT TRANSMEM 187 207 POTENTIAL.
 FT TRANSMEM 218 238 POTENTIAL.
 FT TRANSMEM 254 274 POTENTIAL.
 FT TRANSMEM 284 304 POTENTIAL.
 FT TRANSMEM 438 458 POTENTIAL.
 FT TRANSMEM 464 484 POTENTIAL.
 FT TRANSMEM 485 505 POTENTIAL.
 FT TRANSMEM 627 647 POTENTIAL.
 FT TRANSMEM 733 753 POTENTIAL.
 FT TRANSMEM 779 799 POTENTIAL.
 FT TRANSMEM 801 821 POTENTIAL.
 FT DOMAIN 4 821 HMA 1.
 FT DOMAIN 100 163 HMA 2.

FT	METAL	110	110		COPPER (POTENTIAL)
FT	METAL	113	113		COPPER (POTENTIAL)
FT	MOD_RES	523	523		PHOSPHORYLATION (PROBABLE)
FT	CONFLICT	162	181		EVIDENCEKREDOCTAVAT ->
FT	CONFLICT	508	508		A >> R (IN REF. 1).
FT	CONFLICT	576	576		O -> R (IN REF. 1).
SO	SEQUENCE	834 AA:	87873 MM:		C6R4A1BF2E08EB6F6 CRO64:
Db	Query Match	57.5%	Score 46:	DB 1:	Length 834:
	Best Local Similarity	66.7%:	Pred. No. 6.4:		
Oy	Conservative	3:	Mismatches	1:	Indels
Db	712 GROMAYDDGIN 723				Gaps 0:
	4 GROLATIDDIN 15				
	:: ::				
RESULT	5				
PAT2_CAEEL	STANDARD:	PRT:	1226 AA.		
ID	PAT2_CAEEL				
PC	P34446:				
DT	01-FEB-1994 (Rel. 28, Created)				
DT	01-FEB-1994 (Rel. 28, Last sequence update)				
DT	01-MAR-2002 (Rel. 41, Last annotation update)				
DE	Integrin alpha pat-2 precursor.				
CS	PAT-2 OR F54P2.1				
ON	Caenorhabditis elegans.				
CC	Caenorhabditis elegans.				
OC	Eukaryota; Metazoa; Nematoda; Chromodorea; Rhaditida; Rhaditolidae.				
OC	Rhaditidae; Peloderinae; Caenorhabditis.				
OX	NCBI_TaxID=6239:				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-BRISTOL N2:				
RX	MEDLINE=94150718: PubMed-7906398:				
RA	Wilson R., Almschoor K., Anderson K., Baynes C., Berks M.,				
RA	Cratton J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,				
RA	Fulton L., Gardner K., Green P., Hawkins T., Hillier D., Jeter M.,				
RA	Johnson E., Jones M., Keshav V., Kirsten J., Laister N., Lester N.,				
RA	Lattelle J.P., Lightning Y., Lloyd C., Motilone B., O'Callaghan M.,				
RA	Parsons J., Percy C., Rifkin L., Roop A., Saunders E., Shorkkeen R.,				
RA	Sims W., Smalton N., Smith A., Smith M., Sonnenhammer E., Staden R.,				
RA	Waterston J., Thiller-Mieg J., Thomas K., Vaubin M., Vaughan K.,				
RA	Wohlman P.; Watson A., Welnsstock L., Wilkinson-Sproat J.,				
RT	*2.2 Mb of contiguous nucleotide sequence from chromosome III of C.				
RL	Nature 368:32-38(1994).				
CC	-1- FUNCTION: POSSIBLE ROLE IN CELL-CELL INTERACTIONS (BY SIMILARITY).				
CC	-1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA PAT-2 ASSOCIATES WITH BETA PAT-3.				
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).				
CC	-1- SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.				
CC	-1- SIMILARITY: CONTAINS 7 FC-GAP REPEATS.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to licenses@isb-sib.ch).				
CC	EMBL: L23645; AKZ6134.1: -.				
DR	PIR: S44824; S44824.				
DR	HSSP: P11215; LABX.				
DR	WormPeP: F54P2.1; CE00194.				
DR	InterPro: IPRO00413; Integrin_alpha.				
DR	pfam: PF01839; FC-GAP; 5.				
DR	pfam: PF01839; Integrin_A; 1.				
DR	PRINTS: PRO1185; INTERGRINA.				

DB	SMART: SM00191; int_alpha.5.	DR PROSITE: PS00242; INTERNA_ALPHA.1.	KM Integrin: Cell adhesion; Receptor; Glycoprotein; Transmembrane; Signal; Repeat.	FT SIGNAL	1	25	POTENTIAL.
FT	CHAIN	26	1226	INTERGRIN ALPHA PAT-2.			
FT	DOMAIN	26	1154	EXTRACELLULAR (POTENTIAL).			
FT	TRANSSEM	1155	1177	POTENTIAL.			
FT	DOMAIN	1178	1226	CYTOPLASMIC (POTENTIAL).			
FT	REPEAT	40	103	PG-GAP 1.			
FT	REPEAT	120	143	PG-GAP 2.			
FT	REPEAT	189	242	PG-GAP 3.			
FT	REPEAT	244	297	PG-GAP 4.			
FT	REPEAT	300	372	PG-GAP 5.			
FT	REPEAT	373	433	PG-GAP 6.			
FT	REPEAT	437	485	PG-GAP 7.			
FT	CARBOHYD	108	108	N-LINKED (GLCNAc. . .) (POTENTIAL).			
FT	CARBOHYD	228	228	N-LINKED (GLCNAc. . .) (POTENTIAL).			
FT	CARBOHYD	280	280	N-LINKED (GLCNAc. . .) (POTENTIAL).			
FT	CARBOHYD	608	608	N-LINKED (GLCNAc. . .) (POTENTIAL).			
FT	CARBOHYD	679	679	N-LINKED (GLCNAc. . .) (POTENTIAL).			
FT	CARBOHYD	775	775	N-LINKED (GLCNAc. . .) (POTENTIAL).			
FT	CARBOHYD	819	819	N-LINKED (GLCNAc. . .) (POTENTIAL).			
SQ	SEQUENCE	1226 AA; 135939 MW; B9169AD758B901D CRC64;					
QY	1 GVGQRLATIGDD 13	57.5%; Score 46; DB 1; Length 1226;					
DB	I : : : : : I	Best Local Similarity 53.8%; Pred. No. 9.6;					
	359 GVEGKQIAVGD 371	Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;					
RESULT 6							
ENO_HELPJ	ENO_HELPJ	STANDARD:	PRT: 426 AA.				
AC	09ZMS5:						
DT	16-OCT-2001 (rel. 40, Created)						
DT	16-OCT-2001 (rel. 40, Last sequence update)						
DT	16-OCT-2001 (rel. 40, Last annotation update)						
DE	Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase).						
DE	Eno OR JRP0142.						
OS	Helicobacter pylori j99 (campylobacter pylori j99).						
OC	Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group; Helicobacter.						
OX	NCBI_TaxID=85963;						
RN	1)						
RP	SEQUENCE FROM N.A.						
RX	MEDLINE=9120557; PubMed=9923682;						
RA	Alm R.A., Ling L.-S.L., Møllr D.T., King B.L., Brown E.D., Dolg P.C., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tumbino P.J., Caruso A., Uria-McNelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jlang Q., Taylor D.E., Yovis G.F., Trust T.J.;						
RA	*Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.*;						
RT	Nature 397:176-180(1999).						
RL	-1 CATALYTIC ACTIVITY: 2-phospho-D-glycerate + phosphoenolpyruvate + H(2)O.						
CC	-1 COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).						
CC	-1 PATHWAY: GLYCOLYSIS.						
CC	-1 SUBUNIT: HOMODIMER (BY SIMILARITY).						
CC	-1 SUBCELLULAR LOCATION: Cytoplasmic (By similarity).						
CC	-1 SIMILARITY: BELONGS TO THE ENOLASE FAMILY						
CC	-----						
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way						

```

CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.lsb-slb.ch/announce/
CC or send an email to license@lsb-slb.ch).
CC -----
DR EMBL: A6001453; AAD05723.1. -.
DR HSSP: P00924; 4ENL.
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; enolase; 1.
DR PRINTS: PR00148; ENOLASE.
DR Prodom: PD000902; ENOLASE.
DR PROSITE: PS00164; ENOLASE; 1.
DR Lyase: Glycolysis; Magnesium; Complete proteome.
DR ACT_SITE 155 154 BY SIMILARITY.
DR METAL 242 242 MAGNESIUM (BY SIMILARITY).
DR METAL 286 286 MAGNESIUM (BY SIMILARITY).
DR METAL 313 313 MAGNESIUM (BY SIMILARITY).
DR CONFLICT 85 85 V >> T (IN REF. 2).
DR SEQUENCE 426 AA; 46534 MW; EDFA73EABE877BEE CAC64;

Query Match 56.2%; Score 45; DB 1; Length 426;
Best Local Similarity 46.2%; Prod. No. 4.6;
Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 2 OVGROLATIGDII 14
Db 303 ELGRQIQVGDLL 315

RESULT 7
ENO_HELPY STANDARD; PRT; 426 AA.
AC P48285;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-
DE glycerate hydro-lyase).
GN ENO OR HP0154.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=26595 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9752185;
RA Tomb J.-F., White O., Kesteven A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klein H.-P., Gill S., Dougherty B.A.,
RA Loftus B., Richardson D., Dodson R., Khakhria E.F., Peterson S.,
RA McKenney K., Fitzgerald L.M., Iee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Meldrum J.M., Fujii C., Bowman C., Weisberg I., Mallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.H.,
RA Venter J.C.;
RA "The complete genome sequence of the gastric pathogen Helicobacter
RA pylori."
RL Nature 388:539-547(1997).
RN [2]
RP SEQUENCE OF 1-178 FROM N.A.
RC STRAIN=ATCC 53726 / R4-183;
RX MEDLINE=9528632; PubMed=7768597;
RA Thompson S.A., Blaser M.J.;
RA "Isolation of the Helicobacter pylori recA gene and involvement of
RA the recA region in resistance to low pH."
RL Infect. Immun. 63:2185-2193(1995)
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate ~ phosphoenolpyruvate +
CC H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
CC THE DIMER (BY SIMILARITY).
CC -1- PATHWAY: GLYCOLYSIS
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).

```

```

CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.lsb-slb.ch/announce/
CC or send an email to license@lsb-slb.ch).
CC -----
DR EMBL: A600536; AAD07219.1. -.
DR HSSP: U11750; AKC43380.1. -.
DR TIGR: HP0154; 4ENL.
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; enolase; 1.
DR PRINTS: PR00148; ENOLASE.
DR Prodom: PD000902; ENOLASE.
DR PROSITE: PS00164; ENOLASE; 1.
DR Lyase: Glycolysis; Magnesium; Complete proteome.
DR ACT_SITE 155 154 BY SIMILARITY.
DR METAL 242 242 MAGNESIUM (BY SIMILARITY).
DR METAL 286 286 MAGNESIUM (BY SIMILARITY).
DR METAL 313 313 MAGNESIUM (BY SIMILARITY).
DR CONFLICT 85 85 V >> T (IN REF. 2).
DR SEQUENCE 426 AA; 46534 MW; 7B7A0B7A5DFB398 CAC64;

Query Match 56.2%; Score 45; DB 1; Length 426;
Best Local Similarity 46.2%; Prod. No. 4.6;
Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 2 OVGROLATIGDII 14
Db 303 ELGRQIQVGDLL 315

RESULT 8
ATCU_BACSU STANDARD; PRT; 803 AA.
AC O32220;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Potential copper-transporting ATPase (Ec 3.6.3.4).
GN yycG subunit.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/streptococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Knäuper F., Ogasawara N., Yoshikawa H., Dancho A.;
RA Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RL -1- FUNCTION: INVOLVED IN COPPER TRANSPORT (BY SIMILARITY).
RL -1- CATALYTIC ACTIVITY: ATP + H(2)O ADP + DIPHOSPHATE.
RL -1- SUBCELLULAR LOCATION: Integral membrane protein.
RL -1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
RL (EC-3 ATPASES) SUBFAMILY 1B.
RN -1- SIMILARITY: CONTAINS 2 HMA DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.lsb-slb.ch/announce/
CC or send an email to license@lsb-slb.ch).
CC -----
DR EMBL: 299121; CAB1535.1. -.
DR HSSP: P04129; IATF.

```

```

DR Subtilist; BG14106; yvgX.
DR InterPro: IPR001366; Cad_Atpase.
DR InterPro: IPR000579; Cal_P_AtpaseA.
DR InterPro: IPR001756; Cu_Atpase.
DR InterPro: IPR001877; Cu_Atpase_I.
DR InterPro: IPR001757; E1-E2_Atpase.
DR InterPro: IPR001803; Hg_scaevenger.
DR InterPro: IPR001934; HMA.
DR InterPro: IPR001454; Hydrolyase.
DR Pfam: PF00122; E1-E2_Atpase; 1.
DR Pfam: PF00403; HMA; 2.
DR Pfam: PF00702; Hydrolyase; 1.
DR PRINTS: PRO0940; CATATPASE.
DR PRINTS: PRO0941; CATATPASEA.
DR PRINTS: PRO0943; CATATPASE.
DR PRINTS: PRO0942; CUATPASEI.
DR PRINTS: PRO0946; HSCAVENGER.
DR PROSITE: PS00154; ATPASE_E1_E2; 1.
DR PROSITE: PS01047; HMA_1; 2.
DR PROSITE: PS00846; HMA_2; 2.
DR Hydrolyase; Transmembrane; Phosphorylation; Magnesium; ATP-binding.
KW Metal-binding; Copper; Repeat; Complete proteome.
FT TRANSMEM 163 183 POTENTIAL.
FT TRANSMEM 197 217 POTENTIAL.
FT TRANSMEM 229 249 POTENTIAL.
FT TRANSMEM 260 280 POTENTIAL.
FT TRANSMEM 416 436 POTENTIAL.
FT TRANSMEM 448 468 POTENTIAL.
FT TRANSMEM 610 630 POTENTIAL.
FT TRANSMEM 704 724 POTENTIAL.
FT TRANSMEM 767 787 POTENTIAL.
FT DOMAIN 7 73 HMA 1.
FT METAL 17 17 COPPER (POTENTIAL).
FT METAL 20 20 COPPER (POTENTIAL).
FT METAL 85 85 COPPER (POTENTIAL).
FT METAL 88 88 COPPER (POTENTIAL).
FT MOD_RES 500 500 PHOSPHORYLATION (BY SIMILARITY).
FT METAL 699 699 MAGNESIUM (BY SIMILARITY).
FT METAL 703 703 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 803 AA; 86024 MW; D9C8DA5D40320C69 CRC64;

Query Match 55.0%; Score 44; DB 1; Length 803;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 4 GROLIIDDIN 15
DB 691 GROTAMVGDGIN 702

RESULT 9
ID CRTI_APHSP STANDARD; PRT: 532 AA.
AC P21134.
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DE 01-MAY-2002 (Rel. 41, Last annotation update)
DE Phytoene dehydrogenase (EC 1.14.99.-) (Phytoene desaturase).
CN CRTI.
OS Aphnocapsa sp.
OC Bacteria; Cyanobacteria; Chroococcales; Aphnocapsa.
OX NCBI_TaxID=1120;
PY 11-11-11
PP SEQUENCE FROM N.A.
RC STRAIN=PC 6714;
RC MEDLINE=9038285; PubMed=2119326;
RA Schmidt A., Sandmann G.;
RT Cloning and nucleotide sequence of the crtI gene encoding phytoene
dehydrogenase from the cyanobacterium Aphnocapsa PCC6714.*;
RL Gene 91:113-117(1990).

```

```

CC -1- FUNCTION: THIS ENZYME CONVERTS PHYTOENE INTO ZETA-CAROTENE VIA THE
CC INTERMEDIARY OF PHYTOFLUENE BY THE SYMMETRICAL INTRODUCTION OF TWO
CC DOUBLE BONDS AT THE C-11 AND C-11' POSITIONS OF PHYTOENE.
CC -1- COFACTOR: NAD, NADP, OR FAD (PROBABLE).
CC -1- PATHWAY: CAROTENOID BIOSYNTHESIS.
CC -1- SIMILARITY: BELONGS TO THE PHYTOEN DEHYDROGENASE FAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M56647; M562573.1; -.
DR PIR: J00084; J00084.
DR Carotenoid biosynthesis; Oxidoreductase; FAD; Flavoprotein; NAD.
FT NP_0084 22 49 FAD (ADP PART) (POTENTIAL).
SQ SEQUENCE 532 AA; 56754 MW; 0629C65A914B19F CRC64;

Query Match 54.4%; Score 43.5; DB 1; Length 532;
Best Local Similarity 47.4%; Pred. No. 10;
Matches 9; Conservative 5; Mismatches 2; Indels 3; Gaps 1;

OY 1 GOGKRLAT---IGDDIR 16
DB 141 GOGKRLDLEFGEDVHR 159

RESULT 10
ID ENO_LYCES STANDARD; PRT: 444 AA.
AC P26300.
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-
DE glycerate hydro-lyase).
DE PGI1.
GN Enoloprotein esculentum (Tomato).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
PY 11-11-11
PP SEQUENCE FROM N.A.
RC STRAIN=CV, SUPERSONIC;
RC MEDLINE=93044507; PubMed=1841726;
RA van der Straeten D., Rodriguez-Pousada R.A., Goodman H.M.,
RA van Montagu M.;
RT Plant enolase: gene structure, expression, and evolution.*;
RL Plant Cell 3:719-735(1991).
DE -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
DE H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
CC THE DIMER (BY SIMILARITY).
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X58108; CA441115.1; -.
DR PIR: J01185; J01185.

```


OY 2 OVGROALIGDDI 14
 : : : : :
 Db 319 EICEVOYICDDL 331

RESULT 13
 YRN9_CAEEL STANDARD: PRT: 770 AA.
 AC 009609;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Hypoetical 84.2 kDa protein R07B1.9 in chromosome X.
 GN R07B1.9
 OS Caenorhabditis elegans.
 CC Eukaryota; Metazoa; Nematoda; Chromodorea; Rhaditidae; Rhaditoidae;
 CC Rhaditidae; Reticoderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN 11
 RP SEQUENCE FROM N.A.
 RA STRAIN-BRISTOL N2;
 RA Kestraw J.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL: Z48621; CA48546.1;
 WORMPEP: R07B1.9; CB01635.
 KW Hypothetical protein.
 SQ SEQUENCE 770 AA: 84235 MW: 428A0C59ACBBD8 CRC64:

Query Match 53.8%; Score 43; DB 1; Length 770;
 Best Local Similarity 56.2%; Pred. No. 18;
 Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 GVGROALIGDDINR 16
 : : : : :
 Db 738 GPCQSPANVGDDPR 753

RESULT 14
 ATC2_RHIME STANDARD: PRT: 827 AA.
 AC P58342;
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DE Copper-transporting ATPase 2 (EC 3.6.3.4).
 GN ACTP2 OR ATC2P OR RH1018 OR SM821578.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OS plasmid pSymB (megaplasmid 2).
 CC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 CC Rhizobiaceae; Sinorhizobium.
 OX NCBI_TaxID=382;
 RN 11
 RP SEQUENCE FROM N.A.
 RA STRAIN-1021;
 RA MEDLINE-21396508; Pubmed-11481431;
 RA Flann T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
 RA Vorholter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
 RA Golding B., Puhler A.;
 RT "The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-
 fixing endosymbiont Sinorhizobium meliloti.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
 CC -1- FUNCTION: INVOLVED IN COPPER TRANSPORT (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + ORTHOPHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
 CC -1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
 CC (E1-E2 ATPASES). SUBFAMILY 1B.
 CC -1- SIMILARITY: CONTAINS 2 HMA DOMAINS.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

EMBL: AL603645; CAC49418.1;
 DR PROSITE: PS00154; ATPASE_E1_E2, 1.
 DR PROSITE: PS01047; HMA_1; 2.
 DR PROSITE: PS0846; HMA_2; 2.
 KW Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding;
 KM Metal-binding; Copper; Repeat; Plasmid; Complete proteome.
 FT TRANSMEM 174 194
 FT TRANSMEM 210 230
 FT TRANSMEM 246 266
 FT TRANSMEM 271 291
 FT TRANSMEM 430 450
 FT TRANSMEM 458 478
 FT TRANSMEM 771 793
 FT TRANSMEM 797 819
 FT DOMAIN 16 81
 FT DOMAIN 83 149
 FT METAL 26 26
 FT METAL 29 29
 FT METAL 93 93
 FT METAL 96 96
 FT MOD_RES 515 515
 FT METAL 714 714
 FT METAL 718 718
 SQ SEQUENCE 827 AA: 85861 MW: A3D8DFDD1315FCB CRC64:

Query Match 53.8%; Score 43; DB 1; Length 827;
 Best Local Similarity 64.3%; Pred. No. 20;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 OVGROALIGDDIN 15
 : : : : :
 Db 704 GQGRVAFIGDGIN 717

RESULT 15
 ATC2_RHIME STANDARD: PRT: 827 AA.
 AC Q9A5X3;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Copper-transporting ATPase (EC 3.6.3.4).
 GN ACTP.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OS Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 CC Rhizobiaceae; Sinorhizobium.
 OX NCBI_TaxID=382;
 RN 11
 RP SEQUENCE FROM N.A.
 RA STRAIN-WSM419;
 RA Reeve W.G., Tivari R.P., Kale N.B., Dilworth M.J., Glenn A.R.;
 RT "The role of copper and P-type ATPase in the acid-tolerance of
 RT Rhizobium leguminosarum by viciae and Sinorhizobium meliloti.";
 RL Submitted (Feb-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: INVOLVED IN COPPER TRANSPORT (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + ORTHOPHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY


```

CC      (E1-E2 ATPases). SUBFAMILY 1B.
CC      -1- SIMILARITY: CONTAINS 2 HMA DOMAINS.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@lsb-sib.ch).
CC      -----
CC      EMBL: AF129004; AAD27639.1; -.
CC      HSSP: Q04656; 1AM0.
CC      InterPro: IPR001366; Cad_ATPase.
CC      InterPro: IPR000579; Cat_P_ATPase.
CC      InterPro: IPR001757; E1-E2_ATPase.
CC      InterPro: IPR001802; HG_scamenger.
CC      InterPro: IPR001934; HMA.
CC      InterPro: IPR001454; Hydrolyase.
CC      Pfam: PF00122; E1-E2_ATPase; 1.
CC      Pfam: PF00403; HMA; 2.
CC      Pfam: PF00702; Hydrolyase; 1.
CC      PRINTS: PR00119; CATATPASE.
CC      PRINTS: PR00940; CATPTPASEA.
CC      PRINTS: PR00946; HGSCAVENGER.
CC      PROSITE: PS00154; ATPASE_E1_E2; 1.
CC      PROSITE: PS01047; HMA_1; 2.
CC      PROSITE: PS0846; HMA_2; 2.
CC      KW      Hydrolyase; Transmembrane; Phosphorylation; Magnesium; ATP-binding;
KW      Metal-binding; Copper; Repeat.
FT      TRANSMEM 174 194  POTENTIAL..
FT      TRANSMEM 210 230  POTENTIAL..
FT      TRANSMEM 248 268  POTENTIAL..
FT      TRANSMEM 271 291  POTENTIAL..
FT      TRANSMEM 430 450  POTENTIAL..
FT      TRANSMEM 458 478  POTENTIAL..
FT      TRANSMEM 541 561  POTENTIAL..
FT      TRANSMEM 569 589  POTENTIAL..
FT      TRANSMEM 727 747  POTENTIAL..
FT      TRANSMEM 773 793  POTENTIAL..
FT      TRANSMEM 795 815  POTENTIAL..
FT      DOMAIN 16 81  HMA 1.
FT      METAL 83 149  COPPER (POTENTIAL).
FT      METAL 26 26  COPPER (POTENTIAL).
FT      METAL 29 29  COPPER (POTENTIAL).
FT      METAL 93 93  COPPER (POTENTIAL).
FT      METAL 96 96  COPPER (POTENTIAL).
FT      MOD_RES 515 515  PHOSPHORYLATION (BY SIMILARITY).
FT      METAL 714 714  MAGNESIUM (BY SIMILARITY).
FT      METAL 718 718  MAGNESIUM (BY SIMILARITY).
SQ      SEQUENCE 827 AA; 86239 MW; 707E2148DDA5004 CRC64;

Query Match 53.8%; Score 43; DB 1; Length 827;
Best local similarity 64.3%; Pred. No. 20;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      2  OYGRQLATIGDIN 15
DB      704  QGGRSVAFIGDGIN 717

```

Search completed: September 20, 2002, 11:04:33
 Job time: 1630 sec


```

RESULT 2
O9M2S6 PRELIMINARY: PRT: 163 AA.
AC 09M2S6 (TREMUREL. 15, Created)
DT 01-DEC-2001 (TREMUREL. 15, Last sequence update)
DT 01-DEC-2001 (TREMUREL. 19, Last annotation update)
DE BAK PROTEIN (FRAGMENT).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
RN NCBI_TaxID=9940;
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY.
RA Murray J.F., Leigh A.J., Scaramuzzi R.J., Carter N.D.:
RA "Bak in the sheep ovary";
RL Submitted (JUL-1993) to the EMBL/GenBank/DBJ databases.
DR HSEB: O16611; BCL: BCL2_family.
DR HSEB: O16611; BCL: BCL2_family.
DR Interpro: IP000712; BCL_2.
DR Pfam: PF00452; BCL-2; 1.
DR SMART: SM00337; BCL: 1.
DR PROSITE: PSS0062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BHL: 1.
DR PROSITE: PS01258; BHL: 1.
DR PROSITE: PS01259; BHL: 1.
PT NON_TER
SQ SEQUENCE 163 AA: 18039 MW: 18356A8A8C3AD58 CRC64:

Query Match 98.8%; Score 79; DB 6; Length 163;
Best Local Similarity 93.8%; Pred. No. 2.1e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0:
OY 1 GOVGOALATIGDINR 16
DB 31 GOVGOALATIGDINR 46

RESULT 3
O91WAS PRELIMINARY: PRT: 151 AA.
AC 091WAS (TREMUREL. 19, Created)
DT 01-DEC-2001 (TREMUREL. 19, Last sequence update)
DT 01-DEC-2001 (TREMUREL. 19, Last annotation update)
DE N-BANK1.
GN BANK1.
OS Bank musculus (Mouse).
OC Eukaryota; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI; TISSUE=NEURONAL;
RX MEDLINE=21228300; PubMed=11276671;
RA Sun Y.F., Li L.Y., Saitama M., Timusk T., Arumae U.:
RA "A novel, neuron-specific, domain-only splice variant of Bak in
RA anti-apoptotic in neuron-specific in non-neuronal cells";
RL Submitted (APR-1993) to the EMBL/GenBank/DBJ databases.
DL EMBL: AF02617; AL01876; 1; -.
SQ SEQUENCE 151 AA: 16402 MW: 18C13BF86AF33B CRC64:

Query Match 97.5%; Score 78; DB 11; Length 151;
Best Local Similarity 93.8%; Pred. No. 2.8e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0:

```

```

OY 1 GOVGOALATIGDINR 16
DB 70 GOVGOALATIGDINR 85

RESULT 4
O9UKS9 PRELIMINARY: PRT: 209 AA.
AC 09UKS9 (TREMUREL. 15, Created)
DT 01-OCT-2000 (TREMUREL. 15, Last sequence update)
DT 01-OCT-2000 (TREMUREL. 15, Last annotation update)
DE BAK PROTEIN.
GN BAK.
OS Rattus norvegicus (Rat).
OC Eukaryota; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN NCBI_TaxID=10116;
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Itch T., Itch A., Pleasure D.:
RA Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR HSEB: O16613; BCL: BCL2_family.
DR HSEB: O16613; BCL: BCL2_family.
DR Interpro: IP000712; BCL_2.
DR Pfam: PF00452; BCL-2; 1.
DR SMART: SM00337; BCL: 1.
DR PROSITE: PSS0062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BHL: 1.
DR PROSITE: PS01258; BHL: 1.
DR PROSITE: PS01259; BHL: 1.
PT NON_TER
SQ SEQUENCE 209 AA: 22153 MW: 2493B81491972421 CRC64:

Query Match 97.5%; Score 78; DB 11; Length 209;
Best Local Similarity 93.8%; Pred. No. 4e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0:
OY 1 GOVGOALATIGDINR 16
DB 70 GOVGOALATIGDINR 85

RESULT 5
O9S2S3 PRELIMINARY: PRT: 357 AA.
AC 09S2S3 (TREMUREL. 13, Created)
DT 01-MAY-2000 (TREMUREL. 13, Last sequence update)
DT 01-MAY-2000 (TREMUREL. 13, Last annotation update)
DE PROTEIN PHOSPHATASE 2C-LIKE PROTEIN (AT4G31860/FLIC18_60).
GN FLIC18_60 OR AT4G31860.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Eukaryotae; Streptophyta; Embryophyta; Tracheophyta;
OC Eudicotyledons; Eudicotyledons; Eudicotyledons; Rosidae;
OC Eurosidia II; Brassicales; Brassicaceae; Arabidopsida.
RN NCBI_TaxID=3702;
RP SEQUENCE FROM N.A.
RA Bevan M., Terry N., Ardies W., Buysaert C., Daeseville R.,
RA De Clerck R., De Keyser A., Neyt P., Rouze P., Van den Daele H.,
RA Hildebrandt R., Glatz J., Van Montagu M., Hohnelst J., Mewes H.W.:
RA Submitted (APR-1993) to the EMBL/GenBank/DBJ databases.
DL Submitted (APR-1993) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RA Arabidopsis sequencing project;
RA Submitted (APR-1993) to the EMBL/GenBank/DBJ databases.
DL Submitted (APR-1993) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.

```

Query Match	58.1%	Score 46.5	DB 10	Length 357
Best Local Similarity	58.8%	Pctd. No 13		
Matches 10	Conservative	4	Mismatches 2	Indels 1
Db	104 GORGEWELAVGSKINK 120			
09KP27	6			
ID 09KP27	PRELIMINARY:	PRT:	915 AA.	
AC 09KP27				
DT 01-OCT-2000 (TRIMBrel. 15. Created)				
DT 01-OCT-2000 (TRIMBrel. 15. Last sequence update)				
DE 01-DEC-2001 (TRIMBrel. 10. Last annotation update)				
DE CATION TRANSPORT ATPASE, E1-E2 FAMILY.				
DS VC2215				
GN Vibrio cholerae				
OS Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.				
OC NCBI_TaxId=668				
OX [1]				
RP SEQUENCE FROM N.A.				
RC STRAIN=EL TOR N16961 / SEROTYPE O1;				
RC MEDLINE=26406833; PubMed=10952301;				
RA Heidelberg J.F., Eissen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,				
RA Dodson R.J., Halt D.H., Hickey E.K., Peterson J.D., Umayam L.A.,				
RA Gill S.R., Nelson K.E., Read T.D., Yettelein H., Richardson D.,				
RA Ermonelaeva M.D., Yamachavan J., Bass S., Qin H., Drogoti I., Sellers P.,				
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,				
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,				
RA Fraser C.M.;				
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio				
RL Nature 406:477-483(2000).				
DR EMBL: AE004293; AF95355.1; -				
DR HSSP: P04129; IAFI.				
DR TIGR: VC2215;				
DR InterPro: IPR000579; Cat_P_ATPase.				
DR InterPro: IPR001757; E1-E2_ATPase.				
DR				
DR				
DR SMART: SM00331; P2C2; 1.				
DR PROSITE: PS01032; P2C2; 1.				
DR SEQUENCE 357 AA; 39203 MW; 98PELA05818CAKD03 CRC64;				
RA				
RA Ficker J.R.;				
RA "Arabidopsis cDNA clones";				
RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.				
RL EMBL: AL045607; CAB40756.1; -				
DR EMBL: AL161579; CAB79904.1; -				
DR EMBL: AY057611; M114406.1; -				
DR HSSP: P35813; IAG0.				
DR InterPro: IPR000223; P2C2.				
DR InterPro: IPR001933; P2C2_domain.				
DR Pfam: PF00481; P2C2; 2.				
DR SMART: SM00331; P2C2; 1.				
DR SMART: SM00331; P2C2; 1.				
DR PROSITE: PS01032; P2C2; 1.				
DR SEQUENCE 357 AA; 39203 MW; 98PELA05818CAKD03 CRC64;				
RA				
RA Yerryn N., Ardiles W., Buysahtet C., Dasseville R., De Clerck R.,				
RA De Keyser A., Neyt P., Rouze P., Van den Daele H., Villarroel R.,				
RA Gieken J., Van Montagu M., Mewes H.W., Lemcke K., Meyer K.F.X.;				
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.				
RN [4]				
RN SEQUENCE FROM N.A.				
RN EU Arabidopsis sequencing project;				
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.				
RN [5]				
RN SEQUENCE FROM N.A.				
RN Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,				
RA Bower L., Ganinci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,				
RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,				
RA Kawaji J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,				
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,				
RA Satou M., Seki M., Southwick A., Taag C.C., Toriumi M., Yamada K.,				
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,				
RA Ficker J.R.;				

DR	InterPro:	IPR001802;	HG_scaevenger.	
DR	InterPro:	IPR001934;	HMA.	
DR	InterPro:	IPR001454;	Hydrolase.	
DR	InterPro:	IPR00150;	Hypothet.co.f.	
DR	Pfam:	PF00122;	E1-E2_Afrase; 1.	
DR	Pfam:	PF00403;	HMA; 3.	
DR	Pfam:	pf00702;	Hydrolase; 1.	
DR	PRINTS:	PR00119;	CATAPPAE.	
DR	PRINTS:	PRO0940;	CATPATPASEA.	
DR	PRINTS:	PRO0946;	HGSCAVENGER.	
DR	PROSITE:	PS00154;	ATPPASE_E1.E2; UNKNOWN_1.	
DR	PROSITE:	PS01229;	COF 2; UNKNOWN_1.	
DR	PROSITE:	PS01047;	HMA; 1.	
KW	Complete	proteome.		
SQ	SEQUENCE	915 AA; 97311 MW; 2P3IEB2640ND0D20 CRC64;		
<hr/>				
QY	Query Match	57.5%; Score 46;	DB 16; Length 915;	
	Best Local Similarity	64.3%;	Pctd. No. 44;	
Matches	9; Conservative	3; Mismatches	2; Indels	0; Gaps
OY	2 OVGROLAIIGDDIN 15	:		
Db	786 QDGKRVAMIGGIN 799			
<hr/>				
RESULT	7			
Q9UXV1	PRELIMINARY;	PRT;	258 AA.	
AC	O9UXV1:			
DT	01-MAY-2000 (TrEMBLrel. 13, Created)			
PT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)			
DE	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)			
SY	V-ATPASE PROTEOLIPID.			
GN	PAB189.			
OS	Pyrococcus abyssi.			
NCBI	AChapaa; Burytschaecota; Thermococcales; Pyrococcus.			
OC	NCB1_taxonomy:2592;			
RN	[1]			
RC	SEQUENCE FROM N.A.			
RP	STRAIN-OHSAY;			
RA	Hellig R.;			
RT	"Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure and evolution."			
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: A0246286; CAB50662.1;			
DR	InterPro: IPR004083; Chemcatalix_transducer.			
DR	InterPro: IPR004090; Me_chemoaxis.			
DR	Pfam: PF00015; MCPsignal; 1.			
DR	PRINTS: PR00280; CHEMTRNSDCU.			
DR	SMART: SM00283; MA; 1.			
KW	Complete proteome.			
SQ	SEQUENCE 258 AA; 29033 MW; EDEB44ACAB51512 CRC64;			
<hr/>				
QY	Query Match	55.0%; Score 44;	DB 17; Length 258;	
	Best Local Similarity	43.8%;	Pctd. No. 23;	
Matches	7; Conservative	4; Mismatches	5; Indels	0; Gaps
OY	1 GOVGROLAIGDDIN 16	: :		
Db	122 GEAGRGFAVVADLR 137			
<hr/>				
RESULT	8			
ID	057733	PRELIMINARY;	PRT;	261 AA.
AC	057733:			
DT	01-AUG-1998 (TrEMBLrel. 07, Created)			
PT	01-AUG-1998 (TrEMBLrel. 07, Last sequence update)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)			
DE	261AA LONG HYPOTHETICAL CHEMORECEPTOR PROTEIN.			
PN	PH1970.			

OS Pyrococcus horikoshii.
 OC Archaea: Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
 NX NCBI_TaxID=53953;
 RX (1)
 RC SEQUENCE FROM N.A.
 RA STRAIN=OT3;
 RM MEDLINE=98344137; PubMed=9679194;
 RA Kawarabayashi Y., Sawada M., Horikawa H., Halkawa Y., Hino Y.,
 RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Onikubo Y.,
 RA Funahashi T., Tanaka T., Kudo H., Yamazaki J., Kishida N., Oguchi A.,
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 RA Masuchi Y., Shizuya H., Kikuchi H.;
 RT *Complete sequence and gene organization of the genome of a hyper-
 RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
 RL DNA Res. 5:55-76(1998).
 DR EMBL: AP000007; BAA31097.1;
 DR InterPro: IPR004089; Chemotaxis_transducer.
 DR Pfam: PF00015; MCPsigmal; 1.
 DR SMART: SM00283; MA; 1.
 KM Complete proteome.
 SO SEQUENCE 261 AA; 29234 MW; 2FDDC7CC08223D46 CRC64;

Query Match 55.0%; Score 44; DB 17; Length 261;
 Best Local Similarity 43.8%; Pred. No. 24;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 1 GQVROLATIGDDINR 16
 DB 125 GEAQGRPAVVADEIRR 140

RESULT 9
 ID Q9JHL6 PRELIMINARY; PRT: 556 AA.
 AC Q9JHL6
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE GB|JAF30301.1 (HYPOTHETICAL 63.0 KDa PROTEIN).
 GN T21B14.12.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 NX NCBI_TaxID=3702;
 RX (1)
 RC SEQUENCE FROM N.A.
 RA STRAIN=COLUMBIA;
 RA Kaneo T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
 RM Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
 RL [12]
 RP SEQUENCE FROM N.A.
 RA STRAIN=COLUMBIA;
 RC PubMed=10907853;
 RA Nakamura Y.;
 RT *Structural analysis of Arabidopsis thaliana chromosome 3. II.
 RT Sequence features of the regions of 4,251,695 bp covered by ninety pl,
 RT TAC and BAC clones.";
 RL DNA Res. 7:217-221(2000).
 RX (3)
 RP SEQUENCE FROM N.A.
 RA STRAIN=CV. COLUMBIA;
 RM MEDLINE=21016720; PubMed=11130713;
 RA Salanoubat M., Lemcke K., Rieger M., Ansoorge W., Unsel M.,
 RA Faltmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
 RA Delacny M., Boutry M., Grivell L.A., Mache R., Pulgionemich P.,
 RA de Simone V., Cholene N., Artiguenave F., Robert C., Broillet P.,
 RA Wincker P., Catellano L., Weisenbach J., Surin W., Queller F.,
 RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
 RA Wurmbach E., Drznezek H., Erle H., Jordan N., Bangert S.,
 RA Wielemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,

RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
 RA Conrath A., Hornischer K., Kauer G., Loehner T.-H., Nordick G.,
 RA Reichelt J., Schaefer M., Schen O., Barques M., Terol J., Clement J.,
 RA Navarro P., Collado C., Perez-Perez A., Ottensmeyer B., Duchemin D.,
 RA Cooke R., Landie M., Berger-Liauro C., Purnelle B., Masuy D.,
 RA de Haan R., Angier A.C., Flores M., Liguori R., Vitale D.,
 RA Monfort A., Maure A.C., Schoof F., Ruid S., Zaccaria P., Menges H.-W.,
 RA Maninape G., Kasse D., Schopf F., Koo H.-L., Tallon L.J., Jenkins J.,
 RA Koyner T.F.X., Kaul S., Town C.D., Koo H.-L., Tallon L.J., Jenkins J.,
 RA Cressy T.H., Haas B., Nait R., Wu D., Peterson J., Van Aken S.,
 RA Pal G., Milschener J., Sellers P., Gill J.E., Feldblyum T.V.,
 RA Traus D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
 RA Freus G.M., Kaneo T., Nakamura Y., Sato S., Kato T., Asamizu E.,
 RA Sasamoto S., Kimura T., Ideasa K., Kawashima K., Kishida Y.,
 RA Kiyokawa S., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakayama S., Nakazaki N., Shimpso S., Takeuchi C., Wada T.,
 RA Nakane A., Yamada M., Yasuda M., Tabata S.;
 RT *Sequence and analysis of chromosome 3 of the plant Arabidopsis
 RT thaliana.";
 RL Nature 408:820-822(2000).
 DR EMBL: AP002040; BAB03118.1;
 DR EMBL: AC069473; AAG51057.1;
 KM Hypothetical protein.
 SO SEQUENCE 556 AA; 63004 MW; F697359ABB7213F CRC64;

Query Match 55.0%; Score 44; DB 10; Length 556;
 Best Local Similarity 53.8%; Pred. No. 55;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 4 GROLATIGDDINR 16
 DB 262 GRLVFGVDSINR 274

RESULT 10
 ID P73239 PRELIMINARY; PRT: 593 AA.
 AC P73239
 DT 01-FEB-1997 (TREMblrel. 02, Created)
 DT 01-FEB-1997 (TREMblrel. 02, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE ARC_TRANSPORTER.
 GN SIR2019.
 OS Synecocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
 NX NCBI_TaxID=1148;
 RX (1)
 RC SEQUENCE FROM N.A.
 RM MEDLINE=97061201; PubMed=8905231;
 RA Kaneo T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima T., Hirosewa M., Sugiura M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
 RA Shimpso S., Takeuchi C., Wada T., Nakane A., Yamada M., Yasuda M.,
 RA Tabata S.;
 RT *Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synecocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-136(1996).
 CC -I- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
 CC (ABC TRANSPORTERS).
 CC EMBL: D90904; BAA17266.1;
 DR InterPro: IPR003593; AAA.
 DR InterPro: IPR001140; ABC_transporter_tmem.
 DR InterPro: IPR003439; ABC_transporter.
 DR InterPro: IPR01687; ATP_GTP_A.
 DR Pfam: PF00664; ABC_membrane; 1.
 DR Pfam: PF00005; ABC_tran; 1.
 DR SMART: SM00382; AAA; 1.
 DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
 DR ATP-binding: Complete proteome; Transport.
 KW SEQUENCE 593 AA; 65761 MW; DA48CE31D0EAC6C9 CRC64;

```

Query Match      55.0%; Score 44; DB 16; Length 593;
Best Local Similarity 61.5%; Pred. No. 59;
Matches      8; Conservative      3; Mismatches      2; Indels      0; Gaps      0;

Oy      4 GRGATIGDDINR 16
      11 : 11 : 11 : 11 :
Db      128 GRGATIGDDINQ 140

RESULT 11
O9PG35      PRELIMINARY;      PRT;      608 AA.
AC      O9PG35;
DT      01-MAR-2001 (TREMBLrel. 16, Created)
DT      01-MAR-2001 (TREMBLrel. 17, Last sequence update)
DE      EMBL|CA82953.1
OC      Arabidopsis thaliana (Mouse-ear cress).
OC      Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC      Ericales; I. Brassicales; Brassicaceae; Arabidopsids.
OX      NCBI_TaxID=3702;
RN      111
RP      SEQUENCE FROM N.A.
RC      STRAIN=COLUMBIA;
RA      Kaneo T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kocani H.,
RA      Tabeta S.;
RL      Structural analysis of Arabidopsis thaliana chromosome 5. XI."
DR      EMBL; AF002032; BAB9804.1; -
DR      InterPro: IPR000531; T0M6_BOXC.
DR      PROSITE: PS00430; T0M6_DEPENDENT_ARC_1; UNKNOWN.1.
SQ      SEQUENCE 608 AA; 67923 MW; 75B5DF42E697386C CRC64;

Query Match      55.0%; Score 44; DB 10; Length 608;
Best Local Similarity 53.8%; Pred. No. 60;
Matches      7; Conservative      3; Mismatches      3; Indels      0; Gaps      0;

Oy      4 GRGATIGDDINR 16
      11 : 11 : 11 : 11 :
Db      321 GRGATIGDDINR 333

RESULT 12
O9PG32      PRELIMINARY;      PRT;      693 AA.
AC      O9PG32;
DT      01-OCT-2000 (TREMBLrel. 15, Created)
DT      01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT      01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE      PLUS BIOGENESIS PROTEIN.
GN      XP1953.
OS      Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC      Xylella fastidiosa.
OC      Xylella.
OX      NCBI_TaxID=2371;
RN      111
RP      SEQUENCE FROM N.A.
RC      STRAIN=9A5C;
RA      MEDLINE=20365717; PubMed=10910347;
RA      Simpson A.J.G., Rehnach F.C., Arruda P., Abreu F.A., Acencio C.S.,
RA      Alvarado R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA      Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Bioness M.R.S.,
RA      Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carter H.,
RA      Coutinho L.L., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA      Fachinani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA      Fraaga J.S., Frasca S.C., Franco M.C., Frohme M., Furian L.R.,
RA      Garner M., Goldman G.H., Goldman M.H.S., Gomes S.L., Grubler A.,
RA      Ho P.L., Honeisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,

```

```

RA      Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA      Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA      Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA      Marques M.V., Martins E.A.L., Martins E.M.F., Matsushima A.Y.,
RA      Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA      Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA      Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA      de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA      Pelxoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pessegueiro J.B.,
RA      Quaglio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA      da Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA      da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA      de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubano M.H.,
RA      Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA      Zago M.A., Zatz M., Zeldanis J., Zetubal J.C.;
RT      "The genome sequence of the plant pathogen Xylella fastidiosa."
RL      Nature 406:151-159(2000).
DR      EMBL; AE004014; AAP8475.1; -
DR      HSSP; P02942; 1007.
DR      InterPro: IPR004089; Chemotaxis transducer.
DR      InterPro: IPR004090; Me.chemotaxis.
DR      Pfam; PF00015; MCPsignal. 1.
DR      PRINTS; PR00260; CHEMTRNSDUCR.
DR      SMART; SM00283; MA; 1.
KW      Complete proteome.
SQ      SEQUENCE 693 AA; 74235 MW; EAD08C73BF573D80 CRC64;

Query Match      55.0%; Score 44; DB 16; Length 693;
Best Local Similarity 43.8%; Pred. No. 70;
Matches      7; Conservative      4; Mismatches      5; Indels      0; Gaps      0;

Oy      1 GCGRGTALVDEYQR 16
      11 : 11 : 11 : 11 :
Db      550 GCGRGTALVDEYQR 565

RESULT 13
O81716      PRELIMINARY;      PRT;      355 AA.
AC      O81716;
DT      01-NOV-1998 (TREMBLrel. 08, Created)
DT      01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT      01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE      HYPOHECTICAL 39.4 KDA PROTEIN.
GN      AT2G25070.
OS      Arabidopsis thaliana (Mouse-ear cress).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC      eucotsids II; Brassicales; Brassicaceae; Arabidopsids.
OX      NCBI_TaxID=3702;
RN      111
RP      SEQUENCE FROM N.A.
RC      STRAIN=CV. COLUMBIA;
RA      MEDLINE=20083487; PubMed=10617197;
RA      Lin X., Kaul S., Rounsley S.D., Shua T.P., Benito M.-I., Town C.D.,
RA      Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA      Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Morfitt K.S.,
RA      Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA      Adams M.D., Carreira A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA      Copenhaver G.P., Preuss D., Nierman W.C., White O., Eissen J.A.,
RA      Salzberg S.L., Fraser C.M., Venter M.C.;
RT      "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT      thaliana."
RL      Nature 402:761-768(1999).
RN      121
RP      SEQUENCE FROM N.A.
RC      STRAIN=CV. COLUMBIA;
RA      Lin X.;
RA      Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN      131
RP      SEQUENCE FROM N.A.

```

RA Yamada K., Liu S.-X., Pham P.-K., Banh J., Dale J. W., Goldsmith A. D.,
RA Jiang P.-X., Lee J.-M., Onodera C.-S., Quach H.-L., Tang C., Tortoli M.,
RA Yamamura Y., Yu G., Yu S., Bowers L., Carninci P., Chen H., Cheuk R.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawaji Y., Kim C., Kosgen A., Lam B., Lin J., Meyers M. C., Miranda M.,
RA Narasaka M., Nguyen M., Palm C. J., Sakurai T., Satou M., Seki M.,
RA Shih P., Southwick A., Tracy S. E., Shinozaki K., Davis R. W.,
RA Ecker J. R., Theodoris A., Theodoris I., Alt2925070 (GI:4559345). *;
RT Full length cDNA of gene PZC1.1/A1C2925070 (GI:4559345). *;
RT Full length cDNA of gene PZC1.1/A1C2925070 (GI:4559345). *;
DR EMBL: AY050873; AAC92810.1. -;
DR HSRP: P35813; IAG6.
DR Interpro: IPR000232; PZC.
DR Interpro: IPR001933; PZC_domain.
DR Pfam: PF00481; PZC_2.
DR SMART: SM00333; PZCC_1.
DR SMART: SM00333; PZC_S13.
DR PROSITE: PS01032; PZC; 1.
KO Hypothetical protein.
KO SEQUENCE 355 AA: 39354 MW: CAD638796203C746 CRC64:

	Query Match	Score	DB	Length
Best Local Similarity	54.4%	Ped. No. 40;	355;	
Matches	9;	Conservative	5;	Mismatches 2;
				Indels 1;
				Gaps 1;
OY	1	GCGG-RCQAATGGDDIRK	16	
	11	111111111111	11	
DB	104	GCGGRCRELAVGDDKMK	120	

RESULT	14		
098RM2			
ID	098RM2	PRELIMINARY:	PRT: 421 AA.
AC	098RM2:		
DT	01-OCT-2001 (TREMBlrel, 18, Created)		
DT	01-OCT-2001 (TREMBlrel, 18, Last sequence update)		
DT	01-OCT-2001 (TREMBlrel, 18, Last annotation update)		
DE	PROBABLE FAD-DEPENDENT MONOOXYGENASE.		
GN	ML1411.		
OS	Rhizobium lot1 (Mesorhizobium lot1).		
OC	Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;		
CC	Phyllobacteriaceae; Mesorhizobium.		
OX	NCBI_Taxid=381;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=MAF30309;		
RX	MEDLINE=1082930: PubMed=11214968;		
RA	Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,		
RA	Katsube A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,		
RA	Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,		
RA	Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,		
RA	Takemuchi C., Yamada M., Tabata S.;		
RT	*Complete genome structure of the nitrogen-fixing symbiotic bacterium		
FT	Mesorhizobium lot1.		
RL	DNA Res 7:331-338(2000).		
DR	EMBL: AF002987. BAB46932.1. -		
DR	InterPro: IPR000759. ADRndc_reductase.		
DR	InterPro: IPR001322. FAD_pyr_redox.		
DR	InterPro: IPR007335. Flavo_monooxygenase.		
DR	InterPro: IPR002358. Mox_p4D_binding.		
DR	InterPro: IPR002205. Mtd_binding.		
DR	InterPro: IPR001003. Pyridine_redox_2.		
DR	InterPro: IPR001100. pyr_redox.		
DR	InterPro: IPR003042. Ring_moxoygenase.		
DR	Pfam: PF01494. FAD_binding_3; 1		
DR	Pfam: PF01360. Monooxygenase; 1		
DR	PRINTS: PR00419. ADRDTASE.		
DR	PRINTS: PR00368. FADPVR.		
DR	PRINTS: PR00411. PDRDRTSEL.		
DR	PRINTS: PR00469. PDRDRTSEL.		
DR	PRINTS: PR00420. RGNMONOGENASE.		

KM	Monooxygenase; Complete proteome	421 AA; 45340 MW; 2B1EF11C87476F1E	CRG64;
QW	SEQUENCE	421 AA; 45340 MW; 2B1EF11C87476F1E	CRG64;
Query Match	53.8%;	Score 43;	DB 16;
Physical Similarity	8.0%;	Frete 59;	Length 421;
Matches	8;	Conservative	2;
		Mismatches	0;
		Indels	0;
		Gaps	0;
OY	3 VGR0L1A1D 12	111:11:111	
Db	294 VGR0L1A1D 303		

RESULT	15
09CD42	
ID	09CD42
AC	09CD42; PRELIMINARY; PRT: 447 AA.
DT	01-JUN-2001 (TRIMBLrel. 17, Created)
DT	01-JUN-2001 (TRIMBLrel. 17, Last sequence update)
DT	01-DEC-2001 (TRIMBLrel. 19, Last annotation update)
DE	ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE).
GN	ENO OR M0255.
OC	Mycobacterium leprae.
OC	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC	Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
CC	NCBI_TaxID=1769;
CC	[1]
RN	SEQUENCE FROM N.A.
RP	STRAIN=71;
FX	MEDLINE=21128732; PubMed=11234002;
RA	Cole S.T., Eigmeier K., Parthill J., James K.D., Thomson N.R.,
RA	Wheeler P.R., Honore N., Garfield T., Churchill C., Harris D.,
RA	Mangall K., Asham D., Brown D., Chillingworth T., Connor R.,
RA	Davies R.M., DeLisle K., Duthoy S., Fellinelli T., Fraser A., Hamlin N.,
RA	Morley D.S., Hornby T., Jukes K., Lescot C., Maclean J., Moule S.,
RA	Murphy S., Oliver K., Shal S.A., Rajadnan M.A., Rutherford K.M.,
RA	Rutler S., Seeger K., Simon S., Simons N., Skelton J., Squares R.,
RA	Squares B.G., Stevens R., Taylor K., Whitehead S., Woodward J.R.,
RA	Burrell B.G., decay in the leprosy bacillus.";
RT	Massive "eno" decay in the leprosy bacillus.";
RL	Native 495,1007-1011(2001).
CC	- 1-CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE - PHOSPHOENOLPYRUVATE +
CC	H ₂ O).
CC	- 1-COPROCTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
CC	THE DIMER (BY SIMILARITY).
CC	- 1-PATHWAY: GLYCOLYSIS.
CC	- 1-SUBUNIT: HOMODIMER (BY SIMILARITY).
CC	- 1-SUBCELLULAR LOCATION: CYTOSOLASMIC (BY SIMILARITY).
CC	- 1-SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
DR	EMBL, AL583917; CAC239763.1; -
DR	HSSP, P00924; 4ENL.
DR	LeprPro; M0255; -
DR	InterPro; IPR000941; Enolase.
DR	Pfam; PF00113; enolase; 1.
DR	PRINTS; PR00148; ENOLASE.
DR	PRODOM; P0000902; Enolase; 1.
DR	PROSITE; PS00164; ENOLASE; 1.
DR	NC Complete proteome; Glycolysis; Lyase; Magnesium.
DR	SEQUENCE 447 AA; 47250 MW; 63F03867DAA230B8 CRC64;

Search completed: September 20, 2002, 11:03:46

Fri Sep 20 11:03:13 2002

us-09-544-664-30.rpt

Job time: 1663 sec

PT cell lymphoma/leukemia 2 (bcl-2) function, especially useful for
 PT treating neurodegenerative disorders, stroke, or cancer -
 PS Claim 18: Page 18; 74pp; English.

XX The invention relates to a peptide conjugate having the formula:
 CC (R-X)-n-peptide where n = 1-10; X = C=O when the R-X group is attached
 CC to the N-terminus of the peptide, or a side chain of the peptide where
 CC the functional group of the side chain is NH₂ or OH; or X = O or NH.
 CC When the R-X group is attached to the C-terminus of the peptide, or a
 CC side chain of the peptide, where the side chain functional group is COOH
 CC or CONH₂, and R = 2-18C alkyl or alkoxy, 2-14C alkenyl optionally
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain
 CC alkyl group, or benzyl. The peptides AAR37001-B37058 represent examples
 CC of a bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
 CC the bcl-2 domain of the cell death apoptosis protein. The peptide conjugate is
 CC useful for modulating apoptosis in the cells of a subject or cell
 CC reversing B cell lymphoma/leukemia 2 (bcl-2) mediated blockage of
 CC apoptosis in cancer cells. It is also useful for inhibiting bcl-2
 CC function. In particular, the peptide conjugate is useful for treating a
 CC subject afflicted with a cancer characterized by cancer cells that
 CC express bcl-2. The cancer includes prostate colorectal, gastric, or
 CC non-small lung, renal or thyroid cancers, neuroblastoma, glioma, or
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
 CC conjugate is also useful for treating disorders characterized by
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
 CC
 XX Sequence 16 AA:

Query Match 100.0%; Score 81; DB 21; Length 16;
 Best Local Similarity 100.0%; Pred. No. 9, 3e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KKLSECKLRIGDELS 16
 Db 1 KKLSECKLRIGDELS 16

RESULT 2

AAV05411
 ID AAV05411 standard; peptide: 24 AA.

XX AAV05411;

DT 02-JUL-1999 (first entry)

XX Human BAX BH3 domain.

XX BH3 domain; cell death agonist; bcl homology domain; BCL-2 family;

XX apoptosis; oncofetal cancer; cell virus infected cell; inflammation;

XX anticarcinoma producing cell; cancer; lymphoproliferative condition;

XX arthritis; autoimmune disease; therapy.

XX Homo sapiens.

XX MO9916787-A1.

PD 08-APR-1999.

PF 22-SEP-1998; 96MO-US19765.

XX 07-OCT-1997; 97US-0946039.

XX 26-SEP-1997; 97US-0060133.

XX (UNITM) UNIV WASHINGTON.

XX Kortsmeier SJ;

DR WPI; 1999-255058/21.
 XX Bcl homology domain 3 polypeptide
 PS Claim 4: Fig 17a; 104pp; English.

XX This sequence represents a bcl homology domain 3 (BH3 domain) of the
 CC invention, derived from a proapoptotic member of the BCL-2 family. The
 CC Bcl polypeptide can be used in a method for promoting apoptosis in a
 CC target cell, especially where the cell is a cancer cell, a virus infected
 CC cell or an antibody producing cell. The BH3 polypeptide can be used
 CC in therapeutic compositions for treating disease including cancer, other
 CC lymphoproliferative conditions, arthritis, inflammation, and autoimmune
 CC diseases, which may result from the down regulation of cell death
 CC regulation.

XX Sequence 24 AA:

Query Match 100.0%; Score 81; DB 20; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1, 4e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KKLSECKLRIGDELS 16
 Db 5 KKLSECKLRIGDELS 20

RESULT 3

AAV06298
 ID AAV06298 standard; peptide: 26 AA.

XX AAV06298;

DT 29-JUL-1997 (first entry)

DE CD domain region for Bax amino acid residues 52-77.

XX Apoptosis; follicular lymphoma; tumour; p53; antibody.

XX Synthetic.

XX MO9635951-A1.

PD 14-NOV-1996.

PE 06-MAY-1996; 96MO-US06122.

XX 12-MAY-1995; 95US-0440391.

XX (IMMU-) IMMUNOGEN INC.

XX Chittenden TD; Lutz RJ;

XX WPI; 1996-518805/51.

XX N-PSDB; AAT4431.

XX Peptide(s) comprising CD domains - have similar activities to wild
 PT type Bax, and cause cellular apoptosis for treatment of viral
 PT infection

PS Claim 2: Page 52; 69pp; English.

XX The term CD domain refers to a protein domain first identified in
 CC Bax and shown to be essential for the interaction of Bax with bcl-x(L)
 CC and for Bax's cell killing function, and to peptides and/or molecules
 CC capable of mimicking its structure and/or function. The present sequence
 CC represents a CD domain corresponding to amino acid residues 52-77 of
 CC Bax. An antibody raised against a CD domain may induce or screen for
 CC CDNA expression library for genes complementary DNA inserts encoding
 CC immunorecognitive proteins. Truncated CD domain peptides have been
 CC shown to maintain the protein binding and cell killing function
 CC exhibited by wild type Bax. These molecules may induce apoptosis in

CC tumour cell. These peptides act independently of p53 status. Bax or
 CC CD domain mimetics that inhibit Bcl-2 may be selectively toxic to
 CC certain tumours, e.g. follicular lymphoma, which depend on high levels
 CC of Bcl-2 for their continued growth and survival. CD domain mimetics
 CC may also be used for combatting viral infections by causing apoptosis
 CC of infected cells.

XX Sequence 26 AA;

Query Match 100.0%; Score 81; DB 17; Length 26;

Best Local Similarity 100.0%; Pred. No. 1.5e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 KKLSECLKRIIGDELDS 16

6 KKLSECLKRIIGDELDS 21

RESULT 4

AA96323
 ID AAY96323 standard; Peptide: 26 AA.

XX AC AAY96323;

XX DT 17-AUG-2000 (first entry)

XX DE Mammalian Bax Bcl-2 homology domain 3 domain.

XX KM Mammal; apoptosis; cell death; BGC3; apoptosis promotion; Bax;

XX KW apoptosis inhibition; malignant cell; autoimmune disease.

XX OS Mammalia.

XX PN W0200026228-A1.

XX PD 11-MAY-2000.

XX PF 28-OCT-1999; 99MO-US25285.

XX PR 02-NOV-1998; 9805-0184168.

XX PA (CLON-) CLONTECH LAB INC.

XX PI Zhu L, Yin X, Chittenden T;

XX DR WPI: 2000-365560/31.

XX PT Novel polynucleotide encoding a BGC3 protein which is useful for
 PT modulating apoptosis, especially in the treatment of cancer and
 PT autoimmune diseases -

XX PS Disclosure: Fig 4; 47pp; English.

XX XX The present sequence is the mammalian Bax Bcl-2 homology domain 3
 CC (BH3) domain, which was used in a sequence alignment with the same
 CC domain of a putative version of the mammalian apoptosis

CC regulator BGC3, which was designated BGC3-ORF2. The BGC3 protein,
 CC nucleic acids and antibodies are suitable for use in promoting cell
 CC death or for preventing apoptosis in malignant cells and those causing
 CC autoimmune diseases.

XX XX Sequence 26 AA;

Query Match 100.0%; Score 81; DB 21; Length 26;

Best Local Similarity 100.0%; Pred. No. 1.5e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 KKLSECLKRIIGDELDS 16

3 KKLSECLKRIIGDELDS 18

RESULT 5

AA870373
 ID AAB70373 standard; Peptide: 26 AA.

XX AC AAB70373;

XX DT 02-MAY-2001 (first entry)

XX DE BAX BH3 consensus peptide sequence SEQ ID NO:6.

XX KM Bcl-XL/Bcl-2 associated cell death regulator; BAD; mutant; apoptosis;

XX KW immunostimulant; neuroprotective; neurotropic; antischismic; vulnary;

XX KW cytosolic; antiviral; antiarthritic; antiinflammatory; wound healing;

XX KW immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;

XX KW immunodeficiency disease; neurodegenerative disease; viral infection;

XX KW ischemic cell death; reperfusion cell death; arthritis; infertility;

XX KM lymphoproliferative condition; inflammation; autoimmune disease.

XX OS Unidentified.

XX PN W0200110888-A1.

XX PD 15-FEB-2001.

XX PF 30-MAY-2000; 2000MO-US11864.

XX PR 28-MAY-1999; 99US-0136783.

XX PA (APOF-) APOPTOSIS TECHNOLOGY INC.

XX PI Zhou X;

XX DR WPI: 2001-138734/14.

XX PT New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,
 PT useful for screening for candidate compounds which induce or inhibit
 PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
 PT Ser113 -

XX PS Example 2; Fig 3a; 157pp; English.

XX XX The present invention describes an isolated or synthetic polypeptide
 CC (1) comprising a less than full length amino acid sequence of a mutant
 CC Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its
 CC fragment, which contains amino acid substitutions at Ser118 of a human
 CC BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a murine
 CC BAD (shorter murine BAD). (1) has immunostimulant, neuroprotective,
 CC neurotropic, antischismic, vulnary, cytosolic, antiviral,
 CC antiarthritic, antiinflammatory and immunosuppressive activities, and
 CC can be used as an apoptosis inducer or inhibitor. BAD polypeptides and
 CC polynucleotides can be used for screening candidate compounds and drugs
 CC for activity that promote cell survival or apoptosis. Other uses include
 CC inducing or inhibiting apoptosis in a cell. Candidate compounds
 CC identified and (mutant) BAD polypeptides are useful in treating
 CC immunodeficiency diseases, neurodegenerative diseases, ischemic cell
 CC death, reperfusion cell death, wound healing, cancer, viral infections,
 CC lymphoproliferative conditions, arthritis, infertility, inflammation and
 CC autoimmune diseases. The present sequence represents a Bcl-family member
 CC BH3 domain consensus sequence which is used in an example from the
 CC present invention.

XX XX Sequence 26 AA;

Query Match 100.0%; Score 81; DB 22; Length 26;

Best Local Similarity 100.0%; Pred. No. 1.5e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 KKLSECLKRIIGDELDS 16

3 KKLSECLKRIIGDELDS 18

RESULT 6
ID AAB37006
AC AAB37006 standard; peptide: 27 AA.
DT AAB37006:
XX 28-FEB-2001 (first entry)
DE Bcl2 polypeptide BH3 domain in peptide #6.
KW Cytostatic; neuroprotective; anti-HIV; vitinucide; cerebroprotective;
KW cardiac; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;
KW apoptotic modulation; B cell lymphoma/leukemia 2; cancer; prostate;
KW colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
KW melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
KW stroke; myocardial infarction.
XX Homo sapiens.
XX WO200059526-A1.
XX 12-OCT-2000.
XX 06-APR-2000; 2000WO-US09352.
XX 07-APR-1999; 99US-0128202.
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX Huang Z, Wang J, Zhang Z, Shan S, Lu Z;
XX WPI: 2000-679325/66.
XX
XX New peptide conjugates for modulating apoptosis or for inhibiting B
XX cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
XX treating neurodegenerative disorders, stroke, or cancer
XX
XX Claim 18; Page 17; 74pp. English.
XX
XX The invention relates to a peptide conjugate having the formula:
XX (R-X)-peptide where n = 1-10; X = C=O, when the R-X group is attached
XX to the N-terminus of the peptide, or a side chain of the peptide where
XX the functional group of the side chain is NH2 or OH; or X = O or NH,
XX when the R-X group is attached to the C-terminus of the peptide, or a
XX side chain of the peptide, where the side chain functional group is COOH
XX or CONH2; and R = 2-18C alkyl or alkoxy, 2-14C alkenyl optionally
XX monosubstituted with a 1-5C straight or branched chain alkyl group,
XX or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally
XX phenyl optionally monosubstituted with a 1-5C straight or branched chain
XX alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples
XX of the peptide portion of the conjugate. The peptides represent analogues
XX of the BH3 domain of the cell death agonist Bad. The peptide conjugate is
XX useful for modulating apoptosis in the cells of a subject, or for
XX reversing a cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of
XX apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
XX function. In particular, the peptide conjugate is useful for treating a
XX subject afflicted with a cancer characterized by cancer cells that
XX express Bcl-2. The cancer includes prostate, colorectal, gastric,
XX non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
XX acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
XX conjugate is also useful for treating disorders characterized by
XX increased apoptosis, e.g. neurodegenerative disorders, acquired
XX immunodeficiency syndrome (AIDS), stroke or myocardial infarction.
XX
XX Sequence 27 AA:

QY	1	KKLSECTKRIQDELD	16	
DB	6	KKLSECTKRIQDELD	21	
RESULT	7			
ID	AA05430	standard; peptide: 34 AA.		
AC	AA05430;			
DT	02-JUL-1999	(first entry)		
DE	Human BAX BH3 domain.			
KW	BH3 domain: cell death agonist; bcl homology domain; Bcl-2 family; apoptosis promoter; cancer cell; virus infected cell; inflammation; autolysosome producing cell; cancer; lymphoproliferative condition; arthritis; autoimmune disease; therapy.			
CS	Homo sapiens.			
PN	MO9916787-A1.			
PD	08-APR-1999.			
PE	22-SEP-1998: 96NO-US19765.			
PR	07-OCT-1997: 97US-0946039.			
PR	26-SEP-1997: 97US-0060133.			
PA	(UNIW) UNTY WASHINGTON.			
PI	Korsmeyer SJ:			
DR	WPI: 1999-255058/21.			
PT	Bcl homology domain 3 polypeptide			
PS	Example 10; Fig 17a; 104pp; English.			
CC	This sequence represents a bcl homology domain 3 (BH3 domain) of the			
CC	invention, derived from a proapoptotic member of the BCL-2 family. The			
CC	BH3 polypeptide can be used in a method for promoting apoptosis in a			
CC	target cell, especially where the cell is a cancer cell, a virus infected			
CC	cell, or an autolysosome producing cell. The BH3 polypeptide can be used			
CC	in therapeutic compositions for treating disease including cancer, other			
CC	lymphoproliferative conditions, arthritis, inflammation, and autoimmune			
CC	diseases, which may result from the down regulation of cell death			
CC	regulation.			
XX	Sequence	34 AA:		
XX	50			
QY	Query Match	100.08;	Score 81;	DB 20;
XX	Best Local Similarity	100.08;	Pred. No. 2e-06;	Length 34;
XX	Matches 16;	Conservative 0;	Mismatches 0;	Indels 0;
XX	Gaps 0;			
DB	1 KKLSECTKRIQDELD	16		
XX	5 KKLSECTKRIQDELD	20		
RESULT	8			
ID	AA070818			
AC	AA070818 standard; Protein; 78 AA.			
DT	31-JUL-2000	(first entry)		
DE	Human neuroprotective truncated BAX protein, tBAX78.			

Human: truncated BAX protein; tBAX78; BAX alpha; BCL-2 family; neuron; anti-apoptotic; cerebroprotective; neuroprotective; neurotrophic; treatment; neurodegenerative disease; peripheral nerve injury; spinal cord injury; head trauma; stroke.

Homo sapiens.

Key Location/Qualifiers
Region 1..58 "N-terminal region of BAX alpha"
FT /note="59..73
FT /label="BH3-domain

WO200023083-A1.
27-APR-2000.
22-OCT-1999; 99MO-US24747.
22-OCT-1998; 98US-0177315.
22-OCT-1998; 98US-0177315.
(UNITW) UNIV WASHINGTON.
Johnson EM, Easton R;
WPI: 2000-339513/29.
Truncated BAX polypeptides useful for preventing apoptosis of neurons for the treatment of nervous system disorders -
Claim 4; Page 33; 43pp; English.

The present sequence is a specifically claimed truncated BAX protein tBAX78 which inhibits neuronal apoptosis induced by trophic factor deprivation. The protein consists of first 78 amino acids of human BAX alpha, that includes the N-terminal region and BH3 domain. It lacks the BH1, BH2 and C-terminal transmembrane domains of the full-length BAX alpha. The tBAX protein lacking only the transmembrane domain has been shown to have anti-apoptotic activity. The present sequence is used to treat diseases associated with neuronal apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury, spinal cord injury, head trauma and stroke.

Sequence 78 AA:

Query Match 100.0%; Score 81; DB 21; Length 78;
Best Local Similarity 100.0%; Pred. No. 4,8e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRLSECLKRGDELD 16
Db 57 KRLSECLKRGDELD 72

RESULT 9
ID AAY34149 standard; Protein: 131 AA.
XX AAY34149;
XX 30-NOV-1999 (first entry)
XX Human truncated Bax protein.
XX Apoptosis; adenovirus; dimeric; Bcl-2; p53; cancer; gene therapy.
XX Homo sapiens.
XX Key Location/Qualifiers
XX 59..101
XX /note="Portion of BH3 domain essential for dimerisation"

PN W09946371-A2.
XX 16-SEP-1999.
XX 11-MAR-1999; 99MO-US05359.
XX 11-MAR-1998; 98US-0077541.
XX (TEXA) UNIV TEXAS SYSTEM.
XX McDonald TJ, Swisher SG, Pang B, Bruckheimer EM, Sarkiss MG;
XX Ji L, Roth JR;
XX WPI: 1999-551404/46.
XX N-PSDB; AA219763.
XX New adenovirus vectors, used for killing or inhibiting the growth of cells and for treating cancers -
Claim 26; Page 148-149; 151pp; English.

This sequence represents a human truncated Bax protein. The CDNA contains a single base deletion relative to the wild-type (AA219764), causing a frameshift which leads to translation of a premature stop codon, resulting in a truncated protein. However, the domain responsible for its function is still present in the truncated protein. Bax (Bcl-2 associated X protein) is a proapoptotic member of the Bcl-2 gene family. Bax functions as a primary response gene in the p53-regulated apoptotic pathway. The bax gene promoter has 4 p53 binding sites and the bax expression of Bax is upregulated at the transcriptional level by p53, and Bax mRNA and protein expression have been shown to increase following induction of p53. The protein can function as a homodimer, or it can heterodimerize with Bcl-2 gene family members. Bcl-2 family members antagonize the proapoptotic protein Bcl-2 heterodimer with the "rheostat" model. This model suggests that the relative amounts of Bcl-2 and Bax determine the susceptibility of a cell to undergo apoptosis. If Bcl-2 is in excess, Bcl-2/Bax heterodimers predominate and cell death is inhibited. If Bax is in excess, however, Bax homodimers predominate and the cell becomes susceptible to apoptosis following exposure to an apoptotic stimulus. Additionally, Bax can function in its monomeric form to accelerate cell death. Use of novel adenoviral vectors containing this Bax gene may augment and complement wild-type p53 gene therapy, which induces a G1 cell cycle arrest and/or apoptosis in malignant cells carrying p53 mutations. In addition, Bax overexpression could provide the apoptotic effect of p53 without the need for p53 itself.

Sequence 131 AA:

Query Match 100.0%; Score 81; DB 20; Length 131;
Best Local Similarity 100.0%; Pred. No. 8,3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRLSECLKRGDELD 16
Db 57 KRLSECLKRGDELD 72

RESULT 10
ID AAR71406 standard; Protein: 192 AA.
XX AAR71406;
XX 15-NOV-1995 (first entry)
XX Human Bax protein.
XX Human: Bcl-2; alpha; beta; proto-oncogene; hematopoietic cell line; apoptosis; membrane-associated cytoplasmic protein; B cell; T cell; proliferation; cell cycle progression; Bax; apoptotic cell death; apoptosis; cytokine; death repressor; BH1; BH2; cancer therapy.

KW hyperplasia; immunodeficiency disease; AIDS; neurodegeneration;
KW ischaemic cell death.

XX Homo sapiens.

XX MO9505750-A.

XX 02-MAR-1995.

XX 24-AUG-1994; 94MO-US09701.

XX 26-AUG-1993; 93US-0112208.

XX 25-MAY-1994; 94US-0248819.

XX (UNIT) UNIV WASHINGTON.

XX Korsmeyer SJ;

XX WPI: 1995-106605/14.

XX N-PSDB: AA097806.

XX Method for producing and identifying mutant bcl-2 proteins -
XX that lack death repressor activity and/or lacks binding to Bax.

XX Disclosure; Fig 3; 133pp; English.

XX This sequence represents human Bax protein. Bax is a protein which is
XX associated with the human bcl-2 gene and beta proteins, the sequences
XX of which are given in PAR71404-05 respectively. Bcl-2 is encoded by a
XX proto-oncogene and is capable of inhibiting apoptosis in many
XX hematopoietic cell systems. bcl-2 is a 26 kD membrane-associated
XX cytoplasmic protein and is thought to function by enhancing the survival
XX of hematopoietic cells of B and T origins rather than directly promoting
XX proliferation of these cell types. bcl-2 has not been shown to directly
XX promote cell cycle progression nor does it necessarily alter the dose
XX response to limiting concentrations of IL-3. bcl-2 has been shown to
XX form heterodimers with this 21 kD protein, Bax. Overexpressed Bax
XX accelerates apoptotic cell death induced by cytokine deprivation in an
XX IL-3 dependent cell line, and it also acts to counter the death repressor
XX activity of bcl-2. Therefore, the ratio between bcl-2 and Bax determines
XX cell survival or death following an apoptotic stimulus. The invention
XX gives a mutant form of bcl-2 in which there is at least one amino acid
XX substitution or deletion in the BH1 or BH2 domains. This makes the
XX mutant protein substantially incapable of binding Bax and/or incapable
XX of death repressor activity. Down regulation of bcl-2 is useful in
XX cancer therapy, controlling hyperplasias and eliminating self-reactive
XX clones in autoimmunity by favouring death effector molecules. Up
XX regulating bcl-2 is beneficial in treatment and diagnosis of immuno-
XX deficiency diseases, including AIDS and neurodegenerative and ischaemic
XX cell death.

XX Sequence 192 AA:

Query Match 100.0%; Score 81; DB 16; Length 192;

Best Local Similarity 100.0%; Pred. NO. 1.2e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLSECLKRIQDELDLS 16

DB 57 KKLSECLKRIQDELDLS 72

RESULT 11

AAV34150 standard: ProteIn: 192 AA.

XX AAV34150;

XX 30-NOV-1999 (first entry)

XX Human wild-type Bax protein.

XX

KW Apoptosis; adenovirus; dimeric; Bcl-2; p53; cancer; gene therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

XX 59..101

XX Domain /note="Portion of BH3 domain essential for dimerisation"

XX MO9946371-A2.

XX 16-SEP-1999.

XX 11-MAR-1999; 99MO-US05359.

XX 11-MAR-1998; 98US-0077541.

XX (TEXA) UNIV TEXAS SYSTEM.

XX McDonnell TV, Swisher SG, Fang B, Bruckheimer EM, Sarkiss MG;

XX JI L, Roth JA;

XX WPI: 1999-551404/46.

XX N-PSDB: AA219764.

XX New adenovirus vectors, used for killing or inhibiting the growth of
XX cells and for treating cancers -

XX Disclosure; Page 149-150; 151pp; English.

XX This sequence represents human wild-type Bax protein. A naturally
XX occurring mutant protein (AAV34149) was also isolated. Bax (Bcl-2
XX associated X protein) is a proapoptotic member of the bcl-2 gene family.
XX Bax functions as a primary response gene in the p53-regulated apoptotic
XX pathway. The Bax gene promoter has 4 p53 binding sites and the
XX expression of Bax is upregulated at the transcriptional level by p53, and
XX Bax mRNA and protein expression have been shown to increase following
XX induction of p53. Bax protein can function as a homodimer, or it can
XX heterodimerise with other Bcl-2 gene family members such as the
XX antiapoptotic protein Bcl-2. Heterodimerisation of Bcl-2 family members
XX provides a means of controlling cell death via the "rheostat" model. This
XX model suggests that the relative amounts of Bcl-2 and Bax determine the
XX susceptibility of a cell to undergo apoptosis. If Bcl-2 is in excess,
XX Bcl-2/Bax heterodimers predominate and cell death is inhibited. If Bax is
XX in excess, however, Bax homodimers predominate and the cell becomes
XX susceptible to apoptosis following exposure to an apoptotic stimulus.
XX Additionally, Bax can function in its monomeric form to accelerate cell
XX death. Use of novel adenoviral vectors containing the Bax gene may
XX augment and complement wild-type p53 gene therapy, which induces a G1
XX cell cycle arrest and/or apoptosis in malignant cells carrying p53
XX mutations. In addition, Bax overexpression could provide the apoptotic
XX effect of p53 without the need for p53 itself.

XX Sequence 192 AA:

Query Match 100.0%; Score 81; DB 20; Length 192;

Best Local Similarity 100.0%; Pred. NO. 1.2e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLSECLKRIQDELDLS 16

DB 57 KKLSECLKRIQDELDLS 72

RESULT 12

AAV05435 standard: pepptide: 192 AA.

XX AAV05435;

XX 02-JUL-1999 (first entry)

XX Human Bax protein sequence.

XX

XX BH3 domain: cell death agonist; bcl homology domain; Bcl-2 family;
 KW apoptosis promoter; cancer cell; virus infected cell; inflammation;
 KW antibody producing cell; cancer; lymphoproliferative condition;
 KW arthritis; autoimmune disease; therapy.
 XX
 OS Homo sapiens.
 XX
 PN M09916787-A1.
 PD
 XX 08-APR-1999.
 XX
 XX 22-SEP-1998: 98MO-0519765.
 XX
 XX 07-OCT-1997: 97US-0946039.
 PR 26-SEP-1997: 97US-0060133.
 XX
 XX (UNIW) UNIV WASHINGTON.
 PA
 XX
 PI Korsmeyer SJ;
 XX
 DR WPI: 1999-255058/21.
 XX
 XX Bcl homology domain 3 polypeptide
 PT
 XX
 PS Disclosure: Fig 21c; 104pp; English.
 XX
 XX This sequence represents the human BAX protein.
 CC The invention relates to a bcl homology domain 3 (BH3 domain).
 CC derived from a proapoptotic member of the Bcl-2 family. The
 CC BH3 polypeptide can be used in a method for promoting apoptosis in a
 CC target cell, especially where the cell is a cancer cell, a virus infected
 CC cell or an autacell producing cell. The BH3 polypeptide can be used
 CC in therapeutic compositions for treating disease including cancer, other
 CC lymphoproliferative conditions, arthritis, inflammation, and autoimmune
 CC diseases, which may result from the down regulation of cell death
 CC regulation.
 CC
 XX
 SQ Sequence 192 AA:

Query Match 100.0%: Score 81; DR 20; Length 192;
 Best Local Similarity 100.0%: Pred. No. 1.2e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRISCKLRIGDELD 16
 |||
 DB 57 KRISCKLRIGDELD 72

RESULT 13

AAW87804
 ID AAW87804 standard; Protein: 192 AA.
 XX
 AC AAW87804;
 XX
 DT 10-MAR-1999 (first entry)
 XX
 XX A human Bcl-2 associated protein designated Bax.
 KW Human: Bcl-2 associated protein; Bax; bcl-2; antibody; modulator;
 KW bcl-2-related function; apoptosis.
 XX
 OS Homo sapiens.
 XX
 PN US5856171-A.
 PD
 XX 07-118 Location/Qualifiers
 FT Domain /note="BH1 domain"
 FT 146..168
 FT Domain /note="BH2 domain"
 XX
 PN US5856171-A.

PD 05-JAN-1999.
 XX
 XX 10-NOV-1994: 94US-0337646.
 PF
 XX 10-NOV-1994: 94US-0337646.
 PR 26-AUG-1993: 93US-0112208.
 PR 25-MAY-1994: 94US-0248819.
 XX
 XX (UNIW) UNIV WASHINGTON.
 PA
 XX
 PI Korsmeyer SJ;
 XX
 DR WPI: 1999-105119/09.
 DR N-FSDS: AAW84005.
 XX
 XX DNA composition encoding bcl-2 two-hybrid and reporter system - for
 XX identifying modulators of bcl-2 function
 XX
 XX Example 1: Columns 71-74; 105pp; English.
 XX
 XX The present sequence represents a human bcl-2 associated protein
 CC designated Bax. The Bax protein is used in a composition which
 CC comprises a bcl-2 family member polypeptide, a naturally occurring
 CC Bax polypeptide and an antibody that binds to the Bax polypeptide.
 CC The composition is used to identify modulators of bcl-2-related
 CC function, e.g. substances that inhibit binding of Bax to bcl-2,
 CC which would be potentially useful as drugs for modulating
 CC apoptosis.
 CC
 XX
 SQ Sequence 192 AA:

Query Match 100.0%: Score 81; DR 20; Length 192;
 Best Local Similarity 100.0%: Pred. No. 1.2e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRISCKLRIGDELD 16
 |||
 DB 57 KRISCKLRIGDELD 72

RESULT 14

AAW87809
 ID AAW87809 standard; Protein: 192 AA.
 XX
 AC AAW87809;
 XX
 DT 10-MAR-1999 (first entry)
 XX
 XX A human Bcl-2 associated protein designated Bax.
 DE
 XX Human: Bcl-2 associated protein; Bax; bcl-2; antibody; modulator;
 KW bcl-2-related function; apoptosis.
 XX
 OS Homo sapiens.
 XX
 PN US5856171-A.
 PD
 XX 05-JAN-1999.
 XX
 XX 10-NOV-1994: 94US-0337646.
 PR 26-AUG-1993: 93US-0112208.
 PR 25-MAY-1994: 94US-0248819.
 XX
 XX (UNIW) UNIV WASHINGTON.
 PA
 XX
 PI Korsmeyer SJ;
 XX
 DR WPI: 1999-105119/09.
 DR
 XX DNA composition encoding bcl-2 two-hybrid and reporter system - for

10/10/02

Fri Sep 20 11:03:13 2002

us-09-544-664-32.rai

Page 1

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2002, 10:37:21 ; Search time 75.64 seconds
(without alignments) 5.167 Million cell updates/sec

Title: US-09-544-664-32

Perfect score: 81

Sequence: 1 KKLSECLRKRGDELDS 16

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents, AA:*

1: /cgn2_6/prodate/2/1aa/5a_COMB.pep:*
2: /cgn2_6/prodate/2/1aa/5b_COMB.pep:*
3: /cgn2_6/prodate/2/1aa/6a_COMB.pep:*
4: /cgn2_6/prodate/2/1aa/6b_COMB.pep:*
5: /cgn2_6/prodate/2/1aa/6c_COMB.pep:*
6: /cgn2_6/prodate/2/1aa/6d_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	81	100.0	20 4	US-09-236-385A-40
2	81	100.0	20 1	US-09-236-385A-40
3	81	100.0	26 1	US-08-440-381-24
4	81	100.0	26 2	US-08-908-597A-24
5	81	100.0	26 2	US-08-908-597A-24
6	81	100.0	26 4	US-09-236-385A-6
7	81	100.0	26 4	US-09-236-385A-6
8	81	100.0	26 5	PCT-US96-06122-6
9	81	100.0	26 5	PCT-US96-06122-6
10	81	100.0	34 1	US-08-440-391-13
11	81	100.0	34 2	US-08-908-597A-13
12	81	100.0	34 4	US-09-236-385A-13
13	81	100.0	34 5	PCT-US96-06122-13
14	81	100.0	42 2	US-08-798-897-22
15	81	100.0	42 2	US-08-798-897-22
16	81	100.0	132 1	US-08-112-208C-8
17	81	100.0	132 1	US-08-112-208C-8
18	81	100.0	132 1	US-08-248-819A-8
19	81	100.0	132 1	US-08-248-819A-8
20	81	100.0	192 1	US-08-607-269-25
21	81	100.0	192 1	US-08-471-058-13
22	81	100.0	192 2	US-08-337-646A-2
23	81	100.0	192 2	US-08-337-646A-2
24	81	100.0	192 2	US-08-856-531-8
25	81	100.0	192 2	US-08-856-531-8
26	81	100.0	192 2	US-08-856-531-8
27	81	100.0	192 2	US-08-856-531-8

28	81	100.0	192 3	US-08-471-057-13	Sequence 13, Appl
29	81	100.0	192 4	US-09-127-048-7	Sequence 7, Appl
30	81	100.0	192 4	US-08-927-326-2	Sequence 2, Appl
31	81	100.0	192 4	US-08-927-326-2	Sequence 9, Appl
32	81	100.0	192 5	PCT-US95-04600-25	Sequence 25, Appl
33	81	100.0	221 1	US-08-616-742A-9	Sequence 3, Appl
34	81	100.0	221 1	US-08-616-742A-9	Sequence 5, Appl
35	78	96.3	192 1	US-08-112-208C-3	Sequence 3, Appl
36	78	96.3	192 1	US-08-112-208C-3	Sequence 8, Appl
37	78	96.3	192 1	US-08-248-819A-3	Sequence 8, Appl
38	78	96.3	192 1	US-08-248-819A-3	Sequence 8, Appl
39	78	96.3	192 2	US-08-337-646A-3	Sequence 3, Appl
40	78	96.3	192 2	US-08-337-646A-3	Sequence 8, Appl
41	78	96.3	192 2	US-08-856-531-3	Sequence 3, Appl
42	78	96.3	192 2	US-08-856-531-3	Sequence 8, Appl
43	78	96.3	192 2	US-08-856-531-3	Sequence 8, Appl
44	78	96.3	192 2	US-08-856-531-3	Sequence 8, Appl
45	78	96.3	192 4	US-09-127-048-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-236-385A-40
; Sequence 40, Application US/09236385A
; Patent No. 6221615
; GENERAL INFORMATION:
; APPLICANT: CHITTENDEN, Thomas D.; and
; LUTZ, Robert J.
; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
; MODULATE APOPTOSIS
; NUMBER OF SEQUENCES: 41
; CORRESPONDING ADDRESS:
; STREET: 1455 pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/09/236,385A
; FILING DATE: 25-Jan-1999
; PUBLICATION DATE: 15-Jun-2000
; ATTORNEY INFORMATION:
; NAME: WIXON, HENRY N.
; REGISTRATION NUMBER: 32,073
; TELECOMMUNICATION INFORMATION:
; (C) ATTORNEY DOCKET NO. 104322.147CIP
; TELEPHONE: 202-942-8400
; TELEFAX: 202-942-8484
; INFORMATION FOR SEQ ID NO: 40
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 40
US-09-236-385A-40

Query Match 100.0%; Score 81; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLSECLRKRGDELDS 16
|||||
DB 3 KKLSECLRKRGDELDS 18

```

RESULT 2
US-08-440-391-6
: Sequence 6, Application US/08440391
: Patent No. 5656725
: GENERAL INFORMATION:
: APPLICANT: CHITTENDEN, Thomas D.: and
: APPLICANT: LUTZ, Robert J.
: TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
: MODULATE APOPTOSIS
: NUMBER OF SEQUENCES: 34
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Hale and Dorr
: STREET: 1455 Pennsylvania Avenue, N.W.
: CITY: Washington
: STATE: D.C.
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: OPERATING SYSTEM: PC/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/440,391
: FILING DATE: 12-MAY-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: WIXON, HENRY N.
: REGISTRATION NUMBER: 32,073
: REFERENCE/DOCKET NUMBER: 104322.147
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-942-8400
: TELEFAX: 202-942-8400
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 26 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: Peptide
: US-08-440-391-6

Query Match 100.0%; Score 81; DB 1; Length 26;
Best Local Similarity 100.0%; Freq. No. 5,4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRISECKRIDEELS 16
DB 6 KRISECKRIDEELS 21

RESULT 3
US-08-440-391-24
: Sequence 24, Application US/08440391
: Patent No. 5656725
: GENERAL INFORMATION:
: APPLICANT: CHITTENDEN, Thomas D.: and
: APPLICANT: LUTZ, Robert J.
: TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
: MODULATE APOPTOSIS
: NUMBER OF SEQUENCES: 34
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Hale and Dorr
: STREET: 1455 Pennsylvania Avenue, N.W.
: CITY: Washington
: STATE: D.C.
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: OPERATING SYSTEM: PC/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:

```

```

: APPLICATION NUMBER: US/08/440,391
: FILING DATE: 12-MAY-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: WIXON, HENRY N.
: REGISTRATION NUMBER: 32,073
: REFERENCE/DOCKET NUMBER: 104322.147
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-942-8400
: TELEFAX: 202-942-8400
: INFORMATION FOR SEQ ID NO: 24:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 26 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-440-391-24

Query Match 100.0%; Score 81; DB 1; Length 26;
Best Local Similarity 100.0%; Freq. No. 5,4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRISECKRIDEELS 16
DB 6 KRISECKRIDEELS 21

RESULT 4
US-08-908-597A-6
: Sequence 6, Application US/08908597A
: Patent No. 5656795
: GENERAL INFORMATION:
: APPLICANT: CHITTENDEN, Thomas D.: and
: APPLICANT: LUTZ, Robert J.
: TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
: MODULATE APOPTOSIS
: NUMBER OF SEQUENCES: 34
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Hale and Dorr
: STREET: 1455 Pennsylvania Avenue, N.W.
: CITY: Washington
: STATE: D.C.
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: OPERATING SYSTEM: PC/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/908,597A
: FILING DATE:
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/440,391
: FILING DATE: 12-MAY-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: WIXON, HENRY N.
: REGISTRATION NUMBER: 32,073
: REFERENCE/DOCKET NUMBER: 104322.147
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-942-8400
: TELEFAX: 202-942-8400
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 26 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-908-597A-6

Query Match 100.0%; Score 81; DB 2; Length 26;

```

Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLSECLKRIIDDELDS 16
Db 6 KKLSECLKRIIDDELDS 21

RESULT 5
US-08-908-597A-24

; Sequence 24, Application US/08908597A

; Patent No. 5863795

; GENERAL INFORMATION:

; APPLICANT: CHITTENDEN, Thomas D.; and

; ATTORNEY/AGENT INFORMATION:

; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hale and Dorr

; STREET: 1455 Pennsylvania Avenue, N.W.

; CITY: Washington

; STATE: D.C.

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; FILING DATE: US/08/908, 597A

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/440, 391

; FILING DATE: 12-MAY-1995

; ATTORNEY/AGENT INFORMATION:

; REGISTRATION NUMBER: N. 32, 073

; REFERENCE/DOCKET NUMBER: 104322.147

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-942-8400

; INFORMATION FOR SEQ ID NO: 24:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 26 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-908-597A-24

Query Match 100.0%; Score 81; DB 2; Length 26;

Best Local Similarity 100.0%; Pred. No. 5.4e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLSECLKRIIDDELDS 16

Db 6 KKLSECLKRIIDDELDS 21

RESULT 6

US-09-236-385A-6

; Sequence 6, Application US/09236385A

; Patent No. 6221615

; GENERAL INFORMATION:

; APPLICANT: CHITTENDEN, Thomas D.; and

; ATTORNEY/AGENT INFORMATION:

; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH

; NUMBER OF SEQUENCES: 41

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hale and Dorr

STREET: 1455 Pennsylvania Avenue, N.W.

CITY: Washington

STATE: D.C.

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/236, 385A

FILING DATE: 25-Jan-1999

CLASSIFICATION: <unknown>

ATTORNEY/AGENT INFORMATION:

NAME: WIXON, HENRY N.

REGISTRATION NUMBER: 32, 073

(C) ATTORNEY DOCKET NO. 104322.147CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-942-8400

TELEFAX: 202-942-8484

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 6;

US-09-236-385A-6

Query Match 100.0%; Score 81; DB 4; Length 26;

Best Local Similarity 100.0%; Pred. No. 5.4e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLSECLKRIIDDELDS 16

Db 6 KKLSECLKRIIDDELDS 21

RESULT 7

US-09-236-385A-24

; Sequence 24, Application US/09236385A

; Patent No. 6221615

; GENERAL INFORMATION:

; APPLICANT: CHITTENDEN, Thomas D.; and

; ATTORNEY/AGENT INFORMATION:

; TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH

; NUMBER OF SEQUENCES: 41

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Hale and Dorr

; STREET: 1455 Pennsylvania Avenue, N.W.

; CITY: Washington

; STATE: D.C.

; ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/236, 385A

FILING DATE: 25-Jan-1999

CLASSIFICATION: <unknown>

ATTORNEY/AGENT INFORMATION:

NAME: WIXON, HENRY N.

REGISTRATION NUMBER: 32, 073

(C) ATTORNEY DOCKET NO. 104322.147CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-942-8400

TELEFAX: 202-942-8484

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-236-385A-24

Query Match 100.0%; Score 81; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 5,4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLSECKLRIGDELD 16
DB 6 KKLSECKLRIGDELD 21

RESULT 8
PCT-US96-06122-6
Sequence 6, Application PC/TUS9606122
GENERAL INFORMATION:
APPLICANT: IMMUNOGEN, INC.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESS: Hale and Dorf
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06122
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/440,391
FILING DATE: 12-MAY-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.147PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US96-06122-6

Query Match 100.0%; Score 81; DB 5; Length 26;
Best Local Similarity 100.0%; Pred. No. 5,4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLSECKLRIGDELD 16
DB 6 KKLSECKLRIGDELD 21

RESULT 9
PCT-US96-06122-24
Sequence 24, Application PC/TUS9606122
GENERAL INFORMATION:

APPLICANT: IMMUNOGEN, INC.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESS: Hale and Dorf
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06122
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/440,391
FILING DATE: 12-MAY-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION/DOCKET NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.147PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US96-06122-24

Query Match 100.0%; Score 81; DB 5; Length 26;
Best Local Similarity 100.0%; Pred. No. 5,4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLSECKLRIGDELD 16
DB 6 KKLSECKLRIGDELD 21

RESULT 10
US-08-440-391-13
Sequence 13, Application US/08440391
Patent No. 5656725
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESS: Hale and Dorf
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,391
FILING DATE: 12-MAY-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: WIXON, HENRY N.
 REGISTRATION NUMBER: 32,073
 REFERENCE/DOCKET NUMBER: 104322.147
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-942-8400
 TELEFAX: 202-942-8484
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 34 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-440-391-13

Query Match 100.0%; Score 81; DB 1; Length 34;
 Best Local Similarity 100.0%; Pred. No. 7.2e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRLSECLKRIQDELD 16
 DB 8 KRLSECLKRIQDELD 23

RESULT 11
 US-08-908-597A-13
 Sequence 13, Application US/08908597A
 Patent No. 5863795
 GENERAL INFORMATION:
 APPLICANT: CHITTENDEN, Thomas D.; and
 ATTORNEY/AGENT INFORMATION:
 NAME: WIXON, HENRY N.
 REGISTRATION NUMBER: 32,073
 REFERENCE/DOCKET NUMBER: 104322.147
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-942-8400
 TELEFAX: 202-942-8484
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 34 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-908-597A-13

Query Match 100.0%; Score 81; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 7.2e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRLSECLKRIQDELD 16
 DB 8 KRLSECLKRIQDELD 23

RESULT 12
 US-09-236-385A-13
 Sequence 13, Application US/09236385A
 Patent No. 6221615
 GENERAL INFORMATION:
 APPLICANT: CHITTENDEN, Thomas D.; and
 ATTORNEY/AGENT INFORMATION:
 NAME: WIXON, HENRY N.
 REGISTRATION NUMBER: 32,073
 REFERENCE/DOCKET NUMBER: 104322.147CIP

TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
 MODULATE APOPTOSIS
 NUMBER OF SEQUENCES: 41
 CORRESPONDENCE ADDRESS:
 ADDRESSER: Hale and Dorr
 STREET: 1455 Pennsylvania Avenue, N.W.
 CITY: Washington
 STATE: D.C.
 ZIP: 20004

COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA: US/09/236,385A
 FILING DATE: 25-Jan-1999
 CLASSIFICATION: UNKNOWN

ATTORNEY/AGENT INFORMATION:
 NAME: WIXON, HENRY N.
 REGISTRATION NUMBER: 32,073

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-942-8400
 TELEFAX: 202-942-8484
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 34 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 13:

US-09-236-385A-13

Query Match 100.0%; Score 81; DB 4; Length 34;
 Best Local Similarity 100.0%; Pred. No. 7.2e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KRLSECLKRIQDELD 16
 DB 8 KRLSECLKRIQDELD 23

RESULT 13
 PCT-US96-06122-13
 Sequence 13, Application PC/TUS9606122
 GENERAL INFORMATION:
 APPLICANT: IMMUNOGEN, INC.
 TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS
 WHICH MODULATE APOPTOSIS
 NUMBER OF SEQUENCES: 34
 CORRESPONDENCE ADDRESS:
 ADDRESSER: Hale and Dorr
 STREET: 1455 Pennsylvania Avenue, N.W.
 CITY: Washington
 STATE: D.C.
 ZIP: 20004

COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 SOFTWARE: Patent In Release #1.0, Version #1.25

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06122
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/440,391
FILING DATE: 12-MAY-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322,147PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US96-06122-13

Query Match 100.0%; Score 81; DB 5; length 34;
Best local similarity 100.0%; Pred. No. 7.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Yy 1 KKLSECKLRIGDELD 16
Db 8 KKLSECKLRIGDELD 23

RESULT 14
US-08-798-897-22
Sequence 22, Application US/08798897
Patent No. 5789201
GENERAL INFORMATION:
APPLICANT: Gastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
NUMBER OF INVENTIONS: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483,0140001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-798-897-22

Query Match 100.0%; Score 81; DB 1; length 42;
Best local similarity 100.0%; Pred. No. 8.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Yy 1 KKLSECKLRIGDELD 16
Db 27 KKLSECKLRIGDELD 42

RESULT 15
US-08-978-523-22
Sequence 22, Application US/08978523
Patent No. 5883229
GENERAL INFORMATION:
APPLICANT: Gastella, John
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
NUMBER OF INVENTIONS: Homologue
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,523
FILING DATE: herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/798,897
FILING DATE: February 11, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1483,0140002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-978-523-22

Query Match 100.0%; Score 81; DB 2; length 42;
Best local similarity 100.0%; Pred. No. 8.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Yy 1 KKLSECKLRIGDELD 16
Db 27 KKLSECKLRIGDELD 42

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2002, 10:39:10 : Search time 95.59 Seconds

(without alignments)
16.084 Million cell updates/sec

Title: US-09-544-664-32

Perfect score: 81

Sequence: 1 KKLSECLRIKIDELDS 16

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 28318 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	179	2 JC7255	Bax-delta protein
2	81	100.0	192	2 M47538	bcl-2-associated p
3	81	100.0	218	2 M47538	bcl-2-associated p
4	81	100.0	192	2 M47538	bcl-2-associated p
5	75	92.6	133	2 I53295	bcl-2-associated p
6	65	66.5	669	2 A60506	ser/threonine k1
7	47	58.0	862	1 P4D0A	alpha-actinin-81
8	44	54.3	500	2 S64320	hypothetical prote
9	43	53.1	92	2 E71868	hypothetical prote
10	43	53.1	197	2 PC2235	GTPase protein - Syn
11	43	53.1	213	2 E69057	molybdenum-iron
12	43	53.1	217	2 E71098	probable atom prot
13	43	53.1	339	2 S08981	malate dehydrogen
14	43	53.1	1002	2 AF1909	two-component hybr
15	42.5	52.5	460	2 C65964	SAM-dependent meth
16	42	51.9	677	2 T93106	hypothetical prote
17	42	51.9	1325	2 T42722	hypothetical prote
18	41	50.6	151	2 S61384	male-enhanced anti
19	41	50.6	345	2 AF1936	icmw protein - Leg
20	41	50.6	772	2 T93469	fructose-1,6-bisph
21	41	50.6	1280	2 T43457	hypothetical prote
22	40	49.4	118	2 D64347	hypothetical prote
23	40	49.4	126	2 G64311	hypothetical prote
24	40	49.4	159	2 AB0413	2-amino-4-hydroxy-
25	40	49.4	177	2 S25492	gene 28 protein -
26	40	49.4	349	2 B35114	anuranian phosph
27	40	49.4	382	2 H72255	myo-inositol-1-ph
28	40	49.4	384	2 A64230	dihydropyranolide a
29	40	49.4	435	2 A66492	hypothetical prote

ALIGNMENTS

30	40	49.4	435	2 H72129	hypothetical prote
31	40	49.4	460	2 B67455	DNA repair protein
32	40	49.4	485	2 F64157	hypothetical prote
33	40	49.4	713	2 JC7255	Kyle protein
34	40	49.4	968	2 C62392	hypothetical prote
35	40	49.4	1193	2 C68492	hypothetical prote
36	40	49.4	1113	2 D84481	probable retroviral
37	40	49.4	1465	2 T21056	hypothetical prote
38	39	48.1	112	2 AD1756	hypothetical gene
39	39	48.1	229	2 B97035	lacc protein ortho
40	39	48.1	236	2 T45897	hypothetical prote
41	39	48.1	257	2 G88021	protein M409.2 (1
42	39	48.1	254	2 H84115	ribonuclease RbK 11
43	39	48.1	317	2 A53212	probable type II m
44	39	48.1	327	2 C69419	phosphate ABC tran
45	39	48.1	375	2 D97268	toxic anion resist

RESULT 1
JC7255
Bax-delta protein - human
C:Species: Homo sapiens (man)
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 17-Nov-2000
C:Accession: JC7255
R:Schmitt, E.; Paquet, C.; Beauchemin, M.; Dever-Bertrand, J.; Bertrand, R.
Biochem. Biophys. Res. Commun. 270, 886-879, 2000
A:Title: Characterization of Bax-delta, a cell death-inducing isoform of Bax.
A:Reference number: JC7255
A:Accession: JC7255
A:Molecule type: mRNA
A:Residues: 1-179 <SN>
A:Cross-references: GB:AF247393
A:Experimental source: cancer promyelocytic cells
C:Comment: This protein, a member of the Bcl-2 family, has a proapoptotic effect. It
C:Superfamily: bcl transforming protein
C:Keywords: Transmembrane protein

Query Match 100.0% Score 81. DB 2: Length 179.
Best Local Similarity 100.0% Pred. No. 1.5e-05;
Matches 16: Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
Gy 1 KKLSECLRIKIDELDS 16
Db 57 KKLSECLRIKIDELDS 72

RESULT 2
M47538
bcl-2-associated protein x, alpha splice form - human
N:Alternate names: BAX; programmed cell death membrane protein x alpha
C:Species: Homo sapiens (man)
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C:Accession: M47538
R:Oltval, T.N.; Millman, C.L.; Korsmeyer, S.J.
Cell 74, 609-619, 1993
A:Title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates
A:Reference number: M47538; MUID:93364978
A:Accession: M47538
A:Molecule type: mRNA
A:Residues: 1-192 <SN>
A:Cross-references: GB:L22473; NID:9388165; PIDN:AAA03619.1; PID:9388166
C:Note: The amino end of the mature protein is blocked
C:Genetics:
A:Gene: GDB:BAX
A:Cross-references: GDB:228082; OMIM:600040
A:Map position: 19q13.3-19q13.4
C:Superfamily: bcl transforming protein
C:Keywords: alternative splicing; blocked amino end; heterodimer; homodimer; transmem

F:172-191/Domain: transmembrane #status predicted <TM1>

Query Match 100.0%; Score 81; DB 2; Length 192;

Best Local Similarity 100.0%; Pred. No. 1.6e-05;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KXISECLKRIIDELDS 16
|||||
DB 57 KXISECLKRIIDELDS 72

RESULT 3

bcl-2-associated protein x, beta splice form - human

N:Alternate names: BAX; programmed cell death membrane protein x beta

C:Species: Homo sapiens (man)

C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000

C:Accession: B47538

R:Olival, Z.N.; Millman, C.L.; Korsmeyer, S.J.

Cell 74, 609-619, 1993

A>Title: bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates F

A:Reference number: A47538; MUID:93364978

A:Accession: B47538

A:Molecule type: mRNA

A:Residues: 1-218 <OLTV>

A:Cross-References: GB:L22474; NID:9388167; PIDN:AA03620.1; PID:9388168

A>Note: The amino end of the mature protein is blocked

C:Genetics:

A:Gene: GDB:BAX

A:Cross-References: GDB:228082; OMIM:600040

A:Map position: 19q13.3:19q13.4

C:Superfamily: bcl transforming protein

C:Keywords: alternative splicing; blocked amino end; cytosol; heterodimer; homodimer

Query Match 100.0%; Score 81; DB 2; Length 218;

Best Local Similarity 100.0%; Pred. No. 1.8e-05;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KXISECLKRIIDELDS 16
|||||
DB 57 KXISECLKRIIDELDS 72

RESULT 4

bcl-2-associated protein x - mouse

N:Alternate names: BAX; programmed cell death membrane protein x

C:Species: Mus musculus (house mouse)

C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000

C:Accession: D47538

R:Olival, Z.N.; Millman, C.L.; Korsmeyer, S.J.

Cell 74, 609-619, 1993

A>Title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates F

A:Reference number: A47538; MUID:93364978

A:Accession: D47538

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-192 <OLTV>

A:Cross-References: GB:L22472

C:Genetics:

A:Gene: bax

C:Superfamily: bcl transforming protein

Query Match 96.3%; Score 78; DB 2; Length 192;

Best Local Similarity 93.8%; Pred. No. 4.9e-05;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KXISECLKRIIDELDS 16
|||||
DB 57 KXISECLKRIIDELDS 72

RESULT 5

bcl-2-associated protein x - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 03-Nov-2000

C:Accession: I53295

R:Tilly, J.L.; Tilly, K.I.; Kerton, M.L.; Johnson, A.L.

Endocrinology 136, 232-241, 1995

A>Title: Expression of members of the bcl-2 gene family in the immature rat ovary: eq

constitutive bcl-2 and bcl-x-long messenger ribonucleic acid levels.

A:Reference number: I53295; MUID:95129487

A:Accession: I53295

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-133 <RES>

A:Cross-References: EMBL:U032098; NID:9975869; PIDN:AAA75200.1; PID:9975870

C:Genetics:

A:Gene: bax

C:Superfamily: bcl transforming protein

Query Match 92.6%; Score 75; DB 2; Length 133;

Best Local Similarity 87.5%; Pred. No. 0.0001;

Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 KXISECLKRIIDELDS 16
|||||
DB 21 KXISECLKRIIDELDN 36

RESULT 6

src/erb protein kinase, probable [imported] - Sulfolobus solfataricus

C:Species: Sulfolobus solfataricus

C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001

C:Accession: A90504

R:Shen, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aweyer, M.J.; Ch

Jong, T.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.T.; Redder

arefelt, R.A.; Ragan, M.A.; Samsen, C.W.; Van der Oost, J.

submitted to Genbank April 2001

A:Description: Sulfolobus solfataricus complete genome.

A:Reference number: A9139

A:Accession: A90506

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-669 <XUP>

A:Cross-References: GB:A6006641; NID:913816645; PIDN:AAK43304.1; GSRID:GN00155

C:Genetics:

A:Gene: SS01207

Query Match 60.5%; Score 49; DB 2; Length 669;

Best Local Similarity 50.0%; Pred. No. 6.9e-05;

Matches 7; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

OY 3 LSECLKRIIDELDS 16
:::|::|
DB 175 VACMERIDDELTA 188

RESULT 7

FA00A

alpha-actinin - slime mold (Dictyostelium discoideum)

C:Species: Dictyostelium discoideum

C>Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 22-Jun-1999

C:Accession: S00103; A29006

R:Noegel, A.; Witke, W.; Schlieker, M.

FEBS Lett. 221, 391-396, 1987

A>Title: Calcium-sensitive non-muscle alpha-actinin contains EF-hand structures and h

A:Reference number: S00103; MUID:87304850

A:Accession: S00103
 A:Molecule type: mRNA
 A:Residues: 1-662 <MOPS>
 A:Cross-references: EMBL:Y00669; NID:g7177; PIDD:CA68685.1; PID:g7178
 J:Wolke, M.; Schlegel, M.; Woltschke, F.; Noegel, A.
 J:Cell Biol. 100, 963-975, 1996
 A:Title: Studies on the transcription, translation, and structure of alpha-actinin in D.
 A:Reference number: A25006; M0ID:86304574
 A:Accession: A25006
 A:Molecule type: DNA
 A:Residues: 92-359, p', 361-500, T', 502-505 <MT>
 A:Cross-references: EMBL:X04324; NID:g7202; PIDD:CA27855.1; PID:g929034
 C:Superfamily: alpha-actinin; alpha-actinin actin-binding domain homology; calmodulin re
 C:Species: actin binding; calcium binding; duplication; EF hand; homodimer
 F:262-377/Domain: alpha-actinin actin-binding domain homology <Act>
 F:386-497/Domain: spectrin/dystrophin repeat homology <SP>
 F:502-607/Domain: spectrin/dystrophin repeat homology <SP>
 F:616-717/Domain: spectrin/dystrophin repeat homology <SP>
 F:720-762/Domain: spectrin/dystrophin repeat homology <SP>
 F:766-798/Domain: calmodulin repeat homology <EF2>

Query Match 58.0%; Score 47; DB 1; Length 862;
 Best Local Similarity 69.2%; Pred. No. 18;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 K1SECLKRRIGDEL 14
 DB 754 EFSCLASIGDEL 766

RESULT 8

hypothetical protein YG1202a - yeast (Saccharomyces cerevisiae)
 A:Accession: S64220
 A:Residues: 1-500 <R10>
 A:Cross-references: EMBL:Z7724; NID:g1322833; PIDD:CA56914.1; PID:e243502; PID:g132283
 A:Experimental source: strain S288C
 C:Genetics:
 A:Gene: SCD:NR08
 A:Cross-references: SCD:S0003170; MIPs:YG1202a
 A:Map position: 7L

Query Match 54.3%; Score 44; DB 2; Length 500;
 Best Local Similarity 64.3%; Pred. No. 33;
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 K1SECLKRRIGDEL 14
 DB 479 EKTRGKLRKRDLE 492

RESULT 9

hypothetical protein Jhp0948 - Helicobacter pylori (strain J99)
 C:Species: Helicobacter pylori
 A:Variety: strain j99
 C:Date: 13-Feb-1999 #sequence-revision 12-Feb-1999 #cont-change 08-Oct-1999
 C:Accession: F71868
 R:Alm, R.A.; Ling, L.S.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.
 ; Ives, C.; Gibson, R.; Metteny, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
 Nature 397, 176-180, 1999
 A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path

A:Reference number: A71800; M0ID:99120557
 A:Accession: F71868
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-92 <AR>
 A:Cross-references: GB:AE001524; GB:AE001439; NID:g4155523; PIDD:AA006526.1; PID:g415
 A:Experimental source: strain J99
 C:Genetics:
 A:Gene: Jhp0948

Query Match 53.1%; Score 43; DB 2; Length 92;
 Best Local Similarity 53.3%; Pred. No. 9.2;
 Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 K1SECLKRRIGDEL 15
 DB 58 KDSCECFKGGKVD 72

RESULT 10

PC2235
 GPE protein - *Synechococcus* sp. (strain PCC 7942) (fragment)
 C:Species: *Synechococcus* sp.
 C:Date: 20-Feb-1995 #sequence-revision 20-Feb-1995 #text-change 03-Nov-2000
 C:Accession: PC2235; PC2156
 K:Minura, K.; Yoshikawa, H.; Takahashi, H.
 Biochem. Biophys. Res. Commun. 201, 466-471, 1994
 A:Title: Identification of dnaK multigene family in *Synechococcus* sp. PCC7942.
 A:Reference number: PC2156; M0ID:94257015
 A:Accession: PC2235
 A:Molecule type: DNA
 A:Residues: 1-197 <NIM>
 A:Cross-references: DDBJ:D28550; NID:g507816; PIDD:BA05902.1; PID:d1006452; PID:g507
 C:Genetics:
 A:Gene: gpe
 C:Superfamily: heat shock protein gpe
 C:Keywords: heat shock; stress-induced protein

Query Match 72.7%; Score 43; DB 2; Length 197;
 Best Local Similarity 72.7%; Pred. No. 19;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 K1SECLKRRIG 11
 DB 120 KQVDCLEKRI 130

RESULT 11
 E63057
 molycopherin-guanine dinucleotide biosynthesis Moba related protein - *Methanobacteri*
 C:Species: *Methanobacterium thermoautotrophicum*
 C:Date: 05-Dec-1997 #sequence-revision 05-Dec-1997 #text-change 22-Oct-1999
 C:Accession: E63057
 R:Smith, D.R.; Doucette-Stamm, L.A.; Delonguey, C.; Lee, H.; Dubois, J.; Aldredge, T.
 ; Qiu, D.; Spadatore, R.; Vitale, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jivan,
 J.; Becker, L.; Church, G.W.; Dales, J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 J:Biotechnol. 179, 1135-1159, 1997
 A:Title: Complete genome sequence of *Methanobacterium thermoautotrophicum* Delta H: fu
 A:Reference number: A69000; M0ID:98037514
 A:Accession: E63057
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-213 <NH>
 A:Cross-references: GB:AE000803; GB:AE000666; NID:g2621179; PIDD:AA84649.1; PID:g262
 A:Experimental source: strain Delta H
 C:Genetics:
 A:Gene: MTH143

Query Match 53.1%; Score 43; DB 2; Length 213;
 Best Local Similarity 42.9%; Pred. No. 21;

Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 3 LSECLKRIKDGLD 16
 DB 130 MKECFKRLDSCDA 143

RESULT 12

E71098
 Probable arom protein - Pyrococcus horikoshii
 C:Species: Pyrococcus horikoshii
 C:Date: Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
 R:Accession: AF1909
 R:Keywords: Y.; Spande, M.; Horikawa, H.; Hatakeyama, Y.; Hino, Y.; Yamamoto, S.; Seki, M.; Ohnaka, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kishida, N.; Oguchi, M.
 DNA Res 5: 55-76 1998
 A>Title: Complete sequence and gene organization of the genome of a hyperthermophilic
 A:Reference number: A71000; MUID:98344137
 A:Accession: E71098
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-217 <KAW>
 A:Cross-references: GB:AP000004; NID:93236131; PIDN:BA30147.1; PID:93257464
 A:Experimental source: strain O73
 A:Note: this accession replaces an interim accession for a sequence replaced by Genbank
 C:Genetics:
 A:Gene: PH1049
 C:Superfamily: arom protein

Query Match 53.1%; Score 43; DB 2; Length 217;
 Best Local Similarity 43.8%; Pred. No. 21;
 Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 KRLSECLKRIKDGLD 16
 DB 74 KRLQECIDKLEKEDA 89

RESULT 13

S08981
 male dehydrogenase (EC 1.1.1.37) - Methanothermobacter feravidus
 C:Species: Methanothermobacter feravidus
 C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 18-Sep-1998
 C:Accession: S08981; S08689
 R:Accession: S08981; S08689
 R:Honka, E.; Fabry, S.; Niermann, T.; Palm, P.; Hensel, R.
 Eur. J. Biochem. 188, 623-632, 1990
 A>Title: Properties and primary structure of the L-malate dehydrogenase from the extreme
 A:Reference number: S08981; MUID:90235834
 A:Accession: S08981
 A:Molecule type: DNA
 A:Residues: 1-339 <HON>
 A:Cross-references: EMBL:X51840
 R:Honka, E.; Fabry, S.; Niermann, T.; Palm, P.; Hensel, R.
 submitted to the EMBL Data Library, February 1990
 A:Reference number: S08689
 A:Accession: S08689
 A:Molecule type: DNA
 A:Residues: 1-339 <HON>
 A:Cross-references: EMBL:X51714
 C:Genetics:
 A:Start codon: TTG
 C:Superfamily: malate dehydrogenase ylbC
 C:Keywords: oxidoreductase; tricarboxylic acid cycle

Query Match 53.1%; Score 43; DB 2; Length 339;
 Best Local Similarity 66.7%; Pred. No. 32;
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 KRLSECLKRIKDGLD 15
 DB 320 KRLVECLKRIKDELN 334

RESULT 14

AF1909
 Two-component hybrid sensor and regulator af10824 [imported] - Anabaena sp. (strain P
 C:Species: Anabaena sp.
 A:Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120
 A:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
 C:Accession: AF1909
 R:Accession: AF1909
 R:Keywords: Y.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iritsu, N.; Nakai, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
 DNA Res 8: 205-213 2001
 A>Title: Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AF1909
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1002 <UR>
 A:Cross-references: GB:BA000019; PIDN:BA872781.1; PID:917130169; GSPDB:GN00179
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: af10824

Query Match 53.1%; Score 43; DB 2; Length 1002;
 Best Local Similarity 46.7%; Pred. No. 93;
 Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 KRLSECLKRIKDGLD 15
 DB 571 KRLQTKIKKVGNDLN 585

RESULT 15

C96964
 SAM-dependent methyltransferase related to CRNA(uracyl-5-)-methyltransferase (trmA fa
 C:Species: Clostridium acetobutylicum
 C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
 C:Accession: C96964
 R:Rolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L.
 J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183, 4823-4838, 2001
 A>Title: Genome sequence and comparative analysis of the solvent-producing bacterium
 A:Reference number: A96900; MUID:21359325; PMID:21359325
 A:Accession: C96964
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-460 <KUR>
 A:Cross-references: GB:AE001437; PIDN:AAK78502.1; PID:915023386; GSPDB:GN00168
 A:Experimental source: Clostridium acetobutylicum ATCC824
 C:Genetics:
 A:Gene: CAC0523

Query Match 52.5%; Score 42.5; DB 2; Length 460;
 Best Local Similarity 71.4%; Pred. No. 52;
 Matches 10; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 2 KRLSECLKRIKDGLD 15
 DB 103 KRLVECLKRIK-KID 115

Search completed: September 20, 2002, 10:39:12
 Job time: 484 sec

Fri Sep 20 11:03:14 2002

us-03-544-664-32.rpt


```

DR SMART: SM00337; BCL: 1.
DR PROSITE: PS01080; BH1: 1.
DR PROSITE: PS01258; BH2: 1.
DR PROSITE: PS01259; BH3: 1.
DR PROSITE: PS00062; BCL2 FAMILY: 1.
KW Apoptosis; Transmembrane; Alternative splicing.
FT DOMAIN 59 73 BH3.
FT DOMAIN 98 118 BH1.
FT DOMAIN 150 165 BH2.
FT TRANSMEM 172 192 POTENTIAL.
SQ SEQUENCE 192 AA: 21259 MW: 68455BAFBD5F87E CRC64:

Query Match 100.0%; Score 81; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KKESECKRIQDEIDS 16
DB 57 KKESECKRIQDEIDS 72

RESULT 2
BAXA_HUMAN STANDARD; PRT; 192 AA.
AC 007812;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Apoptosis regulator Bax, membrane isoform alpha.
GN BAX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RX MEDLINE=93364978; PubMed=8358790;
RA Oliva L Z.N., Millman C.L., Korsmeyer S.J.;
RT Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that
RT accelerates programmed cell death.
RT Cell 74:609-619(1993).
RN (2)
RP MORTGENESIS AND FUNCTION OF BH3 DOMAIN.
RX MEDLINE=9601131; PubMed=8521816;
RA Chittenden F., Flemington C., Houghton A.B., Edd R.G., Gallo G.J.,
RA Elangovan B., Chinnadurai G., Holz R.J.;
RT A conserved domain in Bax, distinct from BH1 and BH2, mediates cell
RT death and protein binding functions.
RT Leukemia 14:3589-3596(1995).
RN (3)
RP VARIANT T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA ARG-67.
RX MEDLINE=98200607; PubMed=9531611;
RA Mollnes A.V., de Witte T., Vekeman G., Korsmeyer S.J.;
RT Hematopoietic malignancies demonstrate loss-of-function mutations of
RT Bax.
RT Blood 91:2991-2997(1998).
RN (4)
RP FUNCTION: ACCELERATES PROGRAMED CELL DEATH BY BINDING TO, AND
RN ANTIAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS
RN HOMOLOG E1B 19K PROTEIN, INDUCES THE RELEASE OF CYTOCHROME C,
RN ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS.
RN (5)
RP SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,
RN E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.
RN (6)
RP SUBCELLULAR LOCATION: Membrane-bound.
RN (7)
RP ALTERNATIVE PRODUCTS: THE MEMBRANE ISOCYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY
RN CYTOPLASMIC SPLICING.
RN (8)
RP TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
RN (9)
RP DOMAIN: INACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
RN BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
RN WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.

```

```

CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC -1- DISEASE: DEFECTS IN BAX ARE FOUND IN SOME PATIENTS WITH T-CELL
CC ACUTE LYMPHOBLASTIC LEUKEMIA.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L22473; AAA03619.1;
CC DR PIR: A47538; A47538.
CC DR HSP: Q07817; IMAZ.
CC DR MIM: 600040;
CC DR InterPro: IPR002475; BCL2 family.
CC DR InterPro: IPR000712; BCL2.
CC DR Pfam: PF00452; BCL2; 1.
CC DR SMART: SM00337; BCL: 1.
CC DR PROSITE: PS01080; BH1: 1.
CC DR PROSITE: PS01258; BH2: 1.
CC DR PROSITE: PS01259; BH3: 1.
CC KW Apoptosis; Transmembrane; Alternative splicing; Disease mutation.
CC FT DOMAIN 59 73 BH3.
CC FT DOMAIN 98 118 BH1.
CC FT DOMAIN 150 165 BH2.
CC FT TRANSMEM 172 192 POTENTIAL.
CC FT VARIANT 67 67 G->R (IN T-CELL ACUTE LYMPHOBLASTIC
CC LEUKEMIA).
CC FT G->R (IN T-CELL ACUTE LYMPHOBLASTIC
CC LEUKEMIA).
CC SQ SEQUENCE 192 AA: 21184 MW: 600DB0A7DBE4994 CRC64:

Query Match 100.0%; Score 81; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KKESECKRIQDEIDS 16
DB 57 KKESECKRIQDEIDS 72

RESULT 3
BAXA_HUMAN STANDARD; PRT; 218 AA.
AC 007814;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Apoptosis regulator Bax, cytoplasmic isoform beta.
GN BAX.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RX MEDLINE=93364978; PubMed=8358790;
RA Oliva L Z.N., Millman C.L., Korsmeyer S.J.;
RT Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that
RT accelerates programmed cell death.
RT Cell 74:609-619(1993).
RN (2)
RP FUNCTION: ACCELERATES PROGRAMED CELL DEATH BY BINDING TO, AND
RN ANTIAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS
RN HOMOLOG E1B 19K PROTEIN.
RN (3)
RP SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,

```

```

CC      E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.
CC      -1- SUPRCELLULAR LOCATION: CYTOPLASMIC.
CC      -1- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE
CC      CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY
CC      ALTERNATIVE SPLICING.
CC      -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
CC      -1- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
CC      BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
CC      WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC      -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 1 (BH1).
CC      -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 3 (BH3).
CC      -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC      -----
CC      THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: L22474; AAA03620.1;
CC      PIR: B47538; B47538.
CC      HSSP: Q07817; IMA2.
CC      MIM: 600040;
CC      InterPro: IPR002475; BCL2_family.
CC      InterPro: IPR000712; BCL_2.
CC      Pfam: PF00452; BCL-2; 1.
CC      SMART: SM00337; BCL; 1.
CC      PROSITE: PS01080; BH1; 1.
CC      PROSITE: PS01258; BH2; 1.
CC      PROSITE: PS01259; BH3; 1.
CC      PROSITE: PS50062; BCL2_FAMILY; 1.
CC      KMW Apoptosis: Alternative splicing.
CC      FT DOMAIN 59 73 BH3.
CC      FT DOMAIN 98 118 BH1.
CC      FT DOMAIN 150 165 BH2.
CC      SO SEQUENCE 218 AA; 24220 MW; F69DGD70F960192F CRC64;

Query Match 100.0%; Score 81; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 7; 9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLSECLKRRIGDELDS 16
DB 57 KKLSECLKRRIGDELDS 72

RESULT 4
BAXA_MOUSE STANDARD; PRT; 192 AA.
ID BAXA_MOUSE
AC Q07813;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Apoptosis regulator BAX, membrane isoform alpha.
GN BAX.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
OX NCBI_Taxid=10090;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X DBA/2;
RX MEDLINE=93364978; PubMed=8358790;
RA Oliveira 2.N., Millman C.L., Korsmeyer S.J.;
RT "Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that
RT accelerates programmed cell death.";
RL Cell 74:609-619(1993).
-1- FUNCTION: ACCELERATES PROGRAMED CELL DEATH BY BINDING TO, AND

```

```

CC      ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS
CC      HOMOLOG E1B 19K PROTEIN, INDICES THE RELEASE OF CYTOCHROME C,
CC      ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS. BAX DEFICIENCY
CC      LEADS TO LYMPHOID HYPERPLASIA AND MALE STERILITY, BECAUSE OF THE
CC      CESSATION OF SPERM PRODUCTION
CC      -1- SUPPNT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2.
CC      E1B 19K PROTEIN, BCL-X(L), BCL-1 AND A1.
CC      -1- SUPRCELLULAR LOCATION: Membrane bound.
CC      -1- ALTERNATIVE PRODUCTS: A 21 kDa MEMBRANE PROTEIN ALPHA AND THE TWO
CC      CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE
CC      SPLICING.
CC      -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
CC      -1- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
CC      BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
CC      WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC      -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 1 (BH1).
CC      -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 2 (BH2).
CC      -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 3 (BH3).
CC      -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC      -----
CC      THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: L22472; AAA03622.1;
CC      HSSP: Q07817; IMA2.
CC      MIM: 607810; Bax.
CC      InterPro: IPR002475; BCL2_family.
CC      InterPro: IPR000712; BCL_2.
CC      Pfam: PF00452; BCL-2; 1.
CC      SMART: SM00337; BCL; 1.
CC      PROSITE: PS01080; BH1; 1.
CC      PROSITE: PS01258; BH2; 1.
CC      PROSITE: PS01259; BH3; 1.
CC      PROSITE: PS50062; BCL2_FAMILY; 1.
CC      KMW Apoptosis: Transmembrane; Alternative splicing.
CC      FT DOMAIN 59 73 BH3.
CC      FT DOMAIN 98 118 BH1.
CC      FT DOMAIN 150 165 BH2.
CC      FT TRANSMEM 172 192 POTENTIAL.
CC      SO SEQUENCE 192 AA; 21394 MW; D2E0H3566579PAFF CRC64;

Query Match 96.3%; Score 78; DB 1; Length 192;
Best Local Similarity 93.8%; Pred. No. 2; 1e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKLSECLKRRIGDELDS 16
DB 57 KKLSECLKRRIGDELDS 72

RESULT 5
BAXA_RAT STANDARD; PRT; 192 AA.
ID BAXA_RAT
AC Q63690; Q62995; Q64383;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Apoptosis regulator BAX, membrane isoform alpha.
GN BAX.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus;
OX NCBI_Taxid=10116;
[1]
RN SEQUENCE FROM N.A.
RC MEDLINE=96178771; PubMed=8600029;
RX

```

RA Han J., Sabbatini P., Perez D., Rao L., Modha D., White E.;
 RT "The E1B 19K protein blocks apoptosis by interacting with and
 RL inhibiting the p53-inducible and death-promoting Bax protein.";
 RL Genes Dev. 10:461-477(1996).
 RN (2)
 RN SEQUENCE OF 75-192 FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE=97147318; PubMed=8994223;
 RA Madison D.L., Pfeiffer S.E.;
 RT "Cloning of the 3' end of rat bax-alpha and corresponding
 RT developmental down-regulation in differentiating primary, cultured
 RT oligodendrocytes.";
 RL Neurosci. Lett. 220:183-186(1996).
 RN [3]
 RN SEQUENCE OF 37-169 FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-Ovary;
 RX MEDLINE=95129487; PubMed=7828536;
 RA Tilly J.L., Tilly K.I., Kerton M.L., Johnson A.L.;
 RT "Expression of members of the bcl-2 gene family in the immature rat
 RT ovary: equine chorionic gonadotropin-mediated inhibition of granulosa
 RT cell apoptosis is associated with decreased bax and constitutive
 RT bcl-2 and bcl-x long messenger ribonucleic acid levels.";
 RL Endocrinology 136:232-241(1995).
 CC -1- FUNCTION: ACCELERATES PROGRAMED CELL DEATH BY BINDING TO, AND
 CC ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS
 CC HOMOLOG E1B 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C,
 CC ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS.
 CC -1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,
 CC E1B 19K PROTEIN, BCL-X(L), MCL-1 AND AL.
 CC -1- SUBCELLULAR LOCATION: Membrane-bound.
 CC -1- CYTOPLASMIC PROTEINS: A 21 KDa MEMBRANE PROTEIN ALPHA AND THE TWO
 CC SPLICING
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES, WITH
 CC HIGHEST LEVELS IN THE TESTIS AND OVARY
 CC -1- DOMAIN: IMPACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
 CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
 CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 1 (BH1).
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 2 (BH2).
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 3 (BH3).
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U49729; AAC26327.1; -
 CC EMBL: U59184; AAC52898.1; -
 CC EMBL: U52098; AAA75200.1; -
 CC EMBL: S76511; AAC60700.2; -
 CC HSSP: Q07817; 1MAZ.
 CC InterPro: IPR002475; BCL2_family.
 CC InterPro: IPR000712; BCL_2.
 CC Pfam: PF00452; BCL-2; 1.
 CC SMART: SM00337; BCL; 1.
 CC PROSITE: PS01080; BH1; 1.
 CC PROSITE: PS01258; BH2; 1.
 CC PROSITE: PS01259; BH3; 1.
 CC PROSITE: PS00062; BCL2_FAMILY; 1.
 CC Apoptosis; Transmembrane; Alternative splicing.
 CC FT DOMAIN 59 73 BH3
 CC FT DOMAIN 98 118 BH3
 CC FT DOMAIN 150 165 BH2.
 CC TRANSMEM 172 192 POTENTIAL.
 CC CONFLICT 72 72 S->N (IN REF. 3).
 CC CONFLICT 76 76 L->M (IN REF. 2).
 CC CONFLICT 126 126 C->Y (IN REF. 2).

FT CONFLICT 149 149 L->F (IN REF. 3).
 FT CONFLICT 159 159 D->E (IN REF. 1).
 SQ SOURCE 192 AA; 21350 MW; 783CD196D58D589 CRC64;
 DB 57 KRUSCLRRIGDELD5 72
 QY 1 KRUSCLRRIGDELD5 16
 DB 57 KRUSCLRRIGDELD5 72
 Query Match 96.38; Score 78; DB 1; Length 192.
 Best Local Similarity 93.86; Pred. No. 2,1e-05;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 ID AACT_DICDI STANDARD; PRT; 862 AA.
 AC P05095;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alpha-actinin, non-muscular (F-actin cross linking protein).
 GN ABPA.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-AX2.
 RX MEDLINE=87304850; PubMed=3622778;
 RA Noegel A., Witke W., Schleicher M.;
 RT "Calcium-sensitive non-muscle alpha-actinin contains EF-hand
 RT structures and highly conserved regions.";
 RL FEBS Lett. 221:391-396(1987).
 RN [2]
 RP SEQUENCE OF 92-505 FROM N.A.
 RC STRAIN-AX2.
 RX MEDLINE=86304574; PubMed=3745276;
 RA Witke W., Schleicher M., Lottspeich F., Noegel A.;
 RT "Studies on the transcription, translation, and structure of alpha-
 RT actinin in dictyostelium discoideum.";
 RL J. Cell Biol. 103:969-975(1986).
 CC -1- FUNCTION: F-ACTIN CROSS-LINKING PROTEIN WHICH IS THOUGHT TO ANCHOR
 CC ACTIN TO A VARIETY OF INTRACELLULAR STRUCTURES. THIS IS A BUNDLING
 CC PROTEIN.
 CC -1- SUBUNIT: HOMODIMER, ANTIPARALLEL.
 CC -1- SIMILARITY: CONTAINS 1 ACTIN-BINDING DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 CALPONTIN-HOMOLOG (CH) DOMAINS.
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
 CC -1- SIMILARITY: CONTAINS 4 SPECTRIN REPEATS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: Y00689; CA668685.1; -
 CC EMBL: X04324; CAA27855.1; -
 CC PIR: S00103; FAD0AA.
 CC HSSP: G01082; 1BKR.
 CC DictyDb: DP01003; abpa.
 CC InterPro: IPR001589; Actinin_act_bind.
 CC InterPro: IPR001715; Calpontin_hom.
 CC InterPro: IPR002048; EF-hand.
 CC InterPro: IPR002017; Spectrin.
 CC Pfam: PF00307; CH; 2.
 CC Pfam: PF00036; efhand; 2.
 CC Pfam: PF00435; spectrin; 4.
 CC SMART: SM00033; CH; 2.
 CC SMART: SM00054; EPH; 2.

DR SMART: SMO0150; SPEC: 3.
 DR PROSITE: PS00019; ACTININ_1; 1.
 DR PROSITE: PS00020; ACTININ_2; 1.
 DR PROSITE: PS00021; CH; 2.
 DR PROSITE: PS00018; EF-HAND; 2.
 KW Actin-binding; Calcium-binding; Repeat.
 FT DOMAIN 1 240 ACTIN-BINDING.
 FT DOMAIN 22 128 CH 1.
 FT DOMAIN 137 240 CH 2.
 FT REPEAT 241 366 SPECTRIN 1.
 FT REPEAT 367 481 SPECTRIN 2.
 FT REPEAT 482 602 SPECTRIN 3.
 FT REPEAT 603 715 SPECTRIN 4.
 FT CA-BIND 743 754 EF-HAND 1 (BY SIMILARITY).
 FT CA-BIND 779 790 EF-HAND 2 (BY SIMILARITY).
 FT CA-BIND 360 360 EF-HAND 2 (BY SIMILARITY).
 FT CONFLICT 501 501 T -> P (IN REF. 2).
 FT CONFLICT 501 501 I -> T (IN REF. 2).
 SQ SEQUENCE 862 AA; 97598 MW; 15608ADB71213226 CRC64;

Query Match 58.0%; Score 47; DB 1; Length 862;
 Best Local Similarity 69.2%; Pred. No. 6.4;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 KLSECLKRIQDEL 14
 Db 754 EFSECLKRIQDEL 765

RESULT 7
 AR08_YEAST STANDARD; PRT; 500 AA.
 ID AR08_YEAST
 AC P53050;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Aromatic amino acid aminotransferase I (EC 2.6.1.-).
 GN AR08 OR YG1202M.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SIGMA 1278B;
 RX MEDLINE=98151785; PubMed=9491083;
 RA Iregui I., Vissers S., Cartiaux M., Urrestarazu A.;
 RT "Characterisation of Saccharomyces cerevisiae AR08 and AR09 genes
 encoding aromatic aminotransferases I and II reveals a new
 aminotransferase subfamily.";
 RT Mol. Genet. 257:238-248(1998).
 RL [2]
 RN SEQUENCE FROM N.A.
 RA Bjourson A.J., McReynolds A.D.K., Wright L.F.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 CC -i- SIMILARITY: TO YEAST AR09.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>;
 CC or send an email to license@isb-sib.ch).

DR EMBL: Y13624; CAA7946.1; -;
 DR EMBL: 272724; CAA9594.1; -;
 DR SGD: S0003170; AR08.
 KW Transferrase; Aminotransferase.
 SQ SEQUENCE 500 AA; 56177 MW; D0D111640D2C560D CRC64;

Query Match 54.3%; Score 44; DB 1; Length 500;

Best Local Similarity 64.3%; Pred. No. 12;
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 KLSECLKRIQDEL 14
 Db 479 EKLSECLKRIQDEL 492

RESULT 8
 GRPE_SYNP7 STANDARD; PRT; 197 AA.
 ID GRPE_SYNP7
 AC O59984;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE GRPE protein (HSP-70 cofactor) (Fragment).
 GN GRPE.
 OS Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
 OX NCBI_TaxID=1140;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94257019; PubMed=8198610;
 RA Nimura K., Yoshikawa H., Takahashi H.;
 RT "Identification of dnaK multigene family in Synechococcus sp.
 PCC7942.";
 RT PCC7942.";
 RL Biochem. Biophys. Res. Commun. 201:466-471(1994).
 CC -i- FUNCTION: STIMULATES, JOINTLY WITH DNAJ, THE APPASE ACTIVITY OF
 CC DNAK. HELPS TO RELEASE ADP FROM DNAK THUS ALLOWING DNAK TO RECYCLE
 CC MORE EFFICIENTLY (BY SIMILARITY).
 CC -i- SIMILARITY: BELONGS TO THE GRPE FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>;
 CC or send an email to license@isb-sib.ch).

CC EMBL: D29850; BAA05902.1; -;
 CC DR HSPF: P09372; JDRG
 DR InterPro: IPR000740; GRPE.
 DR Pfam: PF01025; GRPE; 1.
 DR PROSITE: PS01071; GRPE; 1.
 KW Heat shock; Chaperone.
 FT NON_TER 1
 SQ SEQUENCE 197 AA; 21833 MW; FDFED6FC98E96E9 CRC64;

Query Match 53.1%; Score 43; DB 1; Length 197;
 Best Local Similarity 72.7%; Pred. No. 7;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLSECLKRIQ 11
 Db 120 KQLVDCIKRIG 130

RESULT 9
 MOBA_MERTH STANDARD; PRT; 197 AA.
 ID MOBA_MERTH
 AC O26246;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable molybdopter-in-guanine dinucleotide biosynthesis protein A.
 GN MOBA OR MTH143.
 OS Methanobacterium thermoautotrophicum.
 OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
 OC Methanobacter.
 OX NCBI_TaxID=145262;
 RN [1]

```

RP SEQUENCE FROM N.A.
RC STRAIN-DETA H;
RA MEDLINE-98037514; PubMed-9371463;
RA Smith D.R., Duccette-Stamm L.A., Delonguey C., Lee H.-M., Dubois J.,
RA Aldridge T., Basalitzaden R., Blakey D., Cook R., Gilbert K.,
RA Harrison R., Hoang L., Keagle P., Lum W., Pocher B., Qiu D.,
RA Spadator R., Viare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jilani N., Catus A., Bush D., Sater H., Petwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Petrovski S., Church G.M.,
RA Daniels C.S., Mao J.-T., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
delah: functional analysis and comparative genomics."
RL Bacteriol. 179:7135-7155(1997);
CC -1- FUNCTION: LINKS A GUANOSINE 5'-PHOSPHATE TO MOLYBDOTERIN (MPT)
CC FORMING MOLYBDOTERIN GUANINE DINDUCTIDE (MGD) (BY SIMILARITY).
CC -1- PATHWAY: MOLYBDENUM COFACTOR BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
CC -1- SIMILARITY: BELONGS TO THE MOBA FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: A800803; AAB84649.1; ALT_INT.
CC Molybdenum cofactor biosynthesis; GTP-binding; Complete proteome.
CC SEQUENCE 197 AA; 21556 MW; 6A8029D2B0AD8619 CRC64;

```

Query Match 53.1%; Score 43; DB 1; Length 197;
 Best Local Similarity 42.9%; Pred. No. 7;
 Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

```

Oy 3 LSECLKRICDELD 16
Db 114 MKCFRRLDSCDA 127

```

RESULT 10
 KAD-ARATH STANDARD; PRT: 246 AA.

AC 082514; 09FWM2; (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).
 GN ADK1 OR AFG53400 OR MLE2.3
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eudicots 11; rosales; brassicales; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV, COLUMBIA;
 RA Weiers B., Thonburg R.;
 RT "Characterization of the cDNA and gene for the Arabidopsis thaliana
 RT adenylate kinase.";
 RL (in) Plant Gene Register PCR98-166.
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV, COLUMBIA;
 RX MEDLINE-98162728; PubMed-9501997;
 RA Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. III.
 RT Sequence features of the regions of 1,191,918 bp covered by seventeen
 RT physically assigned P1 clones.";
 RL DNA Res. 4:401-414(1997).
 CC -1- FUNCTION: THIS SMALL UBQUITOUS ENZYME IS ESSENTIAL FOR

```

CC MAINTENANCE AND CELL GROWTH.
CC -1- CATALYTIC ACTIVITY: ATP + AMP -> ADP + ADP.
CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: AF082882; AAC78478.1; -
CC EMBL: AB007649; BAB08805.1; -
CC HSSP: P07170; LAKY.
CC DR Mendel; 33102; Arabid. 27111.33102.
CC DR InterPro: IPR000850; Adenylate_kin.
CC DR Pfam: PF00406; adenylatekinase; 1.
CC DR PRINTS: PR00094; ADENYLKINASE.
CC DR PRODOM: PD000657; Adenylate_kin. 1.
CC DR PROSITE: PS00113; ADENYLATE_KINASE; 1.
CC KW Transferase: Kinase; ATP-binding; Multigene family.
CC FT NP_BIND 40 48 ATP (BY SIMILARITY).
CC FT CONFLICT 144 152 LNFADDAI -> STILLMTOS (IN REF. 1).
CC SEQUENCE 246 AA; 26932 MW; 659903FBD4B39C7 CRC64;

```

Query Match 53.1%; Score 43; DB 1; Length 246;
 Best Local Similarity 60.0%; Pred. No. 8;
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```

Oy 1 KKLSECLKRICDELD 15
Db 127 EKLDMLKRRGTEID 141

```

RESULT 11
 MDH-METFE STANDARD; PRT: 339 AA.

AC P16142;
 ID MDH-METFE
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Malate/DL-sulfolactate dehydrogenase (EC 1.1.1.37) (EC 1.1.1.82).
 GN MDH.
 OS Methanothermobacter ferrireducens.
 OC Archaea; Euryarchaeota; Methanobacteriales; Methanothermaceae;
 OC Methanothermobacter.
 OX NCBI_TaxID=2180;
 RN 11
 RP SEQUENCE FROM N.A. AND SEQUENCE OF 1-24.
 RC STRAIN-V745; DSM 2088;
 RX MEDLINE-90235634; PubMed-2110059;
 RA Holsa E., Fabry S., Niemann T., Palm P., Hensel R.;
 RT "Properties and primary structure of the L-malate dehydrogenase from
 RT the extremely thermophilic archaeobacterium Methanothermobacter ferrireducens.";
 RL Eur. J. Biochem. 188:623-632(1990).
 RN 12
 RP FUNCTION
 RX MEDLINE-70309698; PubMed-10850983;
 RA Grauper M., Xu H., White R.R.;
 RT Identification of an archaeal 2-hydroxy acid dehydrogenase catalyzing
 RT reactions involved in coenzyme biosynthesis in methanocorchaeta.";
 RL Bacteriol. 182:3686-3692(2000).
 CC -1- FUNCTION: Acts on oxalacetate, sulfolysinate but not on pyruvate.
 CC Has a higher selectivity for the coenzyme NADH than for NADPH.
 CC -1- CATALYTIC ACTIVITY: (S)-malate + NAD(P)(+) -> oxalacetate +
 CC NAD(P)H.
 CC -1- CATALYTIC ACTIVITY: (R)-sulfolactate + NAD(P)(+) -> sulfolysinate +
 CC NAD(P)H.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE LDH2/MDH2 OXIDOREDUCTASE FAMILY.


```

CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X51714; CMA36010.1; .
DR EMBL; X51840; CMA36133.1; .
DR PIR; S08689; S08689.
DR PIR; S08981; S08981.
DR InterPro; IPR003767; Idb_2.
DR Pfam; PF02615; Idb_2; 1
DR Oxidoreductase; Tricarboxylic acid cycle; NAD; NADP.
SO SEQUENCE 339 AA; 36/62 MW; 2319D822DB275835 CRC64;

OY 1 KKLSECKRLRICDELD 15
| | | | | | | | | | | | | | |
Db 320 KLLVETKLEIDELN 334

RESULT 12
C1SD_MOUSE STANFORD PRF 1225 AA.
1 R1ED MOUSE
AC P55937
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Goidin-160 (Male-enhanced antigen-2) (MEX 2).
GN GOLGA3 OR WEA2
OS Mus musculus (Mouse).
CS Fukuysuka; Metazoa; Chordata; Craniata; Vertebrata; Euarchontoi;
CS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CD-1; TISSUE=Testis;
RX MEDLINE=97217683; PubMed=9063644;
RA Kondo M., Satou S.;
RT "Cloning and molecular characterization of cDNA encoding a mouse
RT male-enhanced antigen-2 (Wea-2): a putative family of the Golga3
RT autologous."
RL DNA Seq. 7:71-82(1997).
CC -1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN SPERMATOGENESIS AND/OR
CC TESTES DEVELOPMENT. PROBABLY IDENTICAL WITH THE SEROLOGICALLY
CC DETECTABLE MALE ANTIGEN (SDM).
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS. TRANSCRIPTS CAN BE
CC FOUND IN SPERMATIDS DURING SPERMATOGENESIS. NO EXPRESSION IN
CC LEYDIG CELLS, SPERMATOGENIA, OR SPERMATOCYTES.
CC -1- SIMILARITY: HIGH TO HUMAN GOLGIN-160.
CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1, MET-19 OR MET-30 IS THE
CC INITIATOR.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D78270; BAA16612.1; .
DR HSSP; P18857; ISCQ.
DR MGD; MG1:9695B; Gola3a.
KW Spermatogenesis; Developmental protein.
PT DOMAIN 201 204 POLY-AAL.
```

QY	1	KRUSECKIRIGDEIDS	16
DB	1259	KRLNKLQLOQKQEMDS	1274
SEQUENCE	1325 AA:	149880 MW:	323063696ZC687B0 CRC64:
Query Match		51.9%	Score 42; DB 1; Length 1325;
Best Local Similarity	43.8%	Prod. No. 59;	
Matches	7; Conservative	5; Mismatches	4; Indels 0; Gaps

RESULT	13
CP1R-AAVATH	STANDARD: PRT: 499 AA.
ID	CP1R-AAVATH
AC	065436; (Rel. 40, Last sequence update)
DP	16-OCT-2001 (Rel. 40, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
DE	Cytochrome P450C1A2 (EC 1.11.1.1).
GN	CYP1A2 Or A19C0240 Or FIC12.160
OS	Anilidopsis thaliana (Mouse-ear cress).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsiis.
OC	NCBI_TaxID=3702;
SP	SPENCE FROM N. A.
RP	SPRAIN-CV, COLUMBIA.
PC	MEDLINE=00983488; PubMed=10617198;
XX	MEDLINE=00983488; PubMed=10617198;
RA	Medlin K.F.X. Schueler C. Weinberg R. Murphy G. Volkhaert G.
RA	Boil T. Duesterhoof A. Stiekema W. Ertlan K.-D. Meyn N.
RA	Harris B. Anorgie W. Brandt P. Griell L.A. Rieger M.
RA	Reis M. Delaney M. de Simone V. Obermayer B. Mahe R. Mueller M.
RA	Reichert B. Portetle D. Perez-Alonso M. Botley M. Bancroft I.
RA	Vos P. Hohisel J. Zimmermann W. Medler H. Ridley P.
RA	Latham S.-W. McCullagh B. Bilham L. Robben J.
RA	Van der Schueren J. Gynopprez B. Chuang Y.-J. Vandebussche F.
RA	Bracken M. Weltjens J. Voet M. Bastiaens I. Aert R. Defoor E.
RA	Weitzenecker T. Bohe G. Ramsperger U. Hilbert H. Braun M.
RA	Holzer E. Brandt A. Peters S. van Staveren M. Dirks W.
RA	Mocjman P. Klein Lankhorst R. Rose M. Hauf J. Koetter P.
RA	Boreiser S. Hempel S. Feldpausch M. Lambertz S. Van den Daele H.
RA	De Keyser A. Buysnaert C. Gieken J. Villarroel R. De Clercq R.
RA	Van Montagu M. Rogers J. Cronin A. Quail M. Bray-Allen S.
RA	Clark L. Doggett J. Hall S. Kay M. Leonard N. McKay K. Mayes R.
RA	Reichert A. Rajendram M.A. Lyne M. Benes V. Reehmann S.
RA	Bortova D. Bloeker H. Schafte M. Grimm M. Loehner T.-H.
RA	Dose S. de Haan M. Maes A.C. Scheerl M. Moeller-Auer S.
RA	Gabel C. Fuchs M. Fattman B. Ganderath K. Danner D. Herzl A.
RA	Neumann S. Argiron A. Vitale D. Liguori R. Piravandi E.
RA	Messent O. Quigley F. Calabaud G. Muehlen A. Falber R.
RA	Schabl S. Hiler R. Schmidt W. Lechany A. Aubourg S.
RA	Cheffor F. Cooke R. Berger C. Morfont A. Casacuberta E.
RA	Gibbons T. Weber N. Vandenbol M. Baryges M. Terol J. Torres A.
RA	Perez-Perez A. Purnelle B. Bent E. Johnson S. Tacon D. Jesse T.
RA	Felsten I. Schwarz S. Scholler P. Heber S. Francis P. Bielke C.
RA	Fishman D. Haes D. Lemcke K. Mewes H.-W. Stocker S.
RA	Zaccaria P. Bevan M. Gijon R.K. de la Bastide M. Hebenmann K.
RA	Parnell L. Dehlla N. Guo L. Schutz K. Huang E. Spiegel L.
RA	Sekhon M. Murray J. Sheet P. Cordes M. Abn-Thiridch J.
RA	Stonking T. Kalicki J. Graves T. Harmon G. Edwards J.
RA	Latreille P. Courtney L. Clowd J. Abbott A. Scott K. Johnson D.
RA	Mun P. Bentley D. Fulton B. Miller N. Greco T. Kemp K.
RA	Kramer J. Fulton L. Madis E. Dante M. Pepin K. Hillier L.
RA	Nelson J. Splich J. Ryan E. Andrews S. Geisel C. Layman D.
RA	Du H., Ali J. Berghoff A. Jones K. Dione K. Cotton M. Joshi C.
RA	Antonou B. Zidanic M. Strong C. Sun H. Lamar B. Yordan C.
RA	Swab P. I. O'Shaughnessy A. Rodriguez M. Matero A. Shah R.
RA	May P. Zhong Z. Preston R. Villaluz M. Hoffman J. Tili S.
RA	Grant S. Sholdy N. Hasegawa A. Hamed A. Locht M. Johnson A.
RA	Chen E. Marra M. Martensen R. McCombie W.R.

RT *Sequence and analysis of chromosome 4 of the plant Arabidopsis
 RT chelina. 402:769-777(1999).
 RN Molecule 402:769-777(1999).
 RN (12)
 RN CONCEPTUAL TRANSLATION.
 RA Axelsson K.B.;
 RA Unpublished observations (Apr-2001).
 CC -1- STRIKELINE: BELONGS TO THE CYTOCHROME P450 FAMILY.
 CC -1- CAUTION: NEW 1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO WRONG EXON
 CC PREDICTIONS FROM THE GENOMIC SEQUENCE. THE PREDICTION MIX UP
 CC CYP1A2 WITH CYP1A28. THERE IS FURTHERMORE A FRAMESHIFT IN THE
 CC GENOMIC SEQUENCE.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AL022224; CA18249.1; ALT_FRAME.
 DR EMBL: AL161552; CAB79024.1; ALT_FRAME.
 DR InterPro: IPR001128; Cyt_P450.
 DR Pfam: PF00067; P450_1.
 DR PRINTS: PR00385; P450.
 DR PROSITE: PR00086; CYTOCHROME_P450_1.
 DR KMOxidoreductase; Monooxygenase; Transmembrane; Heme; Multigene family.
 FT TRANSMEM 3 23
 FT BINDING 438 438 HEME (BY SIMILARITY).
 FT DOMAIN 164 169 POLY-SER.
 SQ SEQUENCE 499 AA; 56990 MW; A5FB2BF183780B0A CRC64;
 Query Match 50.6%; Score 41; DB 1; Length 499;
 Best Local Similarity 50.0%; Pred. No. 34;
 Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 Oy 5 ECLARIGDELDS 16
 Db 320 ECMKRLDEINS 331
 RESULT 14
 Y380_METJA STANDARD; PRT; 118 AA.
 ID Y380_METJA
 AC Q57825;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein M70380.
 GN M70380.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
 CC Methanococcus.
 OX NCBI_TaxID=2190;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8688087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reisch C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodok A.,
 RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,
 RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Ventor J.C.;
 RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
 RA jannaschii";
 RT Science 273:1058-1073(1996).
 RL Science 273:1058-1073(1996).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U67491; AAB98377.1; .
 DR TIGR: M70380; .
 CC Hypothetical protein; Complete proteome.
 KW SEQUENCE 118 AA; 13736 MW; 32ZC1759E435B1DD CRC64;
 SQ

Query Match 49.4%; Score 40; DB 1; Length 118;
 Best Local Similarity 66.7%; Pred. No. 13;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 KXISECKRIGED 12
 Db 77 KXLEFIREICD 88

RESULT 15
 Y095_METJA STANDARD; PRT; 126 AA.
 ID Y095_METJA
 AC Q57560;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein M70095.
 GN M70095.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
 CC Methanococcus.
 OX NCBI_TaxID=2190;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8688087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reisch C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodok A.,
 RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,
 RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Ventor J.C.;
 RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
 RA jannaschii";
 RT Science 273:1058-1073(1996).
 RL Science 273:1058-1073(1996).
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U67467; AAB98086.1; .
 DR TIGR: M70095; .
 CC Hypothetical protein; Complete proteome.
 KW SEQUENCE 126 AA; 14709 MW; D4ID24ABDD043E9B CRC64;
 SQ

Query Match 49.4%; Score 40; DB 1; Length 126;
 Best Local Similarity 40.0%; Pred. No. 14;
 Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 Oy 1 KXISECKRIGED 15
 Db 54 KEVKELIDKVDIED 68

Fri Sep 20 11:03:15 2002

us-09-544-664-32.rsp

Page 9

Search completed: September 20, 2002, 11:04:34
Job time: 1691 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OK protein - protein search, using sw model

Run on: September 20, 2002, 11:03:46 : Search time 172.19 Seconds,
(without alignments)
16.075 Million cell updates/sec

Title: US-09-544-664-32

Perfect score: 1 KRLSECLKRRIDELDS 16

Sequence: BIOSUM62

Scoring table: GAPOP 10.0 , GAPEXT 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database : Maximum Match 100%
Listing first 45 summaries

SPRDBML:19:*

1: sp-archaea:*

2: sp-bacteria:*

3: sp-fungi:*

4: sp-human:*

5: sp-invertebrate:*

6: sp-mammal:*

7: sp-misc:*

8: sp-organelle:*

9: sp-phase:*

10: sp-plant:*

11: sp-rodent:*

12: sp-virus:*

13: sp-vertebrate:*

14: sp-unclassified:*

15: sp-virus:*

16: sp-bacteriap:*

17: sp-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	149	6	09GNG7
2	81	100.0	164	4	09GNG7
3	81	100.0	179	4	09GNG7
4	75	92.6	173	11	09GNG7
5	69	85.2	221	13	09GNG7
6	60	74.1	192	13	09GNG7
7	51	63.0	1124	12	09GNG7
8	49	60.5	669	17	09GNG7
9	46	56.8	485	11	09GNG7
10	45	55.6	508	17	09GNG7
11	44	55.6	2376	10	09GNG7
12	44	54.3	226	11	09GNG7
13	44	54.3	303	11	09GNG7
14	43	53.1	72	15	09GNG7
15	43	53.1	92	16	09GNG7
16	43	53.1	169	2	P95332

17	43	53.1	217	17	058748	058748 pyrococcus
18	43	53.1	403	5	09V608	09V608 drosophila
19	43	53.1	527	12	09JGP5	09JGP5 epistictic h
20	43	53.1	661	17	09JGP7	09JGP7 sulfolobus
21	42.5	52.5	302	17	09JGP1	09JGP1 thermoplasma
22	42.5	52.5	460	16	09JGP4	09JGP4 clostridium
23	42	51.9	148	12	09JGP5	09JGP5 tulipa herp
24	42	51.9	275	10	09JGP2	09JGP2 oryza sativ
25	42	51.9	356	2	P66145	P66145 uncultured
26	42	51.9	677	2	09JGP8	09JGP8 streptomyces
27	42	51.9	1447	11	09JGP7	09JGP7 mus musculus
28	42	51.9	1487	11	09JGP3	09JGP3 mus musculus
29	41	50.6	15	15	09JGP7	09JGP7 homo sapien
30	41	50.6	151	2	09JGP0	09JGP0 leishmania
31	41	50.6	166	5	09JGP4	09JGP4 amebae
32	41	50.6	286	5	09JGP2	09JGP2 amebae
33	41	50.6	286	5	09JGP2	09JGP2 amebae
34	41	50.6	286	5	09JGP2	09JGP2 amebae
35	41	50.6	520	3	09JGP8	09JGP8 amebae
36	41	50.6	520	3	09JGP8	09JGP8 amebae
37	41	50.6	520	3	09JGP8	09JGP8 amebae
38	41	50.6	520	3	09JGP8	09JGP8 amebae
39	41	50.6	520	3	09JGP8	09JGP8 amebae
40	41	50.6	662	16	09JGP1	09JGP1 rat
41	41	50.6	665	4	09JGP4	09JGP4 homo sapien
42	41	50.6	670	4	09JGP4	09JGP4 homo sapien
43	41	50.6	1260	5	09JGP5	09JGP5 caenorhabditis
44	40	49.4	119	2	09JGP2	09JGP2 amebae
45	40	49.4	152	9	09JGP7	09JGP7 bacteriophaga

ALIGNMENTS

RESULT	ID	PRELIMINARY	PRF	149 AA
1	09GNG7			
2	09GNG7			
3	09GNG7			
4	09GNG7			
5	09GNG7			
6	09GNG7			
7	09GNG7			
8	09GNG7			
9	09GNG7			
10	09GNG7			
11	09GNG7			
12	09GNG7			
13	09GNG7			
14	09GNG7			
15	09GNG7			
16	09GNG7			
17	09GNG7			
18	09GNG7			
19	09GNG7			
20	09GNG7			
21	09GNG7			
22	09GNG7			
23	09GNG7			
24	09GNG7			
25	09GNG7			
26	09GNG7			
27	09GNG7			
28	09GNG7			
29	09GNG7			
30	09GNG7			
31	09GNG7			
32	09GNG7			
33	09GNG7			
34	09GNG7			
35	09GNG7			
36	09GNG7			
37	09GNG7			
38	09GNG7			
39	09GNG7			
40	09GNG7			
41	09GNG7			
42	09GNG7			
43	09GNG7			
44	09GNG7			
45	09GNG7			

RESULT	1																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
--------	---	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--

```

Db      29  KKLSECLKRRIGDELDLS 44

RESULT  2
Q9U0D6      PRELIMINARY:      PRT:      164 AA.
AC  Q9U0D6:
DT  01-MAY-2000 (TREMBLrel. 13, Created)
DT  01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT  01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE  BAX Epsilon.
OS  Homo sapiens (human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NC  Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX  NCBI_TaxID=9606;

RP  SEQUENCE FROM N.A.
RC  TISSUE=BRAIN;
RA  MEDLINE=99120940; PubMed=9920818;
RA  SHI B; Tlelebe D.; Keilji S.; Iwata K.K.; Bruskin A.; Mahajna J.;
RA  "Identification and characterization of baxepsilon, a novel bax
RA  variant missing the BH2 and the transmembrane domains.";
RL  Biochem Biophys Res Commun. 254:779-785(1999).
DR  EMBL: AF007826; AAD22706.1; -.
DR  InterPro: IPR002475; BCL2_family.
DR  InterPro: IPR000712; BCL_2.
DR  Pfam: PF00452; BCL2_1.
DR  SMART: SM00337; BCL2_1.
DR  PROSITE: PS00062; BCL2_FAMILY; 1.
DR  PROSITE: PS01080; BH1; 1.
DR  PROSITE: PS01259; BH2; 1.
SQ  SEQUENCE 164 AA; 18129 MW; 12CCDB8073EF4C9E CRC64;

Query Match      100.0%; Score 81; DB 4; Length 164;
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  KKLSECLKRRIGDELDLS 16
Db      57  KKLSECLKRRIGDELDLS 72

RESULT  3
Q9NYG7      PRELIMINARY:      PRT:      179 AA.
AC  Q9NYG7:
DT  01-OCT-2000 (TREMBLrel. 15, Created)
DT  01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT  01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE  BAX-SIGNA.
OS  Homo sapiens (human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NC  Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX  NCBI_TaxID=9606;

RP  SEQUENCE FROM N.A.
RA  MEDLINE=20237095; PubMed=10772918;
RA  Schmitt E.; Paquet C.; Beauchemin M.; Dever-Bertrand J.; Bertrand R.;
RA  "Characterization of bax-sigma, a cell death-inducing isoform of
RA  Bax.";
RL  Biochem Biophys Res Commun. 270:868-879(2000).
DR  EMBL: AF247393; AAF71267.1; -.
DR  HSSP: Q07817; IMAZ.
DR  InterPro: IPR002475; BCL2_family.
DR  InterPro: IPR000712; BCL_2.
DR  Pfam: PF00452; BCL2_1.
DR  SMART: SM00337; BCL2_1.
DR  PROSITE: PS00062; BCL2_FAMILY; 1.
DR  PROSITE: PS01080; BH1; 1.
DR  PROSITE: PS01259; BH2; 1.
SQ  SEQUENCE 179 AA; 19718 MW; 5802B0AC73B2EACE CRC64;

```

```

Query Match      100.0%; Score 81; DB 4; Length 179;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  KKLSECLKRRIGDELDLS 16
Db      57  KKLSECLKRRIGDELDLS 72

RESULT  4
Q9JKL3      PRELIMINARY:      PRT:      173 AA.
AC  Q9JKL3:
DT  01-OCT-2000 (TREMBLrel. 15, Created)
DT  01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT  01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE  BAX PROTEIN SPLICED VARIANT K.
OS  Rattus norvegicus (rat).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX  NCBI_TaxID=10116;

RP  SEQUENCE FROM N.A.
RC  TISSUE=BRAIN;
RA  Jin K.; He X.; Greenberg D.A.; Simon R.P.; Graham S.H.;
RA  Submitted (Feb-2000) to the EMBL/GenBank/DBJ databases.
RL  EMBL: AF235993; AAF36411.1; -.
DR  HSSP: Q07817; IMAZ.
DR  InterPro: IPR002475; BCL2_family.
DR  InterPro: IPR000712; BCL_2.
DR  Pfam: PF00452; BCL2_1.
DR  SMART: SM00337; BCL2_1.
DR  PROSITE: PS00062; BCL2_FAMILY; 1.
DR  PROSITE: PS01080; BH1; 1.
DR  PROSITE: PS01259; BH2; 1.
SQ  SEQUENCE 173 AA; 19661 MW; F19A45BCF642C34F CRC64;

Query Match      92.6%; Score 75; DB 11; Length 173;
Best Local Similarity 87.5%; Pred. No. 0.00022;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1  KKLSECLKRRIGDELDLS 16
Db      38  KKLSECLKRRIGDELDN 53

RESULT  5
Q98U13      PRELIMINARY:      PRT:      221 AA.
AC  Q98U13:
DT  01-JUN-2001 (TREMBLrel. 17, Created)
DT  01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT  01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE  Xenopus laevis (African clawed frog).
OS  Xenopus laevis (African clawed frog).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NC  Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC  Xenopodinae; Xenopus.
OX  NCBI_TaxID=8355;

RP  SEQUENCE FROM N.A.
RA  MEDLINE=21107661; PubMed=11158585;
RA  Finkelshtein C.V.; Lewellyn A.L.; Maller J.L.;
RA  "The midblastula transition in Xenopus embryos activates multiple
RA  pathways to prevent apoptosis in response to DNA damage.";
RL  Proc. Natl. Acad. Sci. U.S.A. 98:1006-1011(2001).
DR  EMBL: AF288809; AAK06406.1; -.
DR  HSSP: P53563; IAF3.
DR  InterPro: IPR002475; BCL2_family.
DR  InterPro: IPR000712; BCL_2.
DR  Pfam: PF00452; BCL2_1.

```


RN SEQUENCE FROM N.A.
 RC TISSUE=MAMMARY TUMOR. MAP-TGF ALPHA MODEL. 7 MONTHS OLD. CROSS
 RC TISSUE=MAMMARY TUMOR. MAP-TGF ALPHA MODEL. 7 MONTHS OLD. CROSS
 RA STRAUSBERG R.
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: NC003941; AAR03941.1; -
 DR InterPro: IPR000822; znf-C2H2.
 DR Pfam: PF00096; znf-C2H2; 9.
 DR SMART: SM00355; znf-C2H2; 9.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 4.
 DR PROSITE: PS0157; ZINC_FINGER_C2H2_2; 5.
 DR DNA-binding; Metal-binding; Zinc-finger.
 SO SEQUENCE 485 AA; 55678 MW; 52428549C27A2E4F CRC64;

Query Match 56.8%; Score 46; DB 11; Length 485;
 Best Local Similarity 64.3%; Pred. No. 28;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 KLSECLKRIQDELD 15
 DB 461 KCSECLMRGNDRD 474

RESULT 10
 Q979FS PRELIMINARY; PRT; 508 AA.
 AC Q979FS;
 DT 01-OCT-2001 (TREMBLrel. 18, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DR DNA-DIRECTED RNA POLYMERASE A'.
 GN TGOJ233699.
 OS Thermoplasma volcanium.
 OC Archaea; Euryarchaeota; Thermoplasmales; Thermoplasmaceae;
 OC NCBI_TaxID=50339.
 RN NCBI_L78XID=50339.
 RP SEQUENCE FROM N.A.
 RC STRAIN=GS51 / DSM 4299 / JCM 9571;
 RC MEDLINE=20570466; PubMed=11121031;
 RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,
 RA Kawashima T., Yamamoto Y., Matsunabe K., Kanemori K., Kawamoto T.,
 RA Nunoshima T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
 RT "Archaeal adaptation to higher temperatures revealed by genomic
 RT sequence of Thermoplasma volcanium."
 RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
 DR EMBL: AF000995; BAB60348.1; -
 DR InterPro: IPR002879; RNA_POL_A2.
 DR Pfam: PF01854; RNA_POL_A2; 1.
 DR DNA-directed RNA polymerase; Complete proteome.
 KW SEQUENCE 508 AA; 55949 MW; 0B17ABCEFD018FE CRC64;

Query Match 55.6%; Score 45; DB 17; Length 508;
 Best Local Similarity 64.3%; Pred. No. 42;
 Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KKLSECLKRIQDELD 14
 DB 159 KKYREILKRIQDELD 172

RESULT 11
 Q9FTN7 PRELIMINARY; PRT; 2376 AA.
 AC Q9FTN7;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DR GENOMIC DNA, CHROMOSOME 5, TAC CLONE R10H17.
 OS Aradipops thalians (Mouse-ear cross).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicots; Rosidae;
 OC Eucosids II; Brassicales; Brassicaceae; Arabidopsis.
 ON NCBI_TaxID=3702;

RN SEQUENCE FROM N.A.
 RC STRAIN=COLUMBERA.
 RC MEDLINE=99156233; PubMed=10046488;
 RA Asamizu E., Sato K., Kaneo T., Nakamura Y., Kolan H., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. VIII.
 RT Sequence features of the regions of 1,081,958 bp covered by seventeen
 RT physically assigned P1 and TAC clones."
 RL DNA Res. 5:379-391(1998).
 DR EMBL: AB016884; BAB11228.1; -
 SO SEQUENCE 2376 AA; 266811 MW; 266120288DAFCFB6 CRC64;

Query Match 55.6%; Score 45; DB 10; Length 2376;
 Best Local Similarity 71.4%; Pred. No. 26+02;
 Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 LSECLKRIQDELD 16
 DB 495 LSECLKRIQDELD 508

RESULT 12
 Q9CVNS PRELIMINARY; PRT; 226 AA.
 AC Q9CVNS;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DR 1700095504RIK PROTEIN (FRAGMENT).
 GN 1700095504RIK
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=TESTIS;
 RC MEDLINE=21085650; PubMed=11217831;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kosukawa T., Saito R.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Kaoto K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochava H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schiraldi L.M., Stabli P., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balarelli R., Barh G.,
 RA Blake J., Bonfelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Kamberts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seiya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Wittkater C., Wilmink L.,
 RA Wyszynski B., Yoshida K., Hasegawa Y., Kawaji H., Kohatsu S.,
 RA Wyszynski B., Yoshida K., Hasegawa Y., Kawaji H., Kohatsu S.,
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 407:251-260(2001).
 DR EMBL: AK07251; BAB24916.1; -
 DR MOD: M01191460; 1700095504RIK.
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 SO SEQUENCE 226 AA; 26797 MW; 90DA1783EA675997 CRC64;

Query Match 54.3%; Score 44; DB 11; Length 226;
 Best Local Similarity 56.2%; Pred. No. 27;
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2002, 10:35:59 : Search time 228.86 Seconds
(without alignments)
8.251 Million cell updates/sec

Title: US-09-544-664-57

Perfect score: 1 KQVGRQLAIGDDINR 17

Sequence: BLOSUM62

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A.Geneseq.012802.*
1: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1980.DAT.*
2: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1981.DAT.*
3: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1982.DAT.*
4: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1983.DAT.*
5: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1984.DAT.*
6: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1985.DAT.*
7: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1986.DAT.*
8: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1987.DAT.*
9: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1988.DAT.*
10: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1989.DAT.*
11: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1990.DAT.*
12: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1991.DAT.*
13: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1992.DAT.*
14: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1993.DAT.*
15: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1994.DAT.*
16: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1995.DAT.*
17: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1996.DAT.*
18: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1997.DAT.*
19: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1998.DAT.*
20: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA1999.DAT.*
21: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/hold-geneseq/genesep-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	17	21	AAE37057
2	80	94.1	16	20	AAV05423
3	80	94.1	16	21	AAE37030
4	80	94.1	16	22	AAE71977
5	80	94.1	26	21	AAV96322
6	80	94.1	26	22	AAE70372
7	80	94.1	27	21	AAE37004
8	80	94.1	28	17	AAW06294
9	80	94.1	117	19	AAW79535
10	80	94.1	141	16	AAE77880
11	80	94.1	152	16	AAE77879

12	80	94.1	211	16	AAE77876
13	80	94.1	211	16	AAE77877
14	80	94.1	211	17	AAW03668
15	80	94.1	211	17	AAW03669
16	80	94.1	211	17	AAE81451
17	80	94.1	211	19	AAE79934
18	80	94.1	211	20	AAV05433
19	78	91.8	16	20	AAV05424
20	78	91.8	16	21	AAV37031
21	78	91.8	207	21	AAE37005
22	78	91.8	27	21	AAV05432
23	75	88.2	16	21	AAE37058
24	74	87.1	31	17	AAW06295
25	69	81.2	15	17	AAW06302
26	69	81.2	15	22	AAE85172
27	47.5	35.9	125	21	AAW08500
28	47.5	35.9	162	21	AAW08499
29	47.5	35.9	210	21	AAW08498
30	47.5	35.9	322	21	AAW04329
31	47.5	35.9	329	21	AAW04336
32	47.5	35.9	357	21	AAW04337
33	47.5	35.9	377	21	AAW04338
34	47.5	35.9	15	22	AAE85274
35	47.5	35.9	15	22	AAE85275
36	47.5	35.9	15	22	AAE85276
37	47.5	35.9	15	22	AAE85277
38	47.5	35.9	15	22	AAE85278
39	47.5	35.9	15	22	AAE85279
40	47.5	35.9	15	22	AAE85280
41	47.5	35.9	15	22	AAE85281
42	47.5	35.9	15	22	AAE85282
43	47.5	35.9	15	22	AAE85283
44	47.5	35.9	15	22	AAE85284
45	47.5	35.9	15	22	AAE85285

ALIGNMENTS

RESULT 1
AAE37057 standard; peptide: 17 AA.

AAE37057:

28-FEB-2001 (first entry)

BC12 polypeptide BH3 domain peptide #57.

Cytostatic; neuroprotective; anti-HIV; vituclide; cerebroprotective;
cardiac; BC12 superfamily; BH3 domain; cell death agonist; positive
apoptosis modulation; B cell; lymphoma/leukemia; T; neuroblastoma;
colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
stroke; myocardial infarction.

Homo sapiens.

WO200059526-A1.

12-OCT-2000.

06-APR-2000; 2000WO-US09352.

07-APR-1999; 99US-0128202.

(UYE-) UNIV JEFFERSON THOMAS.

Huang Z, Wang J, Zhang Z, Shan S, Lu Z;

WPI: 2000-679325/66.

New peptide conjugates for modulating apoptosis or for inhibiting B

CC side chain of the peptide, where the side chain functional group is COOH
 CC or CONH₂; and R = 2-18C alkyl or alkoxy, 2-14C alkenyl containing one
 CC or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl, optionally
 CC monosubstituted with a 1-5C straight or branched chain alkyl group,
 CC phenyl optionally monosubstituted with a 1-5C straight or branched chain
 CC alkyl group, or benzyl. The peptides AAB37001-837058 represent analogues
 CC of the peptide portion of the conjugate. The peptides represent analogues
 CC of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of
 CC the Bcl-2 domain of the cell death agonist Bad. The peptide conjugate is
 CC useful for modulating apoptosis in the cells of a subject, or for
 CC reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of
 CC apoptosis in cancer cells. It is also useful for inhibiting Bcl-2
 CC function. In particular, the peptide conjugate is useful for treating a
 CC subject afflicted with a cancer characterized by cancer cells that
 CC express Bcl-2. The cancer includes prostate, colorectal, gastric,
 CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or
 CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide
 CC conjugate is also useful for treating disorders characterized by
 CC increased apoptosis, e.g. neurodegenerative disorders, acquired
 CC immunodeficiency syndrome (AIDS), stroke or myocardial infarction.

Sequence 16 AA:
 Query Match 94.1%; Score 80; DB 21; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GGVGRQLATIGDDINR 17
 DB 1 ggvgrqlatigddinr 16

RESULT 4
 AAB71977
 ID AAB71977 standard; peptide: 16 AA.
 XX AAB71977;
 XX
 DT 11-MAY-2001 (first entry)
 XX
 DE Bak Bcl-2 peptide.
 XX
 KW Bak; Bcl-2 domain; antiapoptotic; cytosolic; antiapoptotic; apoptosis;
 KW Bcl-2; neoplasia; cancer.
 XX
 OS Mammalia.
 XX
 PN WO200114365-A1.
 XX
 PD 01-MAR-2001.
 XX
 PE 18-AUG-2000; 2000WO-US22891.
 XX
 PR 20-AUG-1999; 99US-0149968.
 XX
 PA (HUTCHINSON CANCER RES CENT FRED.
 XX (HUTCHINSON CANCER RES CENT FRED.
 PI Hockenbery DM, Simon JA, Tsung S;
 XX
 DR WPI: 2001-244291/25.
 XX
 PT Novel antiapoptotic derivatives that bind to antiapoptotic Bcl-2 family
 XX protein, useful for modulating the apoptotic state of a cell
 XX
 PS Example 6; Page 41; 60pp; English.
 XX
 CC The present sequence was used in an example illustrating an invention
 CC relating to an antiapoptotic derivative which modulates apoptosis by
 CC binding to a Bcl-2 family protein and preferentially induces apoptosis
 CC in a cell which over-expresses the Bcl-2 family protein. The antiapoptotic
 CC derivative is used in treating an apoptosis-associated disease and for
 CC inducing apoptosis. It is also useful for treating neoplasia and drug

CC resistance. The present sequence binds to the hydrophobic pocket of
 CC Bcl-2. A competitive binding assay was used to determine if the site of
 CC antiapoptotic A3 interaction was the hydrophobic pocket of Bcl-2.

Sequence 16 AA:
 Query Match 94.1%; Score 80; DB 22; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GGVGRQLATIGDDINR 17
 DB 1 ggvgrqlatigddinr 16

RESULT 5
 AA796322 standard; Peptide: 26 AA.
 ID AA796322 standard; Peptide: 26 AA.
 XX
 XX AA796322;
 XX
 DT 17-AUG-2000 (first entry)
 XX
 DE Mammalian Bak Bcl-2 homology domain 3 domain.
 XX
 KW Mammal; apoptosis; cell death; Bcl-2; apoptosis promotion; Bak;
 XX apoptosis inhibition; malignant cell; autoimmune disease.

Mammalia.
 OS
 XX
 PN WO200026228-A1.
 XX
 PD 11-MAY-2000.
 XX
 PE 28-OCT-1999; 99WO-US25285.
 XX
 PR 02-NOV-1998; 98US-0184168.
 XX
 PA (CLON-) CLONTECH LAB INC.
 XX
 PI Zhu L, Yin X, Chittenden T;
 XX
 DR WPI: 2000-365560/31.
 XX
 PT Novel polynucleotide encoding a Bcl-2 protein which is useful for
 XX modulating apoptosis, especially in the treatment of cancer and
 XX autoimmune diseases
 XX
 PS Disclosure: Fig 4; 47pp; English.
 XX
 CC The present sequence is the mammalian Bak Bcl-2 homology domain 3
 CC (Bcl-2) domain, which was used in a sequence alignment with the same
 CC domain of a putative version of the mammalian apoptosis
 CC regulator Bcl-2, which was designated Bcl-2-ORF2. The Bcl-2 protein,
 CC nucleic acids and antibodies are suitable for use in promoting cell
 CC death or for preventing apoptosis in malignant cells and those causing
 CC autoimmune diseases.

Sequence 26 AA:
 QY 2 GGVGRQLATIGDDINR 17
 DB 3 ggvgrqlatigddinr 18

Query Match 94.1%; Score 80; DB 21; Length 26;
 Best Local Similarity 100.0%; Pred. No. 2.4e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
 AAB70372

ID MAE70372 standard; Peptide: 26 AA.
 XX
 AC AAB70372;
 XX
 DT 02-MAY-2001 (first entry)
 XX
 DE BAK BH3 consensus peptide sequence SEQ ID NO:5.
 XX
 KM Bcl-XL/Bcl-2 associated cell death regulator; BAD: mutant; apoptosis;
 KM immunostimulant; neuroprotective; neurotropic; antileukemic; vulnery;
 KM cytotoxic; antiviral; antitumor; antileukemic; wound healing;
 KM immunosuppressive; apoptosis inducer; apoptosis inhibitor; cancer;
 KM immunodeficiency disease; neurodegenerative disease; stroke;
 KM ischemic cell death; reperfusion cell death; arthritis; infectivity;
 KM lymphoproliferative condition; inflammation; autoimmune disease.
 XX
 OS unidentified.
 XX
 PN MO200110886-A1.
 XX
 PD 15-FEB-2001.
 XX
 PF 30-MAY-2000; 2000MO-US11864.
 XX
 PR 28-MAY-1999; 99US-0136783.
 XX
 PA (APOC-) APOPTOSIS TECHNOLOGY INC.
 XX
 PI Zhou X;
 XX
 DR WPI: 2001-138734/14.
 XX
 PT New mutant Bcl-XL/Bcl-2 Associated Cell Death Regulator polypeptide,
 PT useful for screening for candidate compounds which induce or inhibit
 PT apoptosis, comprises amino acid substitutions at Ser118, Ser155 or
 PT Ser113 -
 XX
 PS Example 2; Flg 3a; 157pp; English.

The present invention describes an isolated or synthetic polypeptide (I) comprising a less than full length amino acid sequence of a mutant Bcl-XL/Bcl-2 associated cell death regulator polypeptide (BAD) or its fragment, which contains amino acid substitutions at Ser118 of a human BAD, Ser155 of a murine BAD (longer murine BAD) or Ser113 of a human BAD (shorter murine BAD). (I) has immunostimulant, neuroprotective, neurotropic, antileukemic, vulnery, cytotoxic, antiviral, antitumor, antileukemic, wound healing, cancer, immunosuppressive activities, and can be used as an apoptosis inducer or inhibitor. BAD polypeptides and polynucleotides can be used for screening candidate compounds and drugs for activity that promote cell survival or apoptosis. Other uses include inducing or inhibiting apoptosis in a cell. Candidate compounds identified and (mutant) BAD polypeptides are useful in treating immunodeficiency diseases, neurodegenerative diseases, ischemic cell death, reperfusion cell death, wound healing, cancer, viral infections, lymphoproliferative conditions, arthritis, infertility, inflammation and autoimmune diseases. The present sequence represents a Bcl-Family member Bcl3 domain consensus sequence which is used in an example from the present invention.

Sequence 26 AA:
 SQ

Query Match 94.1%; Score 80; DB 22; Length 26;
 Best Local Similarity 100.0%; Pred. No. 2,4e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GOVGRQLAIIQDDINR 17
 |||
 DB 3 gqvgrqlaligddinr 18

ID AAB37004 standard; peptide: 27 AA.
 XX
 AC AAB37004;
 XX
 DT 28-FEB-2001 (first entry)
 XX
 DE Bcl2 polypeptide BH3 domain peptide #4.
 XX
 KM Cytotoxic; neuroprotective; anti-HIV; vitruclide; cerebroprotective;
 KM cardiotonic; Bcl-2 superfamily; BH3 domain; cell death agonist; Bad;
 KM apoptosis modulator; B cell lymphoma/leukemia 2; cancer; prostate;
 KM osteoclast; gastritis; non-small lung renal; thyroid; neuroblastoma;
 KM melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
 KM stroke; myocardial infarction.
 XX
 OS Homo sapiens.
 XX
 PN MO200059526-A1.
 XX
 PD 12-OCT-2000.
 XX
 PF 06-APR-2000; 2000MO-US09352.
 XX
 PR 07-APR-1999; 99US-0128202.
 XX
 PA (UYJE-) UNIV JEFFERSON THOMAS.
 XX
 PI Huang Z, Wang J, Zhang Z, Shan S, Lu Z;
 XX
 DR WPI: 2000-679325/66.
 XX
 PT New peptide conjugates for mediating apoptosis or for inhibiting B
 PT cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for
 PT treating neurodegenerative disorders, stroke, or cancer -
 XX
 PS Claim 18; Page 17; 74pp; English.

The invention relates to a peptide conjugate having the formula:
 (R-X)_n-peptide where n = 1-10; X = C=O, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is NH₂ or OH; or X = O or NH, when the R-X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COOH or CONH₂; and R = 2-18C alkyl or alkoxy; 2-14C alkenyl containing one or two double bonds; cyclobutyl, cyclopentyl, cyclohexyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, phenyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides AAB37001-B37058 represent examples of the peptide portion of the conjugate. The peptides represent analogues of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of the BH3 domain of the cell death agonist Bad. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing B cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of apoptosis in cancer cells. It is also useful for inhibiting Bcl-2 function. In particular, the peptide conjugate is useful for treating a subject afflicted with a cancer characterized by cancer cells that express Bcl-2. The cancer includes prostate, colorectal, gastric, non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.

Sequence 27 AA:
 SQ

Query Match 94.1%; Score 80; DB 21; Length 27;
 Best Local Similarity 100.0%; Pred. No. 2.5e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GOVGRQLAIIQDDINR 17
 |||
 DB 6 gqvgrqlaligddinr 21

PD 08-JUN-1995.
 XX
 PF 30-NOV-1994: 94WO-US13930.
 XX
 PR 07-OCT-1994: 94US-0320157.
 PR 30-NOV-1993: 93US-0160067.
 XX
 PA (LXRB-) LXR BIOTECHNOLOGY INC.
 XX
 PI Barr PJ, Kiefer MC;
 XX
 DR WPI: 1995-215106/28.
 XX
 PT New nucleic acid sequences encoding Cdn apoptosis modulators - and
 PT related vectors, transformed cells, proteins and antibodies, useful
 PT or diagnosis and treatment e.g. of HIV infection, reperfusion injury
 PT etc.
 PS Disclosure: Fig.11: 66pp: English.
 XX
 CC Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in
 CC increased cell survival in response to anti-Fas-mediated apoptosis.
 CC Deletion of the N-terminal 70 amino acids of Cdn-1 improved this
 CC activity, suggesting that small, truncated Cdn-1 molecules may be
 CC potent therapeutics.
 XX
 SQ Sequence 141 AA:

Query Match 94.1%; Score 80; DB 16; Length 141;
 Best Local Similarity 100.0%; Pred. No. 1.6e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GCGVQLATIGDDINR 17
 |||||
 DB 2 gqvgqrqaligddlnr 17

RESULT 11

AA77879
 ID AA77879 standard: Protein: 152 AA.

XX
 AC AA77879;

XX
 DT 21-NOV-1995 (first entry)

XX
 DE Human Cdn-1(60-211).

XX
 KW Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
 KW autoimmune disease; reperfusion injury; hepatitis; osteoporosis;

KM shock; lymphoma; eczema.
 XX

XX
 OS Homo sapiens.

XX
 PN WO9515084-A.

XX
 PD 08-JUN-1995.

XX
 PF 30-NOV-1994: 94WO-US13930.

XX
 PR 07-OCT-1994: 94US-0320157.

XX
 PR 30-NOV-1993: 93US-0160067.

XX
 PA (LXRB-) LXR BIOTECHNOLOGY INC.

XX
 PI Barr PJ, Kiefer MC;
 XX
 DR WPI: 1995-215106/28.

XX
 PT New nucleic acid sequences encoding Cdn apoptosis modulators - and
 PT related vectors, transformed cells, proteins and antibodies, useful
 PT or diagnosis and treatment e.g. of HIV infection, reperfusion injury
 PT etc.

XX
 PS Disclosure: Fig.11: 66pp: English.

XX
 CC Expression of Cdn-1 in WI-L2 lymphoblastoid cells resulted in
 CC increased cell survival in response to anti-Fas-mediated apoptosis.
 CC Deletion of the N-terminal 59 amino acids of Cdn-1 only slightly
 CC decreased this activity, suggesting that small, truncated Cdn-1
 CC molecules may be potent therapeutics.
 XX

SQ Sequence 152 AA:

Query Match 94.1%; Score 80; DB 16; Length 152;
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GCGVQLATIGDDINR 17
 |||||
 DB 13 gqvgqrqaligddlnr 28

RESULT 12

AA77876
 ID AA77876 standard: Protein: 211 AA.

XX
 AC AA77876;

XX
 DT 21-NOV-1995 (first entry)

XX
 DE Human Cdn-1.

XX
 KW Cdn-1; apoptosis modulator; adoptive immunotherapy; therapy; HIV;
 KW autoimmune disease; reperfusion injury; hepatitis; osteoporosis;

KM shock; lymphoma; eczema.
 XX

XX
 OS Homo sapiens.

XX
 PN WO9515084-A.

XX
 PD 08-JUN-1995.

XX
 PF 30-NOV-1994: 94WO-US13930.

XX
 PR 07-OCT-1994: 94US-0320157.

XX
 PR 30-NOV-1993: 93US-0160067.

XX
 PA (LXRB-) LXR BIOTECHNOLOGY INC.

XX
 PI Barr PJ, Kiefer MC;
 XX
 DR WPI: 1995-215106/28.

XX
 DR N-PSDB: AA095492.

XX
 PT New nucleic acid sequences encoding Cdn apoptosis modulators - and
 PT related vectors, transformed cells, proteins and antibodies, useful
 PT or diagnosis and treatment e.g. of HIV infection, reperfusion injury
 PT etc.

XX
 PS Disclosure: Fig.3A-B: 66pp: English.

XX
 CC Cdn-1 cDNA was isolated from a human heart cDNA library using a
 CC previously isolated clone as probe. Recombinant Cdn-1 was produced
 CC in Sf9 and human colon adenocarcinoma H29 cells. Expression of
 CC Cdn-1 in WI-L2 lymphoblastoid cells resulted in increased cell
 CC survival in response to anti-Fas-mediated apoptosis.
 XX

SQ Sequence 211 AA:

Query Match 94.1%; Score 80; DB 16; Length 211;
 Best Local Similarity 100.0%; Pred. No. 2.5e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PF 19-APR-1996; 96MO-US05639.
 XX
 PR 20-APR-1995; 95US-0426529.
 XX
 PA (LXR8-) LXR BIOTECHNOLOGY INC.
 XX
 PI Barr PJ, Kiefer MC;
 XX
 DR MPI; 1996-485086/48.
 XX
 N-PSDB; AA042139.
 XX
 PT Screening for anti-viral agents - by detecting the ability of an
 PT agent to disrupt the interaction of a Bak protein and a viral
 PT protein
 PS
 PS Disclosure; Fig 2; 24pp; English).
 CC This Bak-2 protein sequence represents a bcl-1 homologue which
 CC interacts with Epstein-Barr virus (EBV) early lytic cycle BHRF1
 CC protein, and is capable of modulating apoptosis. The protein may
 CC be used in complete or partial form, or as an epitope tag fusion.
 CC protein, in a new virucide drug screening method, which involves
 CC combination of Bak-2 protein and a viral protein (e.g. EBV BHRF1),
 CC exposure to a test compound, and monitoring for disruption of the
 CC interaction, e.g. by co-precipitation, protein interaction trapping
 CC or ELISA. Interaction of Bak-2 and viral proteins allows viral
 CC replication latency in the absence of apoptosis. Compounds which
 CC inhibit this interaction may be used as virucide, antitumour or
 CC diagnostic agents.
 XX
 XX
 SQ Sequence 211 AA:

Query Match 94.18; Score 80; BH 17; Length 211;
 Best Local Similarity 100.00; Pred No. 2; Se-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 GCGGCAATIGDDINR 17
 ||||||||||||||||
 Db 72 gqvgqqlalqgddlnr 87

Search completed: September 20, 2002, 10:35:59
 Job time: 427 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2002, 10:37:21 ; Search time 75.64 Seconds
(without alignments)
5.490 Million cell updates/sec

Title: US-09-544-664-57

Perfect score: 85

Sequence: 1 KQVGRQLATIGDDINK 17

BLOSUM62

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents_Aa: *
1: /cgn2-6/p/odata/2/1aa/5A.COMR.pep: *
2: /cgn2-6/p/odata/2/1aa/5B.COMR.pep: *
3: /cgn2-6/p/odata/2/1aa/6A.COMR.pep: *
4: /cgn2-6/p/odata/2/1aa/6B.COMR.pep: *
5: /cgn2-6/p/odata/2/1aa/6C.COMR.pep: *
6: /cgn2-6/p/odata/2/1aa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	80	94.1	19	4	US-09-236-385A-35
2	80	94.1	20	4	US-09-236-385A-36
3	80	94.1	28	1	US-08-440-391-2
4	80	94.1	28	1	US-08-440-391-18
5	80	94.1	28	2	US-08-508-597A-18
6	80	94.1	28	2	US-08-508-597A-18
7	80	94.1	28	4	US-09-236-385A-2
8	80	94.1	28	4	US-09-236-385A-18
9	80	94.1	28	5	PCT-US96-06122-18
10	80	94.1	28	5	PCT-US96-06122-18
11	80	94.1	36	1	US-08-440-391-2
12	80	94.1	36	2	US-08-508-597A-14
13	80	94.1	36	2	US-08-508-597A-14
14	80	94.1	36	5	PCT-US96-06122-14
15	80	94.1	141	1	US-08-471-058-23
16	80	94.1	152	1	US-08-471-058-22
17	80	94.1	210	3	US-08-471-058-22
18	80	94.1	210	3	US-08-471-058-22
19	80	94.1	211	1	US-08-471-058-9
20	80	94.1	211	1	US-08-471-058-9
21	80	94.1	211	1	US-08-471-058-10
22	80	94.1	211	1	US-08-471-058-11
23	80	94.1	211	2	US-08-944-530-2
24	80	94.1	211	2	US-08-944-530-2
25	80	94.1	211	3	US-08-471-057-7
26	80	94.1	211	3	US-08-471-057-9
27	80	94.1	211	3	US-08-471-057-10

28	80	94.1	211	3	US-08-471-057-11	Sequence 11, App1
29	74	87.1	15	4	US-09-236-385A-37	Sequence 37, App1
30	74	87.1	31	1	US-08-440-391-3	Sequence 3, App1
31	74	87.1	31	1	US-08-440-391-16	Sequence 16, App1
32	74	87.1	31	2	US-08-908-597A-3	Sequence 3, App1
33	74	87.1	31	2	US-08-908-597A-16	Sequence 16, App1
34	74	87.1	31	4	US-09-236-385A-3	Sequence 3, App1
35	74	87.1	31	4	US-09-236-385A-16	Sequence 16, App1
36	74	87.1	31	5	PCT-US96-06122-3	Sequence 3, App1
37	74	87.1	31	5	PCT-US96-06122-16	Sequence 16, App1
38	69	81.2	15	1	US-08-440-391-10	Sequence 10, App1
39	69	81.2	15	1	US-08-440-391-20	Sequence 20, App1
40	69	81.2	15	2	US-08-908-597A-10	Sequence 10, App1
41	69	81.2	15	2	US-08-908-597A-20	Sequence 20, App1
42	69	81.2	15	4	US-09-236-385A-10	Sequence 10, App1
43	69	81.2	15	4	US-09-236-385A-20	Sequence 20, App1
44	69	81.2	15	4	US-09-236-385A-38	Sequence 38, App1
45	69	81.2	15	5	PCT-US96-06122-10	Sequence 10, App1

ALIGNMENTS

RESULT 1
US-09-236-385A-35
Sequence 35, Application US/09236385A
Patent No. 6221615
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
LUTZ, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 41
CORRESPONDING ADDRESSES:
ADDRESS: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER ANALYSIS FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/09/236, 385A
APPLICATION NUMBER: US/09/236, 385A
FILING DATE: 25-Jan-1999
CLASSIFICATION: <Intom>
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.; 073
REGISTRATION NUMBER: 32, 073
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-9400
TELEFAX: 202-942-9484
INFORMATION FOR SEQ. ID NO.: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-236-385A-35

Query Match 94.1% Score 80; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 37e08;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 GQVGRQLATIGDDINK 17
DB 2 GQVGRQLATIGDDINK 17

```

RESULT 2
US-09-236-385A-36
: Sequence 36: Application US/09236385A
: Patent No. 6221615
: GENERAL INFORMATION:
: APPLICANT: CHITTENDEN, Thomas D.; and
: TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
: MODULATE APOPTOSIS
: NUMBER OF SEQUENCES: 21
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Hale and Dorr
: STREET: 1455 Pennsylvania Avenue, N.W.
: CITY: Washington
: STATE: D.C.
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION: US/09/236,385A
: FILING DATE: 25-Mar-1999
: CLASSIFICATION: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: WIXON, HENRY N.
: REGISTRATION NUMBER: 32,073
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-942-8400
: TELEFAX: 202-942-8484
: INFORMATION FOR SEQ ID NO: 36
: SEQUENCE CHARACTERISTICS:
: LENGTH: 20 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: SEQUENCE DESCRIPTION: SEQ ID NO: 36
US-09-236-385A-36

Query Match          94.1%; Score 80; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 4e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GOVROLATIGDDIR 17
|1111111111111111|
DB 3 GOVROLATIGDDIR 18

RESULT 3
US-08-440-391-2
: Sequence 2: Application US/08440391
: Patent No. 5656725
: GENERAL INFORMATION:
: APPLICANT: CHITTENDEN, Thomas D.; and
: APPLICANT: LUTZ, Robert J.
: TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
: MODULATE APOPTOSIS
: NUMBER OF SEQUENCES: 34
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Hale and Dorr
: STREET: 1455 Pennsylvania Avenue, N.W.
: CITY: Washington
: STATE: D.C.
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25

```

```

: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/440,391
: FILING DATE: 12-MAY-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: WIXON, HENRY N.
: REGISTRATION NUMBER: 32,073
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-942-8400
: TELEFAX: 202-942-8484
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 28 amino acid
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-08-440-391-2

Query Match          94.1%; Score 80; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GOVROLATIGDDIR 17
|1111111111111111|
DB 6 GOVROLATIGDDIR 21

RESULT 4
US-08-440-391-18
: Sequence 18: Application US/08440391
: Patent No. 5656725
: GENERAL INFORMATION:
: APPLICANT: CHITTENDEN, Thomas D.; and
: APPLICANT: LUTZ, Robert J.
: TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
: MODULATE APOPTOSIS
: NUMBER OF SEQUENCES: 34
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Hale and Dorr
: STREET: 1455 Pennsylvania Avenue, N.W.
: CITY: Washington
: STATE: D.C.
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/440,391
: FILING DATE: 12-MAY-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: WIXON, HENRY N.
: REGISTRATION NUMBER: 32,073
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-942-8400
: TELEFAX: 202-942-8484
: INFORMATION FOR SEQ ID NO: 18:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 28 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-08-440-391-18

Query Match          94.1%; Score 80; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 2 GOVROLAIGDDINR 17
 Db 6 GOVROLAIGDDINR 21

RESULT 5

US-08-908-597A-2
 Sequence 2, Application US/08908597A

Patent No. 5863795

GENERAL INFORMATION:

APPLICANT: CHITTENDEN, Thomas D.; and

APPLICANT: LUTZ, Robert J.

TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH

TITLE OF INVENTION: MODULATE APOPTOSIS

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hale and Dorr

STREET: 1455 Pennsylvania Avenue, N.W.

CITY: Washington

STATE: D.C.

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/908-597A

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION NUMBER: US/08/440,391

APPLICATION NUMBER: US/08/440,391

FILING DATE: 12-MAY-1995

ATTORNEY/AGENT INFORMATION:

NAME: WIXON, HENRY N.

REGISTRATION NUMBER: 32,073

REFERENCE/DOCKET NUMBER: 104322.147

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-942-8400

TELEFAX: 202-942-8484

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 28 amino acid

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

Query Match 94.1%; Score 80; Db 2; Length 28;

Best Local Similarity 100.0%; Pred. No. 5.9e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GOVROLAIGDDINR 17
 Db 6 GOVROLAIGDDINR 21

RESULT 6

US-08-908-597A-18
 Sequence 18, Application US/08908597A

Patent No. 5863795

GENERAL INFORMATION:

APPLICANT: CHITTENDEN, Thomas D.; and

APPLICANT: LUTZ, Robert J.

TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH

TITLE OF INVENTION: MODULATE APOPTOSIS

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hale and Dorr

STREET: 1455 Pennsylvania Avenue, N.W.

CITY: Washington

STATE: D.C.

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/908,597A

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/440,391

FILING DATE: 12-MAY-1995

ATTORNEY/AGENT INFORMATION:

NAME: WIXON, HENRY N.

REGISTRATION NUMBER: 32,073

REFERENCE/DOCKET NUMBER: 104322.147

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-942-8400

TELEFAX: 202-942-8484

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 28 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

Query Match 94.1%; Score 80; Db 2; Length 28;

Best Local Similarity 100.0%; Pred. No. 5.9e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GOVROLAIGDDINR 17
 Db 6 GOVROLAIGDDINR 21

RESULT 7

US-09-236-385A-2
 Sequence 2, Application US/09236385A

Patent No. 6221615

GENERAL INFORMATION:

APPLICANT: CHITTENDEN, Thomas D.; and

APPLICANT: LUTZ, Robert J.

TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH

TITLE OF INVENTION: MODULATE APOPTOSIS

NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hale and Dorr

STREET: 1455 Pennsylvania Avenue, N.W.

CITY: Washington

STATE: D.C.

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/236,385A

FILING DATE: 25-Jan-1999

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: WIXON, HENRY N.

REGISTRATION NUMBER: 32,073

TELECOMMUNICATION INFORMATION: (C) ATTORNEY DOCKET NO. 104322.147CIP

TELEPHONE: 202-942-8400

TELEFAX: 202-942-8484

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 28 amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-236-385A-2

Query Match
Best Local Similarity 100.0%; Pred. No. 5,9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GOVROLAITGDDINR 17
|||||
Db 6 GOVROLAITGDDINR 21

RESULT 8
US-09-236-385A-18
Sequence 18, Application US/09236385A
Patent No. 6221615
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS

NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/236,385A
FILING DATE: 5-Jan-1999
CLASSIFICATION: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073

TELECOMMUNICATION INFORMATION:
ATTORNEY DOCKET NO. 104322.147CIP
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484

SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-236-385A-18

Query Match
Best Local Similarity 100.0%; Pred. No. 5,9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GOVROLAITGDDINR 17
|||||
Db 6 GOVROLAITGDDINR 21

RESULT 9
PCT-US96-06122-2
Sequence 2, Application PC/TUS9606122
GENERAL INFORMATION:
APPLICANT: IMMUNOGEN, INC.

TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS
WHICH MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06122
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/440,391
FILING DATE: 12-MAY-1995

REGISTRATION NUMBER: 32,073
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US96-06122-2

Query Match
Best Local Similarity 100.0%; Pred. No. 5,9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GOVROLAITGDDINR 17
|||||
Db 6 GOVROLAITGDDINR 21

RESULT 10
PCT-US96-06122-18
Sequence 18, Application PC/TUS9606122
GENERAL INFORMATION:
APPLICANT: IMMUNOGEN, INC.

TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS
WHICH MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06122
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/440,391
FILING DATE: 12-MAY-1995

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.147PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US96-06122-18

Query Match 94.1%; Score 80; DB 5; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GOVGQRLAIGDDINR 17
DB 6 GOVGQRLAIGDDINR 21

RESULT 11
US-08-440-391-14
Sequence 14: Application US/08440391
Patent No. 5655725
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
ATTORNEY/AGENT INFORMATION:
FILING DATE: 12-MAY-1995
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,391
FILING DATE: 12-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.147
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-440-391-14

Query Match 94.1%; Score 80; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GOVGQRLAIGDDINR 17
DB 6 GOVGQRLAIGDDINR 21

DB 8 GOVGQRLAIGDDINR 23

RESULT 12
US-08-908-597A-14
Sequence 14: Application US/08908597A
Patent No. 5653795
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
ATTORNEY/AGENT INFORMATION:
FILING DATE: 12-MAY-1995
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/908,597A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/440,391
FILING DATE: 12-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.147
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 36
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-908-597A-14

Query Match 94.1%; Score 80; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GOVGQRLAIGDDINR 17
DB 8 GOVGQRLAIGDDINR 23

RESULT 13
US-09-236-385A-14
Sequence 14: Application US/09236385A
Patent No. 6221615
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
ATTORNEY/AGENT INFORMATION:
FILING DATE: 12-MAY-1995
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/236,385A
 FILING DATE: 25-Jan-1999
 CLASSIFICATION: <unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: WIXON, HENRY N.
 REGISTRATION NUMBER: 32,073
 TELECOMMUNICATION INFORMATION: (C) ATTORNEY DOCKET NO. 104322.147CIP
 TELEPHONE: 202-942-8400
 TELEFAX: 202-942-8484
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 36 base pairs
 TYPE: amino acid
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 14:
 US-09-236-385A-14

Query Match 94.1%; Score 80; DB 4; Length 36;
 Best Local Similarity 100.0%; Pred. No. 7.9e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 G0VGR0LAIIDDDINR 17
 Db 8 G0VGR0LAIIDDDINR 23

RESULT 14
 PCT-US96-06122-14
 Sequence 14, Application PC/TUS9606122
 GENERAL INFORMATION:
 APPLICANT: IMMUNOGEN, INC.
 TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS
 NUMBER OF SEQUENCES: 34
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hale and Dorr
 STREET: 1455 Pennsylvania Avenue, N.W.
 CITY: Washington
 STATE: D.C.
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/06122
 FILING DATE: HEREWITH
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/440,391
 FILING DATE: 12-MAY-1995
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: WIXON, HENRY N.
 REGISTRATION NUMBER: 32,073
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-942-8400
 TELEFAX: 202-942-8484
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 36 base pairs
 TYPE: amino acid
 TOPOLOGY: linear

MOLECULE TYPE: peptide
 PCT-US96-06122-14

Query Match 94.1%; Score 80; DB 5; Length 36;
 Best Local Similarity 100.0%; Pred. No. 7.9e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 G0VGR0LAIIDDDINR 17
 Db 8 G0VGR0LAIIDDDINR 23

RESULT 15
 US-08-471-058-23
 Sequence 23, Application US/08471058
 Patent No. 770413
 GENERAL INFORMATION:
 APPLICANT: Kleber, Michael C.
 APPLICANT: Bitt, Philip J.
 TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING
 PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FORSTER
 STREET: 755 PAGE MILL ROAD
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304-1018
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTESTO for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/471,058
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: B00
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/320,157
 FILING DATE: 07-OCT-1994
 APPLICATION NUMBER: 08/160,067
 FILING DATE: 30-NOV-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Lehnhardt, Susan K.
 REGISTRATION NUMBER: 33,943
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-813-5600
 TELEFAX: 415-494-0792
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 141 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-471-058-23

Query Match 94.1%; Score 80; DB 1; Length 141;
 Best Local Similarity 100.0%; Pred. No. 4e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 G0VGR0LAIIDDDINR 17
 Db 2 G0VGR0LAIIDDDINR 17

Search completed: September 20, 2002, 10:37:21

Job time: 409 sec

Gencore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2002, 10:39:13 ; Search time 95.59 seconds

(without alignments)
17.089 Million cell updates/sec

Title: US-09-544-664-57

Perfect score: 85

Sequence: 1 KGQVGRQLATIGDDINR 17

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Listing first 45 summaries

1: PIR_71:4
2: PIR_71:4
3: PIR_71:4
4: PIR_71:4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	80	94.1	211	2	S58873
2	47.5	55.9	357	2	T06308
3	46	54.1	833	2	A06564
4	46	54.1	834	1	C64779
5	46	54.1	834	2	A90696
6	46	54.1	834	2	E85546
7	46	54.1	915	2	H02104
8	46	54.1	1226	2	S44824
9	45	52.9	263	2	F89890
10	45	52.9	426	2	S58684
11	45	52.9	426	2	H71967
12	45	52.9	426	2	H75027
13	44.5	52.4	355	2	H84643
14	44	51.8	258	2	H75027
15	44	51.8	261	2	B71213
16	44	51.8	593	2	S75352
17	44	51.8	693	1	G82618
18	44	51.8	803	1	E70041
19	43.5	51.2	532	2	JN0084
20	43	50.6	444	2	JQ1185
21	43	50.6	446	2	T03267
22	43	50.6	446	2	T03221
23	43	50.6	447	2	G86940
24	43	50.6	475	2	T48031
25	43	50.6	664	2	D96633
26	43	50.6	770	2	T23999
27	43	50.6	827	2	B93969
28	42	49.4	356	2	S71460
29	42	49.4	356	2	A53453

ALIGNMENTS

30 42 49.4 575 2 T59327
31 42 49.4 826 2 D85330
32 41 48.2 70 2 H13113
33 41 48.2 251 2 T44678
34 41 48.2 383 2 S76964
35 41 48.2 447 2 W13091
36 41 48.2 530 2 C72281
37 41 48.2 539 2 F72288
38 41 48.2 539 2 S22342
39 41 48.2 566 2 A72254
40 41 48.2 570 2 H97244
41 41 48.2 642 2 F84172
42 41 48.2 654 2 F71298
43 41 48.2 656 2 A72428
44 41 48.2 656 2 E72379
45 41 48.2 661 2 G72316

olfactory cyclic n
ACP receptor transp
hypothetical prote
chemotaxis protei
hypothetical prote
probable minor cap
methyl-accepting c
methyl-accepting c
chaperonin Hsp60 -
methyl-accepting c
membrane associate
ABC transport prot
probable methyl-ac
methyl-accepting c
methyl-accepting c
methyl-accepting c

RESULT 1

S58873

Bak protein - human

C:Species: Homo sapiens (man)

C:Date: 15-Feb-1996 #sequence-revision 01-Mar-1996 #ext-change 08-Oct-1999

C:Accession: S58873; S58872; S58874

R:Chittenden, T.; Harrington, E.A.; O'Connor, R.; Flemington, C.; Lutz, R.J.; Evan, G

Nature 374, 733-736, 1995

A:Title: Induction of apoptosis by the Bcl-2 homologue Bak.

A:Reference number: S58873; M01D:95231653

A:Accession: S58873

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-211 <RNP>

A:Cross-references: EMBL:X84213; NID:g804984; PIR:CA58997.1; PIR:g804985

R:Kiefer, M.C.; Brainer, M.J.; Powers, V.C.; Wu, J.J.; Umanovsky, S.R.; Yonem, L.D.; Bar

Nature 374, 736-739, 1995

A:Title: Modulation of apoptosis by interaction with adenovirus E1B 19K.

A:Reference number: S58874; M01D:95231654

A:Accession: S58874

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-211 <RNP>

A:Cross-references: EMBL:U16811; NID:g595923; PIR:AA74466.1; PIR:g595924

C:Genetics:

A:Gene: GDB:BAC

A:Cross-references: GDB:635887

Query Match 94.1%; Score 80; DB 2; Length 211;

Best local similarity 100.0%; Pred. No. 5.4e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 KGQVGRQLATIGDDINR 17

DB 72 KGQVGRQLATIGDDINR 87

RESULT 2

S58875

cdn-2 protein - human

C:Species: Homo sapiens (man)

A:Reidues: 1-834 <HAY>
 A:Cross-references: GB:BA000007; PIDN:BBB33960.1; PID:g1335994; GSPDB:GN00154
 A:Experimental source: strain 0157:H7, substrain RMD 0509952
 C:Genetics:
 A:Gene: EC80537
 C:Superfamily: Bacillus probable copper-transporting ATPase yvgX; ATPase nucleotide-binding

Query Match 54.1%; Score 46; DB 2; Length 834;
 Best Local Similarity 66.7%; Pred. No. 15;
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 5 GROLAIIIGDDIN 16
 |||:::| | |
 DB 712 GROVAMVGDGIN 723

RESULT 7
 E85546
 Probable ATPase ybar [imported] - Escherichia coli (strain 0157:H7, substrain EDL933)
 C:Species: Escherichia coli
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
 C:Accession: E85546
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 Miller, L.; Grobbeck, E.J.; Davis, N.W.; Llm, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; PMID:21074935; PMID:11206551
 A:Accession: E85546
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-834 <SNC>
 A:Cross-references: GB:AE005174; NID:g12513357; PIDN:AGC54833.1; GSPDB:GN00145; UWGP:206
 A:Experimental source: strain 0157:H7, substrain EDL933
 C:Genetics:
 A:Gene: ybar
 C:Superfamily: Bacillus probable copper-transporting ATPase yvgX; ATPase nucleotide-binding

Query Match 54.1%; Score 46; DB 2; Length 834;
 Best Local Similarity 66.7%; Pred. No. 15;
 Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 5 GROLAIIIGDDIN 16
 |||:::| | |
 DB 712 GROVAMVGDGIN 723

RESULT 8
 H82104
 cation transport ATPase, El-E2 family VC2215 [imported] - Vibrio cholerae (strain N16961
 C:Species: Vibrio cholerae
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
 Chardson, D.; Esmailova, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F.
 L, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A:Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A:Reference number: A82035; PMID:20406833
 A:Accession: H82104
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-915 <HEL>
 A:Cross-references: GB:AE004293; GB:AE003852; NID:g9656766; PIDN:AAV95359.1; GSPDB:GN001
 A:Experimental source: serogroup O1; strain N16961; biotype El Tor
 C:Genetics:
 A:Gene: VC2215
 A:Map position: 1
 C:Superfamily: Bacillus probable copper-transporting ATPase yvgX; ATPase nucleotide-binding

Query Match 54.1%; Score 46; DB 2; Length 915;

Best Local Similarity 64.3%; Pred. No. 17;
 Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 3 QVGRQALIIIGDDIN 16
 |||:::| | |
 DB 786 QGRKRVAMIGDGIN 799

RESULT 9
 S44824
 F54F2.1 protein - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 23-Mar-2001
 C:Accession: S44824
 R:Anderson, K.
 submitted to the EMBL data library, September 1993
 A:Description: Sequence of the C. elegans cosmid F54F2.
 A:Reference number: S44817
 A:Accession: S44824
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1226 <AND>
 A:Cross-references: EMBL:123645; NID:g388603; PID:g388605
 C:Genetics:
 A:Insertions: 58/2, 137/3, 179/1, 316/2, 393/1, 551/3, 597/2, 662/2, 899/3, 1178/3
 C:Keywords: cytoskeleton; transmembrane protein

Query Match 54.1%; Score 46; DB 2; Length 1226;
 Best Local Similarity 53.8%; Pred. No. 23;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 2 GQVGRQALIIIGDD 14
 |:::| | |
 DB 359 GVFGRQALVAGSD 371

RESULT 10
 F89890
 conserved hypothetical protein SA1030 [imported] - Staphylococcus aureus (strain N315
 C:Species: Staphylococcus aureus
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C:Accession: F89890
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O
 ma, A.; Mizutani-Oi, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.
 Lancet 357, 1225-1240, 2001
 A:Title: Whole genome sequencing of methicillin-resistant staphylococcus aureus.
 A:Reference number: A89758; PMID:21311952; PMID:11418146
 A:Accession: F89890
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-263 <KUR>
 A:Cross-references: GB:BA000018; PID:g13700986; PIDN:BBBA4282.1; GSPDB:GN00149
 A:Experimental source: strain N315
 C:Genetics:
 A:Gene: SA1030

Query Match 52.9%; Score 45; DB 2; Length 263;
 Best Local Similarity 75.0%; Pred. No. 6.1;
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 KQGVGRQALIIIG 12
 ||| | | | | |
 DB 250 KQGTGRMLAFIC 261

RESULT 11
 S1684
 phosphopyruvate hydratase (EC 4.2.1.11) - Helicobacter pylori (strains 26695 and other
 N/A alternate names: enolase
 C:Species: Helicobacter pylori

C>Date: 29-Nov-1999 #sequence_rev10 17-Sep-1997 #text_change 22-Jun-1999
C>Accession: B64539; S58684
R>Homl, J.F.; Lott, O.; Kerlavage, A.R.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; White, B.; Richardson, D.; Dodson, R.; Kialak, H.G.; Glöckner, J.; McKennam, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Wetthey, L.; son, J.B. 539-547, 1997
A>Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A>Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.
A>Reference number: A64520; MUID:97394467
A>Accession: B64539
A>Status: nucleic acid sequence not shown; translation not shown
A>Molecule type: DNA
A>Residues: 1426 <COM>
A>Cross-References: GB:AE000536; GB:AE000511; NID:g2313230; PIDN:AD07219.1; PID:g2313230
A>Experimental source: strain 26695
C>Schmitt, W.; Odenbreit, S.; Hennermann, D.; Haas, R.
Mol. Gen. Genet. 248: 563-572, 1995
A>Title: Cloning of the *Helicobacter pylori* recA gene and functional characterization of
A>Reference number: S58683; MUID:96027928
A>Accession: S58684
A>Molecule type: DNA
A>Residues: 1425 'T' 27-68 <SCH>
A>Cross-References: EMBL:Z53478
C>Genetics:
A>Gene: HP0154
C>Function:
A>Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to phosphoenolpyruvate
A>Pathway: glycolysis
C>Superfamily: enolase
C>Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; magnesium
F>42/Binding site: magnesium 2 (Sof) #status predicted
F>205 338/Active site: Glu Lys #status predicted
F>242,286,313/Binding site: magnesium 1 (asp, Glu, Asp) #status predicted

Query Match 52.9%; Score 45; DB 2; Length 426;
Best Local Similarity 46.2%; Pred No. 10;
Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
DB 303 EGNOLV6DDL 315
QY 3 OYGNOLV6DDL 15
QY 3 OYGNOLV6DDL 15
QY 3 OYGNOLV6DDL 15

RESULT 12
H71967
enolase - *Helicobacter pylori* (strain J39)
C>Species: *Helicobacter pylori*
A>Variety: str10099
C>Date: 12-Feb-1999 #sequence_rev10 12-Feb-1999 #text_change 22-Jun-1999
C>Accession: H71967
R>Homl, J.F.; Lott, O.; Kerlavage, A.R.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; White, B.; Richardson, D.; Dodson, R.; Kialak, H.G.; Glöckner, J.; McKennam, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Wetthey, L.; son, J.B. 539-547, 1997
A>Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A>Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.
A>Reference number: A64520; MUID:97394467
A>Accession: B64539
A>Status: nucleic acid sequence not shown; translation not shown
A>Molecule type: DNA
A>Residues: 1426 <COM>
A>Cross-References: GB:AE000536; GB:AE000511; NID:g2313230; PIDN:AD07219.1; PID:g2313230
A>Experimental source: strain 26695
C>Schmitt, W.; Odenbreit, S.; Hennermann, D.; Haas, R.
Mol. Gen. Genet. 248: 563-572, 1995
A>Title: Cloning of the *Helicobacter pylori* recA gene and functional characterization of
A>Reference number: S58683; MUID:96027928
A>Accession: S58684
A>Molecule type: DNA
A>Residues: 1425 'T' 27-68 <SCH>
A>Cross-References: EMBL:Z53478
C>Genetics:
A>Gene: HP0154
C>Function:
A>Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to phosphoenolpyruvate
A>Pathway: glycolysis
C>Superfamily: enolase
C>Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; magnesium
F>42/Binding site: magnesium 2 (Sof) #status predicted
F>205 338/Active site: Glu Lys #status predicted
F>242,286,313/Binding site: magnesium 1 (asp, Glu, Asp) #status predicted

```
Db      303 ELRGROIIVGDDL 315

RESULT   13
H84643
Probable protein phosphatase 2C [Imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 15-Jun-2001
C:Accession: H84643
R:Lin.: X.; Kaul, S.; Rounmaley, S.D.; Shea, T.P.; Bentito, M.I.; Town, C.D.; Pujil, C.Y.;
M.; Koo, H.; Moffet, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
M.; D.; Niemann, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-766, 1999
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: AB4420; MIMD.20083487
A:Accession: H84643
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1355 <$NO>
A:Cross-references: GB:AE002093; NID:g4559345; PIDN:AMD2006.1; GSTDB:GN00139
C:Genetics
A:Gene: AT2g25070
A:Map position: 2
C:Superfamily: human phosphoprotein phosphatase 1A

Query Match          52.4%; Score 44.5; DB 2; Length 355;
Best Local Similarity 50.0%; Freq. NO. 10;
Matches 9; Conservative 6; Mismatches 2; Indels 1; Gaps 1;

Ox      1 KGQVG-RQLATIGDDINR 17
       :| | | :||::|| :| :|
Db      103 GGQRGWREIIVAGSDKMK 120
```

```

RESULT 14
H75027
hy v-elpase proteoiclipid PAB1189 - Pyrococcus abyssi (strain Orsay)
C|Species: Pyrococcus abyssi
C|Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C|Accession: H75027
R|anonymous: Genoscope
Submitted to the EMBL Data Library, July 1999
A|Description: Pyrococcus abyssi genome sequence: Insights into archaeal chromosome s
A|Reference number: A75001
A|Accession: H75027
A|Status: preliminary
A|Molecule type: DNA
A|Cross-refs: 1,258 <KB>
A|Cross-references: GB:UJ248288; GB:AL096836; NID:G5458960; PIDN:CAM50662.1; PID:el51
A|Experimental source: strain Orsay
C|Genetics:
A|Gene: PAB1189

Query Match          51.8%; Score 44; DB 2; Length 258;
Best Local Similarity 43.8%; Pred. No. 8,8;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY      2 GCGCATATCGDINDIR 17
      |||::|||
Db      122 GCGCGTAVVADEIR 137

RESULT 15
B71213
probable chemoreceptor protein - Pyrococcus horikoshii
C|Species: Pyrococcus horikoshii
C|Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 21-Jul-2000
C|Accession: B71213
R|Kawabata, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Sa
M.; Ohtsuka, T.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushiida, N.; Og
DNA Res. 5, 55-76, 1998

```

A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A:Reference number: A71000; MUID:98344137
A:Accession: B71213
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-261 <KAM>
A:Cross-references: GB:AP000007; NID:93236134; PIDN:BAA31097.1; PID:93258414
A:Experimental source: strain OT3
A>Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH1970

Query Match 51.8%; Score 44; DB 2; Length 261;
Best Local Similarity 43.8%; Pred. No. 8.9;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Caps 0;
OY 2 GQVGRQLAIIIGDDINR 17
DB 125 GEAGRGFAVVADEIRR 140

Search completed: September 20, 2002, 10:39:13
Job time: 485 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2002, 11:04:35 : Search time 44.99 seconds

(without alignments)
14.631 Million cell updates/sec

Title: US-09-544-664-57

Sequence: 1 KGQYGRQLATIGDDINK 17

Scoring table: BLOSUM62
gapop 10.0 , gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Swissprot_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	80	94.1	211	1	BAK2_HUMAN	Q13014 homo sapien
2	80	94.1	211	1	BAK_HUMAN	Q16931 homo sapien
3	78	91.8	208	1	BAK_MOUSE	Q16931 mus musculus
4	46	54.1	834	1	PRC1_DCOI	Q29385 escherichia
5	46	54.1	1226	1	PRC2_DCOI	Q24446 escherichia
6	45	52.0	262	1	YMD_STRAU	Q24446 streptococcus
7	45	52.9	426	1	ENO_HELPY	Q24446 heliobacter
8	45	52.9	426	1	ENO_HELPY	Q24446 heliobacter
9	44	51.8	833	1	ENO_HELPY	Q24446 heliobacter
10	43.5	50.6	512	1	ENO_HELPY	Q24446 heliobacter
11	43	50.6	444	1	ENO_HELPY	Q24446 heliobacter
12	43	50.6	444	1	ENO_HELPY	Q24446 heliobacter
13	43	50.6	444	1	ENO_HELPY	Q24446 heliobacter
14	43	50.6	444	1	ENO_HELPY	Q24446 heliobacter
15	43	50.6	444	1	ENO_HELPY	Q24446 heliobacter
16	43	50.6	444	1	ENO_HELPY	Q24446 heliobacter
17	42	49.4	575	1	ENO_HELPY	Q24446 heliobacter
18	42	49.4	575	1	ENO_HELPY	Q24446 heliobacter
19	41	48.2	820	1	ENO_HELPY	Q24446 heliobacter
20	41	48.2	820	1	ENO_HELPY	Q24446 heliobacter
21	41	48.2	820	1	ENO_HELPY	Q24446 heliobacter
22	41	48.2	820	1	ENO_HELPY	Q24446 heliobacter
23	41	48.2	820	1	ENO_HELPY	Q24446 heliobacter
24	41	48.2	820	1	ENO_HELPY	Q24446 heliobacter
25	41	48.2	820	1	ENO_HELPY	Q24446 heliobacter
26	41	48.2	820	1	ENO_HELPY	Q24446 heliobacter
27	41	48.2	820	1	ENO_HELPY	Q24446 heliobacter
28	41	48.2	820	1	ENO_HELPY	Q24446 heliobacter
29	41	48.2	820	1	ENO_HELPY	Q24446 heliobacter
30	41	48.2	820	1	ENO_HELPY	Q24446 heliobacter
31	41	48.2	820	1	ENO_HELPY	Q24446 heliobacter
32	41	48.2	820	1	ENO_HELPY	Q24446 heliobacter
33	41	48.2	820	1	ENO_HELPY	Q24446 heliobacter
34	41	48.2	820	1	ENO_HELPY	Q24446 heliobacter
35	41	48.2	820	1	ENO_HELPY	Q24446 heliobacter
36	41	48.2	820	1	ENO_HELPY	Q24446 heliobacter
37	41	48.2	820	1	ENO_HELPY	Q24446 heliobacter
38	41	48.2	820	1	ENO_HELPY	Q24446 heliobacter
39	41	48.2	820	1	ENO_HELPY	Q24446 heliobacter
40	41	48.2	820	1	ENO_HELPY	Q24446 heliobacter
41	41	48.2	820	1	ENO_HELPY	Q24446 heliobacter
42	41	48.2	820	1	ENO_HELPY	Q24446 heliobacter
43	41	48.2	820	1	ENO_HELPY	Q24446 heliobacter
44	41	48.2	820	1	ENO_HELPY	Q24446 heliobacter
45	41	48.2	820	1	ENO_HELPY	Q24446 heliobacter

ALIGNMENTS

Result	ID	STANDARD	PRT	211 AA
BAK2_HUMAN				
Q13014				
01-NOV-1997 (Rel. 35, Created)				
01-NOV-1997 (Rel. 35, Last sequence update)				
16-OCT-2001 (Rel. 40, Last annotation update)				
Bcl-2, hemolysis, antagonist/killer 2 (Apoptosis regulator BAK-2).				
BCL2IP1 or BAK2.				
Homo sapiens (Human)				
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
NCBI_TaxId=9606;				
[1]				
SEQUENCE FROM N.A.				
RA MEDLINE=95231654; PubMed=7715731;				
RA Kletter M.C., Brauer M.J., Powers V.C., Wu J.J., Umansky S.R.,				
RA Kletter L.D., Barr P.J.,				
RA *modulation of apoptosis by the widely distributed Bcl-2 homologue				
BAK-2.				
RA Mature 374-736-739(1995).				
CC - FUNCTION: IN THE PRESENCE OF AN APPROPRIATE STIMULUS, ACCELERATES				
CC PROGRAMED CELL DEATH BY BINDING TO, AND ANTAGONIZING THE A				
CC REPRESSOR BCL-2 OR ITS ADENOVIRUS HOMOLOG E1B 19K PROTEIN.				
CC - SUBUNIT: FORMS HETERODIMERS WITH BCL-2, E1B 19K PROTEIN, AND BCL-				
CC X(L).				
CC - SUBCELLULAR LOCATION: Membrane-associated (potential).				
CC - TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES, WITH				
CC HIGHEST LEVELS IN THE HEART AND SKELETAL MUSCLE.				
CC - DOMAIN: INVOLVED IN THE BCL-2 FAMILY OF PROTEINS, WITH				
CC BAK FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION				
CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.				
CC - SIMILARITY: MEMBERS OF THE BCL-2 FAMILY.				
CC - SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 1 (BH1).				
CC - SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 2 (BH2).				
CC - SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 3 (BH3).				
CC - CAUTION: THIS COULD BE THE PRODUCT OF A PSEUDOGENE.				
CC This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-				
CC The European Bioinformatics Institute. There are no restrictions on its				
CC use by non-profit institutions as long as its content is in no way				
CC modified and this statement is not removed. Usage by and for commercial				
CC entities requires a license agreement (See http://www.isb.ch/announce/				
CC or send an email to license@isb.ch).				
CC EMBL, U16812; AAA7467.1; -				
CC HSPF, Q16611; BAK.				
CC InterPro: IPR002475; BCL2_family.				
CC InterPro: IPR00712; BCL-2.				
CC Pfam: PF00452; BCL-2; 1.				
CC SMART: SM00337; BCL; 1.				
CC SMART: PS01080; BH1; 1.				
CC PROSITE: PS01258; BH2; 1.				
CC PROSITE: PS01259; BH3; 1.				

DR PROSITE: PS50062, BCL2_FAMILY: 1.
 KM Apoptosis1, Transmembrane.
 FT DOMAIN 74 88 BH3.
 FT DOMAIN 117 136 BH1.
 FT DOMAIN 169 184 BH2.
 FT TRANSMEM 188 205 POTENTIAL.
 SO SEQUENCE 211 AA: 23411 MW: 703875CDACDCCLD3 CRC64:

Query Match 94.1%; Score 80; DB 1; Length 211;
 Best Local Similarity 100.0%; Pred. No. 7.7e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GOVGOALATIGDINR 17
 Db 72 GOVGOALATIGDINR 87

RESULT 2
 BAK_HUMAN STANDARD; PRT; 211 AA.
 ID BAK_HUMAN
 AC Q16611: Q92533.
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Bcl-2 homologous antagonist/killer (Apoptosis regulator BAK).
 GN BAK1 OR BAK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 CX NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RC RESIDUE-COUNT: 211.
 RX MEDLINE-95231652, Pubmed-7715729.
 RA Fritton S.N., White J.H.M., MacLennan I., Raven T., Pun K.-T.,
 RA Chinn S.C., MacLennan J.C., Brown R.,
 RT Cloning of a Bcl-2 homologue by interaction with adenovirus E1B
 RT 19k.*.
 RL Nature 374:731-733(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-95231653, Pubmed-7715730.
 RA Chittenden T, Harrington E.A., O'Connor R., Flemington C., Lutz R.J.,
 RA Evan G.I., Guild B.C.,
 RT Induction of apoptosis by the Bcl-2 homologue Bax.*
 RL Nature 374:733-736(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-95231654, Pubmed-7715731.
 RA Klefer M.C., Bauer M.J., Powers V.C., Wu J.J., Umansky S.R.,
 RA Tomei L.D., Barr P.J.,
 RT Modulation of apoptosis by the widely distributed Bcl-2 homologue
 RT Bax.*
 RL Nature 374:736-739(1995).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Williams S.;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 96-206 FROM N.A.
 RA Egnuch H., Hayashi S.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP MUTAGENESIS AND FUNCTION OF BH3 DOMAIN.
 RX MEDLINE-96091131, Pubmed-8521816.
 RA Chittenden T., Flemington C., Houghton A.B., Ebb R.G., Gallo G.J.,
 RA Elangoan B., Chinnadural G., Lutz R.J.;
 RT A conserved domain in Bax, distinct from Bhl and Bh2, mediates cell
 RT death and protein binding functions.*
 RL EMBO J. 14:5589-5596(1995).
 RN [7]
 RP STRUCTURE BY NMR OF 72-87.

RX MEDLINE-97172562, Pubmed-9020082.
 RA Sattler M., Liang H., Nettesheim D., Meadows R.P., Hartlan J.E.,
 RA Eberstadt M., Liang H.S., Shuker S.B., Chang B.S., Milm A.J.,
 RA Thompson C.B., Fesik S.W.;
 RT Structure of Bcl-xL-Bax peptide complex: recognition between
 RT regulators of apoptosis.*
 RL Science 275:983-986(1997).
 CC -1- FUNCTION: IN THE PRESENCE OF AN APPROPRIATE STIMULUS, ACCELERATES
 CC PROGRAMED CELL DEATH BY BINDING TO, AND ANTAGONIZING THE A
 CC REPRESSOR BCL-2 OR ITS ADENOVIRUS HOMOLOG E1B 19K PROTEIN.
 CC -1- SUBUNIT: FORMS HETERODIMERS WITH BCL-2, E1B 19K PROTEIN, AND BCL-
 CC X(1).
 CC -1- SUBCELLULAR LOCATION: Membrane-bound (Potential).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES, WITH
 CC HIGHEST LEVELS IN THE HEART AND SKELETAL MUSCLE.
 CC -1- DOMAIN: INTRACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
 CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
 CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 1 (BH1).
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 2 (BH2).
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 3 (BH3).
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed or used by and for commercial
 CC entities requires a license agreement. (See <http://www.isb.slb.ch/announce/>
 CC or send an email to license@isb.slb.ch.)
 CC -----
 DR EMBL: X84213; CAN58987.1;
 DR EMBL: U23765; AAA93066.1;
 DR EMBL: U16811; AAA74466.1;
 DR EMBL: Z93017; CAB56826.1;
 DR EMBL: D88397; BAA13608.1;
 DR EMBL: D88396; BAA13608.1; JOINED.
 DR DDB: JBX1:29-OCT-97.
 DR MIM: 600516.
 DR InterPro: IPR002475; BCL2 family.
 DR InterPro: IPR007172; BCL-2.
 DR Pfam: PF00452; Bcl-2; 1.
 DR SMART: SMO0337; BCL2; 1.
 DR PROSITE: PS01060; BH2; 1.
 DR PROSITE: PS01258; BH2; 1.
 DR PROSITE: PS01259; BH3; 1.
 DR PROSITE: PS50062; BCL2_FAMILY: 1.
 KW Apoptosis; Transmembrane; 3D-structure.
 FT DOMAIN 74 88 BH3.
 FT DOMAIN 117 136 BH1.
 FT DOMAIN 169 184 BH2.
 FT TRANSMEM 188 205 POTENTIAL.
 SO SEQUENCE 211 AA: 23409 MW: A2200FF72M46D04E CRC64:

Query Match 94.1%; Score 80; DB 1; Length 211;
 Best Local Similarity 100.0%; Pred. No. 7.7e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GOVGOALATIGDINR 17
 Db 72 GOVGOALATIGDINR 87

RESULT 3
 BAK_MOUSE STANDARD; PRT; 208 AA.
 ID BAK_MOUSE
 AC O08734.
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Bcl-2 homologous antagonist/killer (Apoptosis regulator BAK).

ON BAK1 OR BAK.
 CC MUS musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GRIS; TISSUE=Liver;
 RX MEDLINE=9746138; PubMed=9299236;
 RA Chittenden T., Ma A., Ryan G. T.,
 RT "gene structure, cDNA sequence, and expression of murine Bak, a
 RT proapoptotic BCL-2 family member.";
 RL Genomics 1:95-200(1997).
 CC -1- FUNCTION: IN THE PRESENCE OF AN APPROPRIATE STIMULUS, ACCELERATES
 CC PROGRAED CELL DEATH BY BINDING TO, AND ANTAGONIZING THE A
 CC REPRESSOR BCL-2 OR ITS ADENOVIRUS HOMOLOG ELB 19K PROTEIN (BY
 CC SIMILARITY).
 CC -1- SUBUNIT: FORMS HETERODIMERS WITH BCL-2, ELB 19K PROTEIN, AND BCL-
 CC SIMILARITY).
 CC -1- X1L (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Membrane-associated (potential).
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
 CC -1- DOMAIN: INTACT BH3 DOMAIN IS REQUIRED BY BIK, BID, BAK, BAD AND
 CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
 CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 1 (BH1).
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 2 (BH2).
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 3 (BH3).
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC -----
 CC THIS SWISS-PROT entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sdb.civ/announce/>
 CC or send an email to license@isb-sdb.ch).
 CC -----
 CC EMBL: Y13231; CAA73684.1; ..
 CC HSSP: Q16611; 18XL.
 DR MGD: MGI:1097161; Bak1.
 DR InterPro: IPR002475; BCL2_family.
 DR InterPro: IPR00712; BCL_2.
 DR Pfam: PF00452; Bcl-2_1.
 DR SMART: SM00337; BCL, 1.
 DR PROSITE: PS01080; BH1; 1.
 DR PROSITE: PS01258; BH2; 1.
 DR PROSITE: PS01259; BH3; 1.
 DR PROSITE: PS50062; BCL2_FAMILY; 1.
 DR Apoptosis; Transmembrane.
 KW DOMAIN 71 85 BH3.
 FT DOMAIN 114 133 BH1.
 FT DOMAIN 166 181 BH2.
 FT TRANSMEM 185 202 POTENTIAL.
 SQ SEQUENCE 208 AA; 23300 MW; DAFCLIB160C523C9 CRC64;
 QY 2 GOVQROLATIGDDINR 17 91.8%; Score 78; DB 1; Length 208;
 Db 69 GOVQROLATIGDDINR 84 93.8%; Pred. No. 1,6e-05;
 Best Local Similarity 15; Mismatches 0; Indels 0; Gaps 0;
 RESULT 4
 ID ATCU_ECOLI STANDARD; PRT; 834 AA.
 AC 059385; F78245;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT	01-MAR-2002 (Rel. 41, last annotation update)
DE	Probable copper-transferring ATPase (BC 3.6.3.4).
OS	YBAH OR B0484.
OS	Escherichia coli.
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
CC	Escherichia.
CC	Escherichia.
OX	NCBI_TaxID=562;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=RK12.
RL	Das S., Chuang E.Y., Volpe C., Goldman J., Gitschier J.;
RT	Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.
FT	[2]
FP	SEQUENCE FROM N.A.
RC	STRAIN=RK12 / MG1655;
PX	MEDLINE=97426617; Pubmed=9278503;
RA	Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA	Gregory J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA	Mao B., Shoa Y.;
CC	"the complete genome sequence of Escherichia coli K-12.";
CC	Science 277:1453-1474(1997).
CC	[3]
RN	SEQUENCE FROM N.A.
RA	Roberts D., Allen F., Araujo R., Aparicio A., Chung E., David K.,
RA	Duncan M., Federspiel N., Hyman R., Kalman S., Komp G., Kurdi O.,
RA	Kaw H., Lin D., Sanchez A., Smithfield J., Schramm S., Davis R.W.;
KL	Submitted (OAN-1997) to the EMBL/Genbank/DBJ databases.
CL	SUBMITTER INVOLVED IN COPPER TRANSPORT.
CC	- FUNCTION: INVOLVED IN COPPER TRANSPORT.
CC	- CATALYTIC ACTIVITY: ATP-H(2)O ADP + OXYPHOSPHATE.
CC	- SUBCELLULAR LOCATION: Integral membrane protein (potential).
CC	- SIMILARITY: BELONGS TO THE CAPTION TRANSPORT ATPASES FAMILY.
CC	- (EL-E2 ATPASES). SUBFAMILY 1B.
CC	- SIMILARITY: CONTAINS 2 HMA DOMAINS.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL institution -
CC	the European Bioinformatics Institute. There are no restrictions on lists
CC	use by non-profit institutions as long as its contents in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL, U08330; AMB02266.1; --
DR	EMBL, AE000154; AAC73586.1; --
DR	EMBL, U08264; AMB40238.1; --
DR	HSSP, P04129; IAFJ.
DR	Ecogene; ESJ1246; Ybar.
DR	InterPro: IPR00157; EL-E2_ATPase.
DR	InterPro: IPR001934; HMA.
DR	InterPro: IPR001454; Hydrolyase.
DR	Pfam: PF004122; EL-E2_ATPase; 1.
DR	Pfam: PF00403; HMA; 2.
DR	Pfam: PF00702; Hydrolyase; 1.
DR	PRINTS, PR00109; CATATPASE.
DR	PROSITE, PS00154; ATPASE_EL_E2; 1.
DR	PROSITE, PS00447; HMA_1; 1.
DR	PROSITE, PS50846; HMA_2; 2.
KW	Hydrolyase; Transmembrane; Phosphorylation; ATP-binding; Copper;
KW	Metal-binding; Repeat; Complete proteome.
FT	TRANSMEM 187 207 POTENTIAL.
FT	TRANSMEM 218 238 POTENTIAL.
FT	TRANSMEM 254 274 POTENTIAL.
FT	TRANSMEM 284 304 POTENTIAL.
FT	TRANSMEM 438 458 POTENTIAL.
FT	TRANSMEM 464 484 POTENTIAL.
FT	TRANSMEM 485 505 POTENTIAL.
FT	TRANSMEM 627 647 POTENTIAL.
FT	TRANSMEM 733 753 POTENTIAL.
FT	TRANSMEM 779 799 POTENTIAL.
FT	TRANSMEM 801 821 POTENTIAL.
FT	DOMAIN 4 65 HMA 1.
FT	DOMAIN 100 163 HMA 2.

```

FT METAL 110 110 COPPER (POTENTIAL).
FT METAL 113 113 COPPER (POTENTIAL).
FT MOD_RES 523 523 PHOSPHORYLATION (PROBABLE).
FT CONFLICT 162 181 FAIDDADKRRERQOETAVAT ->
FT CONFLICT 508 508 KRLKMTLNAAASAKRPSLA (IN REF. 1).
FT CONFLICT 508 508 A -> R (IN REF. 1).
FT CONFLICT 576 576 Q -> R (IN REF. 1).
SQ SEQUENCE 834 AA: 87873 MW: C84A18FE20E866F6 CRC64:

Query Match 54.1%; Score 46; DB 1; Length 834;
Best Local Similarity 66.7%; Pred. No. 9.2;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 GLOVLAITGDIN 16
Db 712 GROVAVMGDGIN 723

RESULT 5
PAT2_CAEEL STANDARD; PRT: 1226 AA.
AC P34446;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Integrin alpha pat-2 precursor.
GN PAT-2 OR F54F2.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodermidae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RC MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Cooper T., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Fanello A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier S., Juler M.,
RA Latreille P., Lingham J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
RA Sims M., Smalton N., Smith A., Smith M., Sothmanmer E., Staden K.,
RA Sulston J., Thierly-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstock L., Wilkinson-Sprat J.,
RA Woldman P.;
RA *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.
RL Nature 368:32-38 (1994).
CC -1- FUNCTION: POSSIBLE ROLE IN CELL-CELL INTERACTIONS (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA PAT-2
CC ASSOCIATES WITH BETA PAT-3.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: BELONGS TO THE INTEGRIN ALPHA CHAIN FAMILY.
CC -1- SIMILARITY: CONTAINS 7 FG-GAP REPEATS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: L23645; AAK26134.1;
CC PIR: S44824;
CC HSSP: P11215; JABX.
CC Wormpep: F54F2.1; CE00194.
CC InterPro: IPR000413; Integrin_alpha.
CC Pfam: PF01839; FG-GAP; 5.
CC Pfam: PF00357; Integrin_A; 1.
CC PRINTS: PR01185; INTEGRIN.

```

```

DR SMART: SM00191; Int.alpha; 5.
DR PROSITE: PS00242; INTEGRIN ALPHA; 1.
KW Integrin, Cell adhesion; Receptor; Glycoprotein; Transmembrane;
KW Signal; Repeat.
FT CHAIN 1 25 POTENTIAL.
FT SIGNAL 26 1226 INTEGRIN ALPHA PAT-2.
FT DOMAIN 26 1154 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1155 1177 POTENTIAL.
FT DOMAIN 1178 1226 CYTOPLASMIC (POTENTIAL).
FT REPEAT 40 103 FG-GAP 1.
FT REPEAT 120 172 FG-GAP 2.
FT REPEAT 189 243 FG-GAP 3.
FT REPEAT 244 297 FG-GAP 4.
FT REPEAT 300 372 FG-GAP 5.
FT REPEAT 373 433 FG-GAP 6.
FT REPEAT 437 485 FG-GAP 7.
FT CARBOHYD 108 108 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 250 250 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 679 679 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 775 775 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 819 819 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1226 AA: 135939 MW: B9169AD75B88901D CRC64:

Query Match 54.1%; Score 46; DB 1; Length 1226;
Best Local Similarity 53.8%; Pred. No. 14;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 GVGKQLAIVGDD 14
Db 359 GVGKQLAIVGDD 371

RESULT 6
YLMD_STAU STANDARD; PRT: 263 AA.
ID YLMD_STAU
AC Q9ZHA4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 30.1 kDa protein in ftsZ 3'region.
GN YLMD.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 14154;
RC MEDLINE=99061199; PubMed=9846742;
RA Massidda O., Anderluzzi D., Friedli L., Feger G.;
RT *Unconventional organization of the division and cell wall gene
RT cluster of streptococcus pneumoniae.
RL Microbiology 144:3069-3078 (1998).
CC -1- SIMILARITY: BELONGS TO THE UPD0124 FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: A068904; AAC95459.1;
CC PIR: S44824;
CC HSSP: P11215; JABX.
CC Wormpep: F54F2.1; CE00194.
CC InterPro: IPR003730; DUF152.
CC Pfam: PF02576; DUF152; 1.
CC Pfam: PF00357; Integrin_A; 1.
CC PRINTS: PR01185; INTEGRIN.
SQ SEQUENCE 263 AA: 30097 MW: 76A0DA0BFC62AD CRC64:

```

Query Match 52.9%; Score 45; DB 1; Length 263;
 Best Local Similarity 75.0%; Pred. No. 4;
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 KQVGRQALATG 12
 DB 250 KQVGRQALATG 261

RESULT 7

END_HELPY STANDARD; PRT: 426 AA.
 ID ENO_HELPY
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase).
 GN ENO OR HP0142.
 OS Helicobacter pylori J99 (Campylobacter pylori J99).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group; Helicobacter.
 OX NCBI_TaxID=85963;
 RN 111
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99120557; PubMed=9933682;
 RA Alm R.A., Ling L.S.L., Molt D.T., King B.L., Brown E.D., Doig P.C., Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C., Gibson R., Werberg D., Mills S.D., Jhing O., Taylor D.E., Vovis G.F., Trust J.J.;
 RA "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori";
 RT Nature 397:176-180(1999).
 RL Nature 397:176-180(1999).
 CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate + H₂O.
 CC -1- COPFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.

 CC this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL: AE001453; AAC03723.1; --
 DR HSP: P00924; ENL.
 DR Interpro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase; 1.
 DR PRINTS: PR00148; ENOLASE; 1.
 DR Prodom: PD000902; ENOLASE; 1.
 DR PROSITE: PS00164; ENOLASE; 1.
 KW Lyase; Glycolysis; Magnesium; Complete proteome.
 FT ACT_SITE 155
 FT METAL 242
 FT METAL 286
 FT METAL 313
 SQ SEQUENCE 426 AA; 46654 MW; EDFA3FEAB8B7BEE CRC64;

Query Match 52.9%; Score 45; DB 1; Length 426;
 Best Local Similarity 46.2%; Pred. No. 6.6;
 Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 3 QVGRQALATGDDT 15
 DB 303 ELGRQALATGDDT 315

RESULT 8

END_HELPY STANDARD; PRT: 426 AA.
 ID ENO_HELPY
 AC P46285;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase).
 GN ENO OR HP0154.
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group; Helicobacter.
 OX NCBI_TaxID=210;
 RN 111
 RP SEQUENCE FROM N.A.
 RX MEDLINE=26695 / ATCC 700392;
 RX MEDLINE=97394467; PubMed=9252185;
 RA Tomb J.-F., White O., Kierlavage A.R., Clayton R.A., Sutton G.G., Fieldman R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A., Fleischmann R.D., Ketchum K.A., Klein H.-P., Gill S., Dougherty B.A., Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S., Loftus B., Richardson J., Dodson R., Khalak H.G., Glodek A., McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickley E.K., Berg D.E., Gocayne J.D., Ulterback T.R., Peterson J.D., Kelley J.M., Cotton M.D., Weidman J.M., Fujii C., Bowman C., Matthey L., Mallin E., Hayes W.S., Borodovsky M., Rapp P.D., Smith H.O., Fraser C.M., Venter J.C.;
 RA The complete genome sequence of the gastric pathogen Helicobacter pylori.
 RT Nature 388:539-547(1997).
 RL Nature 388:539-547(1997).
 CC -1- SEQUENCE OR 1-178 FROM N.A.
 CC STRAIN=ATCC 53726 / 84-183;
 CC MEDLINS=95280623; PubMed=7768597;
 CC Thompson S.A., Blaser M.J.;
 CC "Isolation of the Helicobacter pylori recA gene and involvement of the recA region in resistance to low pH";
 RT Infect. Immun. 63:2185-2193(1995).
 RL Infect. Immun. 63:2185-2193(1995).
 CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate + H₂O.
 CC -1- COPFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.

 CC this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL: AE000536; AAC07219.1; --
 DR EMBL: U13756; AAC43380.1; --
 DR HSP: P00924; ENL.
 DR Interpro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase; 1.
 DR PRINTS: PR00148; ENOLASE; 1.
 DR Prodom: PD000902; ENOLASE; 1.
 DR PROSITE: PS00164; ENOLASE; 1.
 KW Lyase; Glycolysis; Magnesium; Complete proteome.
 FT ACT_SITE 155
 FT METAL 242
 FT METAL 286
 FT METAL 313
 FT METAL 313
 FT CONFLICT 26
 FT CONFLICT 85
 V -> I (IN REF. 2).
 V -> T (IN REF. 2).

SQ SEQUENCE 426 AA; 46534 MW; 787A0B87A5DFB398 CRC64;
 Query Match 52.9%; Score 45; DB 1; Length 426;
 Best Local Similarity 46.2%; Pred. No. 6.6;
 Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
 OY 3 ONGROLATIGDDI 15
 DB 303 ELGROLATVGGDL 315
 RESULT 9
 ATCU_BACSU STANDARD; PRT: 803 AA.
 AC 032220;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 GN Potential copper-transporting ATPase (EC 3.6.3.4).
 DE YVGG.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Stephylococcus group; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RA Kunst F., Ogatawara N., Yoshikawa H., Danchin A.;
 RA Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: INVOLVED IN COPPER TRANSPORT (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + ORTHOPHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
 CC (E1-E2 ATPASES). SUBFAMILY 1B.
 CC -1- SIMILARITY: CONTAINS 2 HMA DOMAINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@lsb-sib.ch).
 CC -----
 CC EMBL: Z99121; CAB15355.1; -.
 DR HSSP: P04129; IAEJ.
 DR SUBLLIST: BG14106; YVGG.
 DR InterPro: IPR001366; Cad_ATPase.
 DR InterPro: IPR000579; Cat_P_ATPaseA.
 DR InterPro: IPR001756; Cu_ATPase.
 DR InterPro: IPR001877; Cu_ATPase_1.
 DR InterPro: IPR001877; E1-E2_ATPase.
 DR InterPro: IPR001802; HG_schavenger.
 DR InterPro: IPR001934; HMA.
 DR InterPro: IPR001454; Hydrolase.
 DR Pfam: PF001422; E1-E2_ATPase; 1.
 DR Pfam: PF00403; HMA; 2.
 DR Pfam: PF00702; Hydrolase; 1.
 DR PRINTS: PRO0940; CATPATPASE.
 DR PRINTS: PRO0941; CDATPASE.
 DR PRINTS: PRO0943; CUATPASE.
 DR PRINTS: PRO0942; CUATPASEI.
 DR PRINTS: PRO0946; HGSCAVENGER.
 DR PROSITE: PS01047; HMA_1; 2.
 DR PROSITE: PS01047; ATPASE_E1_E2; 1.
 DR PROSITE: PS00846; HMA_2; 2.
 DR Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding;
 KM Metal-binding; Copper; Repeat; Complete proteome.
 FT TRANSMEM 167 183 POTENTIAL.
 FT TRANSMEM 197 217 POTENTIAL.
 FT TRANSMEM 229 249 POTENTIAL.

FT TRANSMEM 260 280 POTENTIAL.
 FT TRANSMEM 416 436 POTENTIAL.
 FT TRANSMEM 448 468 POTENTIAL.
 FT TRANSMEM 610 630 POTENTIAL.
 FT TRANSMEM 704 724 POTENTIAL.
 FT TRANSMEM 767 787 POTENTIAL.
 FT DOMAIN 75 73 HMA 1.
 FT METAL 17 17 COPPER (POTENTIAL).
 FT METAL 17 17 COPPER (POTENTIAL).
 FT METAL 20 20 COPPER (POTENTIAL).
 FT METAL 85 85 COPPER (POTENTIAL).
 FT METAL 88 88 COPPER (POTENTIAL).
 FT MOD_RES 500 500 PHOSPHORYLATION (BY SIMILARITY).
 FT METAL 699 699 MAGNESIUM (BY SIMILARITY).
 FT METAL 703 703 MAGNESIUM (BY SIMILARITY).
 SQ SEQUENCE 803 AA; 86024 MW; D9C8DA5D40326C5B CRC64;

Query Match 51.8%; Score 44; DB 1; Length 803;
 Best Local Similarity 66.7%; Pred. No. 18;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 5 GROLATIGDDIN 16
 DB 691 GROLATVGGDGIN 702

RESULT 10
 CRTI_APHSP STANDARD; PRT: 532 AA.
 ID CRTI_APHSP
 AC P21134;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Phytoene dehydrogenase (EC 1.14.99.-) (Phytoene desaturase).
 GN CRTI
 OS Aphanocapsa sp.
 OC Bacteria; Cyanobacteria; Chroococcales; Aphanocapsa.
 OX NCBI_TaxID=1120;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPRAIN-PC 6714;
 RC MEDLINE=9038265; PubMed=2119326;
 RX Schmidt A., Sandmann G.;
 RA Cloning and nucleotide sequence of the crtI gene encoding phytoene
 RT dehydrogenase from the cyanobacterium Aphanocapsa PCC6714.";
 RL gene 9,113-117(1990)
 CC -1- FUNCTION: THIS ENZYME CONVERTS PHYTOENE INTO ZETA-CAROTENE VIA THE
 CC INTERMEDIARY OF PHYTOFLUENE BY THE SYMMETRICAL INTRODUCTION OF TWO
 CC DOUBLE BONDS AT THE C-11 AND C-11' POSITIONS OF PHYTOENE.
 CC -1- CORRECTOR: NADP OR FAD (PROBABLY).
 CC -1- PATHWAY: CAROTENOID BIOSYNTHESIS.
 CC -1- SIMILARITY: BELONGS TO THE PHYTOENE DEHYDROGENASE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@lsb-sib.ch).
 CC -----
 CC EMBL: M55647; AA62573.1; -.
 DR PIR: JN0084; JN0084.
 DR Carotenoid biosynthesis; Oxidoreductase; FAD; Flavoprotein; NAD.
 KW NP_BIND 22 49 FAD (ADP PART) (POTENTIAL).
 FT NP_BIND 532 AA; 56754 MW; 06296C65A914B19F CRC64;

Query Match 51.2%; Score 43.5; DB 1; Length 532;
 Best Local Similarity 47.4%; Pred. No. 14;
 Matches 9; Conservative 5; Mismatches 2; Indels 3; Gaps 1;

OY 2 GONGROLAT---IGSDINR 17
 DB 141 GONGROLATLEIFGEVHR 159

RESULT 11

ENO_LYCSES STANDARD: PRT: 444 AA.
 AC P26300;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase).
 GN PGH1.
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; eusteriids I; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4081;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. SUPERSONIC;
 RX MEDLINE=93044507; PubMed=1841726;
 RA van der Straeten D., Rodrigues-Pousada R.A., Goodman H.M.,
 RA van Montagu M.;
 RL "Plant enolase: gene structure, expression, and evolution."; Plant Cell 3:719-735(1991).
 CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate + H(2O).
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL collaboration CC the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch)
 CC -----
 CC EMBL: X58108; CAA1115.1; -
 CC PIR: J01185; J01185.
 DR HSSP: P56252; 1PDZ.
 DR Mendel: 611; LYCES: Pgh1.2.
 DR Interpro: IPR000941; Enolase.
 DR Pfam: PF00113; Enolase.1.
 DR PRINTS: PR00148; ENOLASE.1.
 DR PRODOM: PD000902; ENOLASE.1.
 DR PROSITE: PS00164; ENOLASE.1.
 KW Lyase; Glycolysis; Magnesium.
 FT ACT SITE 163 163 BY SIMILARITY.
 FT METAL 250 250 MAGNESIUM (BY SIMILARITY).
 FT METAL 300 300 MAGNESIUM (BY SIMILARITY).
 FT METAL 327 327 MAGNESIUM (BY SIMILARITY).
 SO SEQUENCE 444 AA; 47798 MW; 73C384181BD620D CRC64;

Query Match 50.6%; Score 43; DB 1; Length 444;
 Best Local Similarity 46.2%; Pred. No. 14;
 Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 3 GONGROLATIGDDI 15
 DB 317 EIGEOVOIVGDDL 329

RESULT 12
 ENO2_MAIZE

ID ENO2_MAIZE STANDARD: PRT: 446 AA.
 AC P42855;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2).
 GN ENO2.
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACO clade;
 OC Panicoidae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. B73; TISSUP=Root;
 RX MEDLINE=99063764; PubMed=9847102;
 RA Lai S.K., Lee C., Sachs M.M.;
 RL "Differential regulation of enolase during anaerobiosis in maize."; Plant Physiol. 118:1285-1293(1998).
 CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate + H(2O).
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL collaboration CC the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch)
 CC -----
 CC EMBL: U17973; A004187.1; -
 CC HSSP: P56320; 1PDZ.
 DR MEDLINE: 16623; Zea: Pgh1:16623.
 DR Interpro: IPR000941; Enolase.
 DR Pfam: PF00113; Enolase.1.
 DR PRINTS: PR00148; ENOLASE.1.
 DR PRODOM: PD000902; ENOLASE.1.
 DR PROSITE: PS00164; ENOLASE.1.
 KW Lyase; Glycolysis; Magnesium.
 FT ACT SITE 164 164 MULTIGENE FAMILY.
 FT METAL 251 251 MAGNESIUM (BY SIMILARITY).
 FT METAL 302 302 MAGNESIUM (BY SIMILARITY).
 FT METAL 329 329 MAGNESIUM (BY SIMILARITY).
 SO SEQUENCE 446 AA; 48162 MW; DC27708CF926B80D CRC64;

Query Match 50.6%; Score 43; DB 1; Length 446;
 Best Local Similarity 46.2%; Pred. No. 14;
 Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 3 GONGROLATIGDDI 15
 DB 319 EIGEOVOIVGDDV 331

RESULT 13
 ENO_ORYZA STANDARD: PRT: 446 AA.
 AC Q42971;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (OSEI).
 OS Oryza sativa (Rice).

FT	TRANSMEM	771	793	POTENTIAL.
FT	TRANSMEM	797	819	POTENTIAL.
FT	DOMAIN	16	81	HMA 1.
FT	DOMAIN	83	149	HMA 2.
FT	METAL	26	26	COPPER (POTENTIAL).
FT	METAL	29	29	COPPER (POTENTIAL).
FT	METAL	93	93	COPPER (POTENTIAL).
FT	METAL	96	96	COPPER (POTENTIAL).
FT	MOD.RES	515	515	PHOSPHORYLATION (BY SIMILARITY).
FT	METAL	714	714	MAGNESIUM (BY SIMILARITY).
FT	METAL	718	718	MAGNESIUM (BY SIMILARITY).
SO	SEQUENCE	827 AA:	85861 MW:	A3DBDFDD1315FCB CRC64;

Query Match 50.6%; Score 43; DA 1; Length 827;
 Best Local Similarity 64.3%; Pred. No. 28;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Caps 0;

OY 3 OVGROLAIGDDIN 16
 | | | | | | | | | |
 Db 704 OGRSVAFIGDGIN 717

Search completed: September 20, 2002, 11:04:35
 Job time: 1632 sec


```

RESULT 2
09MZS6 PRELIMINARY: PRT: 163 AA.
AC 09MZS6
DC 01-OCT-2000 (TEMBUREL 15, Created)
DT 01-OCT-2000 (TEMBUREL 15, Last sequence update)
DE 01-DEC-2001 (TEMBUREL 19, Last annotation update)
DE BAK PROTEIN (FRAGMENT).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Ruminantia; Bovidae; Ovis.
OX NCBI_TaxID=9940;
RN 11
RP SEQUENCE FROM N.A.
PC TISSUE=OVARY.
RA Miray J.F., Dong Y.B., Leigh A.J., Scaramuzzi R.J., Carter N.D.;
RA Submitted (Jul-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF64116; MAF9533.1; -.
DR HSP; Q16611; BAK; BCL2_family.
DR InterPro: IPRO02175; BCL2_family.
DR InterPro: IPRO0712; BCL2.
DR Pfam: PF00452; BCL2; 1.
DR SMART; SM00337; BCL2; 1.
DR PROSITE; PS01082; BCL2_FAMILY; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
FM NON_TER
SQ SEQUENCE 163 AA: 18039 MW: 18358A8ACG3AD5B CRC64:

Query Match 92.98; Score 79; DB 6; Length 163;
Best Local Similarity 93.88; Pred. No. 2,6e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGVQLATIGDDINR 17
DB 31 GCGVQLATIGDDINR 46

RESULT 3
09LWX5 PRELIMINARY: PRT: 151 AA.
AC 09LWX5
DC 01-DEC-2001 (TEMBUREL 19, Created)
DT 01-DEC-2001 (TEMBUREL 19, Last sequence update)
DE 01-DEC-2001 (TEMBUREL 19, Last annotation update)
DE N9AK1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 11
RP SEQUENCE FROM N.A.
PC STRAIN=NMRI; TISSUE=NEURONAL;
RA MEDLINE=2128300; PubMed=11278671;
RA Sun Y.F., Yu L.Y., Saarna W., Timusk T., Arumae U.;
RA Neuron-specific Bcl-2 homolog 3 domain-only splice variant of Bak is
RA anti-apoptotic in neurons, but pro-apoptotic in non-neuronal cells.;
RL J. Biol. Chem. 276:16240-16247(2001).
FM EMBL: AF402617; AL01876.1; -.
SQ SEQUENCE 151 AA: 16402 MW: 18C13BFF86E4F33B CRC64:

Query Match 91.88; Score 78; DB 11; Length 151;
Best Local Similarity 93.88; Pred. No. 3,6e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 GCGVQLATIGDDINR 17
DB 70 GCGVQLATIGDDINR 85

RESULT 4
09UKS9 PRELIMINARY: PRT: 209 AA.
AC 09UKS9
DC 01-OCT-2000 (TEMBUREL 15, Created)
DT 01-OCT-2000 (TEMBUREL 15, Last sequence update)
DE 01-DEC-2001 (TEMBUREL 19, Last annotation update)
DE BAK PROTEIN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN 11
RP SEQUENCE FROM N.A.
PC STRAIN=SPRACUE-DAMLEY;
RA Lion T., Lyon A., Measures D.;
RA Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF26104; MAF71760.1; -.
DR HSP; Q16611; BAK; BCL2_family.
DR InterPro: IPRO0712; BCL2.
DR Pfam: PF00452; BCL2; 1.
DR SMART; SM00337; BCL2; 1.
DR PROSITE; PS01082; BCL2_FAMILY; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
SQ SEQUENCE 209 AA: 23153 MW: 2493B814B1972421 CRC64:

Query Match 91.88; Score 78; DB 11; Length 209;
Best Local Similarity 93.88; Pred. No. 5,1e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGVQLATIGDDINR 17
DB 70 GCGVQLATIGDDINR 85

RESULT 5
09SZS3 PRELIMINARY: PRT: 357 AA.
AC 09SZS3
DC 01-MAY-2000 (TEMBUREL 13, Created)
DT 01-MAY-2000 (TEMBUREL 13, Last sequence update)
DE 01-DEC-2001 (TEMBUREL 19, Last annotation update)
DE PROTEIN PHOSPHATASE 2C-LIKE PROTEIN (AT4G31860/P11C18.60).
DE P11C18.60 OR AT4G31860.
OS Arabidopsis thaliana (House-ear creas).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Eudicotyledons; Core eudicotyledons; Rosidae;
OC Eudicotyledons; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN 11
RP SEQUENCE FROM N.A.
RA Bevan M., Terry N., Ardiles W., Blyssshert C., Dasseyville R.,
RA De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,
RA Villalier R., Glehen J., Van Montagu M., Hohnel J., Mewes H.W.,
RA Mayer K.F.X., Schaefer C.;
RA Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF019999.
FM EMBL: AF019999.
SQ SEQUENCE FROM N.A.
PC Arabidopsis sequencing project;
RA Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
RL 13
RN 13
RP SEQUENCE FROM N.A.

```

```
RA Terry P., Avdiels W., Buysshaert C., Dasseville R., De Clerck R.,  
RBA De Keyser A., Neyt P., Rouze P., Van Den Daele H., Villarroel X.,  
RA Gietlen J., Van Montagu M., Mwewa H.W., Lemcke K., Mayer K.F.X.,  
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.  
RP  
RN [4]  
RS SEQUENCE FROM N.A.  
RT EU Arabidopsis sequencing project;  
RU Submitted (MAR-2000) to the EMBL/Genbank/DBAJ databases.  
RV [5]  
RW SEQUENCE FROM N.A.  
RX Chenuk R., Chen H., Kim C.J., Koeseema E., Meyers M.C., Banji J.,  
RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,  
RA Ishida J., Jiang P.-X., Jones T., Kamlay A., Karlin-Newman G.,  
RA Kanai I., Lam B., Lee J.-M., Lin J., Liu S-X., Miranda M., Narusaka M.,  
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Sakurai T., Sakurai T.,  
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,  
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,  
Ecker J.R.;  
RV "Arabidopsis cDNA clones." ;  
WT Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.  
XL EMBL; AL069670; CAB40756.1; -  
DR EMBL; AL161579; CAB79904.1; -  
DR EMBL; AY057611; AA144A06.1; -  
DS HSSP; P35813; IA60.  
DR InterPro: IPRO00222; Pf2C.  
DR InterPro: IPRO01933; PF2C-domain.  
DR Pfam; PF00481; PP2C_2.  
DR SMART; SM00333; PP2CC_1.  
DR SMART; SM00331; PP2CS_Sic_1.  
DR PROSITE; PS01033; PP2C_1.  
SQ SEQUENCE 357 AA; 39203 MW; 9BEETIA09818CA0D3 CRC64;
```

Query Match 55.9%; Score 47.5; DB 10; Length 357;
Best Local Similarity 55.6% Pred. No. 10;
Matches 10; Conservative 5; Mismatches 2; Indels 1; Gaps

Ox 1 KGQVG-RQLATIGDDINR 17
Db 103 QGQRNRELAVALGRKIM 120

ID O9KRZ7 PRELIMINARY: PRT; 915 AA.

DIC O9KRZ7
DI 01-OCT-2000 (YrEmBrel). 15. Created)
DT 01-OCT-2000 (YrEmBrel). 15. Last sequence update)
DT 01-DEC-2001 (YrEmBrel). 19. Last annotation update)
DN CATION TRANSPORT ATPASE, EL-E2 FAMILY.
GN VC2215.
OS Vibrio cholerae.
OC Bacteria; Proteobacteriae; gamma subdivision; Vibrionaceae; Vibriolo.
NCBI_TaxId=666;
OX [1]

RH STRAIN=EL TOR N16961 / SEROTYPE O1;
RC MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.Y., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.U., Haft D.H., Hickley E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Telllellin H., Richardson D.,
RA Ermolenko M.P., Vamathevan J., Bass S., Qin H., Dasgiri I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Newman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.T., Venter J.C.,
Fraser C.M.;
RV "DNA sequence of both chromosomes of the cholera pathogen vibrio
cholerae."
WL Mature 406:477-483(2000).
DL EMBL; AE004429; AACF95359.1; -.
HS SP; POA129; IABT.
TI GR; VC2215; .
InterPro: IPRO00579; Cat_P_ATPase.
InterPro: IPRO01757; El-E2_ATPase.

	DR	InterPro:	IPR001802; HG_scarenger.
	DR	InterPro:	IPR001934; HMA
	DR	InterPro:	IPR001454; Hydrolase
	DR	InterPro:	IPR000150; Hypothet.cof.
	DR	Pfam:	PF00122; E1-E2_ATPase_1.
	DR	Pfam:	PF06403; HMA_3.
	DR	Pfam:	PF07022; Hydrolase_1.
	DR	PRINTS:	PR00119; CATAPPAE.
	DR	PRINTS:	PR00940; CATAPPAE.
	DR	PRINTS:	PR00946; HGSCAVENER.
	DR	PROSITE:	PS00154; ATPASE_E1_E2_UNKNOWN_1.
	DR	PROSITE:	PS01229; COF_2_UNKNOWN_1.
	DR	PROSITE:	PS01047; HMA_1.
	DR	Complete	proteome.
SQ	SEQUENCE	915 AA;	97311 MW; 2F3FE264DAD0D20 CRC64;
OY		3 QVGRQLAITGDDIN 16	
		I I I I I I I I I I	
Db		786 QQGKRYAMIGGIN 799	
RESULT	7		
ID	Q99US8	PRELIMINARY:	PRT; 263 AA.
DC	Q99US8		
DT	01-JUN-2001	(TREMBLrel. 17, Created)	
DT	01-JUN-2001	(TREMBLrel. 17, Last sequence update)	
DE	01-DEC-2001	(TREMBLrel. 19, Last annotation update)	
DE	HYPOTHETICAL PROTEIN SA1030 [HYPOTHETICAL PROTEIN SAV187].		
GN	SA1030 OR SAV187.		
OS	Staphylococcus aureus (strain N315), and		
OC	Staphylococcus aureus (strains M505)		
OC	Bacteria; Firmicutes; Bacillus/Clostridium group;		
CC	Bacillus/Staphylococcus group; Staphylococcus.		
NCBI_TaxID=158879, 158878;			
OX	11		
RE	SEQUENCE FROM N.A.		
RF	SPRIS-S;aureus (strain N315) and S.aureus (strain M505);		
RX	MEDLINE=2111952, PubMed=11418145		
RX	Cutroba H., Ohta T., Uchiyama T., Baba T., Yuzawa H., Kobayashi I.,		
RX	Kel L., Oguchi A., Aoki K.-I., Nagai Y., Liou J.-C., Hori T.,		
RX	Mizumizu T.Y., Takahashi N.K., Miyazaki S., Tanaka Goto S., Inoue R.I., Katano C.,		
RX	Sekimizu K., Hikakawa H., Kohbara S., Putura K., Yoshino C., Shiba T.,		
RX	Rattoli M., Ogasawara N., Hayashi N., Hiramatsu K.;		
RT	*Whole genome sequencing of methicillin-resistant Staphylococcus		
RT	aureus.		
RL	Lancet 357:1225-1240(2001).		
EMBL:	AF003132; BAB52282.1;		
EMBL:	AF003361; BAB57349.1;		
InterPro:	IPR003730; DUF152.		
Pfam:	PF02578; DUF152_1.		
DR	Hypothetical protein: Complete proteome.		
SQ	SEQUENCE 263 AA; 30257 MW; 7AD013BD94EB0759 CRC64;		
Query Match		52.9%; Score 45; DB 16; Length 263;	
Best Local Similarity		75.0%; Pred. No. 19;	
Matches	9; Conservative	0; Mismatches	3; Indels
			0; Gaps
OY	1 QVGRQLAITG 12		
	I I I I I I I I I I		
Db	250 KGQGRMLAFIP 261		
RESULT	8		
			081716

```

ID 081716 PRELIMINARY: PRT: 355 AA.
AC 081716:
DT 01-NOV-1998 (TREMBLERel. 08, Created)
DT 01-NOV-1998 (TREMBLERel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBLERel. 19, Last annotation update)
DE HYPOTHEtical 39.4 KDA PROTEIN.
GN AT2G25070.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae;
OC eurosids II: Brassicales: Brassicaceae: Arabidopsids.
NCBI_TaxID=7702;
RX MEDLINE=20083487; PubMed=10617197;
RC STRAIN=CV. COLUMBIA.
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Honing C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., Vanden S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Cressy T.H., Goodman H.M., Somerville C.R.,
RA Copenhagen G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana."
RL Nature 402:761-768(1999).
RN 12
RS SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA.
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN 13
RS SEQUENCE FROM N.A.
RA Tamada K., Liu S.X., Pham P.K., Banh J., Dale J.M., Goldsmith A.D.,
RA Jiang P.X., Lee J.M., Onodera G.S., Quach H.U., Tang C., Tortum M.,
RA Hatanaka Y., Ye G., Ye S., Bowser T., Carlsbeck P., Chen H., Cheuk R.,
RA Hoshizaki K., Ishida J., Jones T., Kanlaya N., Katlin Neumann G.,
RA Kishimoto K., Kocenas E., Lam B., Lin J., Linn S., Maki M., Kikuchi M.,
RA Matsuda M., Nguyen K., Pal C.M., Saito T., Sakai M., Seki M.,
RA Shinn P., Southeick A., Tracy S.E., Shimozaki K., Davis R.W.,
RA Ecker J.R.
RT "Full length cDNA of gene F27G12.1/AT2G25070 (GI:4559345)."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN 14
RS EMBL: AC006585; AAC23006.1;
DR HSSP: P35813; 1A60
DR InterPro: IPR001922; PP2C
DR InterPro: IPR001932; PP2C_domln.
DR Pfam: PF00481; PP2C_2.
DR SMART: SM00332; PP2C_1.
DR SMART: SM00331; PP2C_Sig_1.
DR PROSITE: PS01032; PP2C_1.
KW Hypothetical protein.
SQ
SEQUENCE 355 AA: 39354 MW; CAGD38796203C746 CRC64;

```

```

GN PA8189.
OS Pyrococcus abyssi.
OC Archaea: Euryarchaeota: Thermococcales: Thermococcaceae: Pyrococcus.
NCBI_TaxID=29292;
RN 11
RS SEQUENCE FROM N.A.
RC STRAIN=ORSAY;
RA Hellis R.;
RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
RT structure and evolution."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ248288; CAB50662.1;
DR InterPro: IPR004089; Chemotaxis-transducer.
DR InterPro: IPR004090; Me-chemotaxis.
DR Pfam: PF00015; MCPsignal; 1.
DR PRINTS: PRO0260; CHEMTRNSDCR.
DR SMART: SM00283; MA; 1.
KW Complete proteome.
SQ
SEQUENCE 258 AA: 29033 MW; EDEB44ACAB515112 CRC64;

Query Match 51.8%; Score 44; DB 17; Length 258;
Best Local Similarity 43.8%; Pred. No. 27;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 1 2 GQVGRQALIGDDINR 17
DB 122 GEGRGFAVADETR 137

RESULT 10
O57733 PRELIMINARY: PRT: 261 AA.
AC O57733:
DT 01-AUG-1998 (TREMBLERel. 07, Created)
DT 01-AUG-1998 (TREMBLERel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBLERel. 19, Last annotation update)
DE 261 AA LONG HYPOTHEtical CHEMOKRECEPTOR PROTEIN.
GN PH1970
OS Pyrococcus horikoshii.
OC Archaea: Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
NCBI_TaxID=53953;
RN 11
RS SEQUENCE FROM N.A.
RC STRAIN=ORS3.
RA MEDLINE=98344137; PubMed=9679194;
RX Kawarabayashi Y., Sawada M., Horikawa H., Halkawa Y., Hino Y.,
RA Yamamoto S., Sotoku M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takemura M., Ohtsuka Y.,
RA Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Kushiida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OR3."
RL DNA Res. 5:55-76(1998).
RN 12
RS EMBL: AF000007; BAA31097.1;
DR InterPro: IPR004089; Chemotaxis_transducer.
DR Pfam: PF00015; MCPsignal; 1.
DR SMART: SM00283; MA; 1.
KW Complete proteome.
SQ
SEQUENCE 261 AA: 29234 MW; 2FDDCTCC0823D46 CRC64;

Query Match 51.8%; Score 44; DB 17; Length 261;
Best Local Similarity 43.8%; Pred. No. 27;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

OY 1 2 GQVGRQALIGDDINR 17
DB 125 GEGRGFAVADETR 140

RESULT 11

```

Q9LHL6
ID Q9LHL6 PRELIMINARY; PRT; 556 AA.
AC Q9LHL6;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE G8IAAF30301.1 (HYPOTHETICAL 63.0 KDA PROTEIN).
GN T2B14.12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RU Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA PubMed:10907853;
RA Nakamura Y.;
RA PubMed:10907853;
RT Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety pl.
RT TAC and BAC clones.
RL DNA Res. 7:217-221(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RC MEDLINE=21016720; PubMed=11130713;
RA Salanoubat B., Valle G., Bloeker H., Perez-Alonso M., Odehman B.,
RA Fattman B., Velle G., Bloeker H., Grivell L.A., Meche R., Fugmann P.,
RA Delesny M., Boutry M., Artiguenave F., Robert G., Brothier P.,
RA de Simone V., Choise N., Artiguenave F., Robert G., Brothier P.,
RA Wincker P., Catolico L., Weissenbach J., Saurin W., Queller F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wilmshaus E., Dronem R., Kranz H., Erdle H., Jordan N., Bangert S.,
RA Wiedemann R., Kranz H., Voss H., Holland N., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppi S., Simionati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nostel K.,
RA Reichelt J., Scharte M., Schoen O., Bauges M., Terol J., Clement J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwelder B., Duchemin D.,
RA Cooke R., Landie M., Berger-Llauro C., Purnelle B., Masuy D.,
RA de Haan M., Maarse A.C., Alcaraz J.-P., Collet A., Casacuberta E.,
RA Monfort A., Argillon A., Flores M., Liguori R., Vitale D.,
RA Manhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Ullrich T., Fujii C.Y., Shea T.P.,
RA Creasy T.H., Haas B., Malt R., Wu D., Peterson J., Van Aken S.,
RA Pal G., Miltcher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Press D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA Frazer C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara T., Matsuno M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shimp S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT *Sequence and analysis of chromosome 3 of the plant Arabidopsis
thaliana.*
RL Nature 408:820-822(2000).
RL EMBL: AP002040; BAB03116.1;
RL EMBL: AC069473; AAG51057.1;
RW Hypothetical protein.
SQ SEQUENCE 556 AA; 63004 MW; F697359AABB7213F CRC64;

RESULT 12
ID P73239 PRELIMINARY; PRT; 593 AA.
AC P73239;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ABC TRANSPORTER.
GN SLR2019.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugita M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Nairu K., Okumura S.,
RA Shimp S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT *Sequence analysis of the genome of the unicellular cyanobacterium
Synechocystis sp. strain PCC6803. II. Sequence determination of the
entire genome and assignment of potential protein-coding regions.*
RT DNA Res. 3:109-136(1996).
CC -1 SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
(ABC TRANSPORTERS).
CC EMBL: D90904; BAA17266.1;
DR InterPro: IPR003593; AAA.
DR InterPro: IPR001140; ABC transporter lmem.
DR InterPro: IPR003439; ABC transporter.
DR InterPro: IPR001687; ATP GTP A.
DR Pfam: PF00664; ABC membrane. 1.
DR Pfam: PF00005; ABC tran. 1.
DR SMART: SM00382; AAA; 1.
DR PROSITE: PS00211; ABC TRANSPORTER; 1.
DR PROSITE: PS00430; TONB_DEPENDENT_RPC_1; UNKNOWN_1.
KW SEQUENCE 593 AA; 65761 MW; DA8CE3D0EDAC69 CRC64;

Query Match 51.8%; Score 44; DB 16; Length 593;
Best Local Similarity 61.5%; Pred. No. 69;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 GROLATIGDDINR 17
DB 128 GRMLATLNDNDIQ 140

RESULT 13
ID Q9FG35 PRELIMINARY; PRT; 608 AA.
AC Q9FG35;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE FMBICAB82953.1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Kato T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
RA Tabata S.;
RT Structural analysis of Arabidopsis thaliana chromosome 5. XI.*
RT Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL: AP002032; BAB09804.1;
DR InterPro: IPR000531; TonB_box.
DR PROSITE: PS00430; TONB_DEPENDENT_RPC_1; UNKNOWN_1.

SC SEQUENCE 608 AA; 67925 MW; 75B5DF426597586C CRC64;

Query Match 51.8%; Score 44; DB 10; Length 608;

Best Local Similarity 53.8%; Pred. No. 70;

Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 5 GQVGLAIIGDINR 17

DB 321 GRRILVFGDSLNR 333

RESULT 14
O9PK32 PRELIMINARY; PRT; 693 AA.
AC O9PK32;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, last sequence update)
DE PLUS BIOGENESIS PROTEIN.
GN XFL1953.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OX Xylella.
NCBI_TaxID=2371;
[1]
SEQUENCE FROM N.A.
RP STRAIN=9ASC;
RC MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Melnick F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvares A.J.G., Alves L.M.C., Araya J.E., Bala G.S., Baptista C.S.,
RA Barros M.P., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carter H.,
RA Colajuno N.B., Colombo C., Costa F.F., Costa M.C., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Facincini A.P., Ferreira A.J.S., Franco M.C., Frohme M., Furian L.R.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furian L.R.,
RA Garner R., Goldman G.H., Goldman M.H., Gomes S.L., Gruber A.,
RA Ho P.L., Hohnel J.D., Junqueira M.L., Kemper E.L., Kikajima J.P.,
RA Kliegel J.E., Kurama E.E., Laliget F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.V., Madalena A.M.B.N., Madalena H.M.F., Matsukuma A.Y.,
RA Marques C.F.M., Miranda E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miraca E.C., Miyaki C.Y., Montello-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nanni A.J.R., Nobrega F.G., Nunes L.R., Oliveira M.A., Paris A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A., Jr., Resqueto J.B.,
RA Peggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E., Jr., de Sa R.G., Santelli R.V., Sawaaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A., Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira M.U., de Souza M.H.,
RA Valada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Zeldanis J., Zetahal J.C.,
RT "The genome sequence of the plant pathogen Xylella fastidiosa".
RL Nature 406:151-159(2000).
DR EMBL: AE004014; AAF84755.1; -;
DR HSSP: P02942; I007.
DR InterPro: IPR004089; Chemotaxis_transducer.
DR InterPro: IPR004090; Me_Chemotaxis.
DR Pfam: PF00015; MCPsignal; 1.
DR PRINTS: PR00260; CHEMTRNSDUCR.
DR SMART: SM00283; MA; 1.
KW Complete proteome.
SQ SEQUENCE 693 AA; 74235 MW; EAD48C73AF573DB0 CRC64;

DB 550 GENGRAIIVAEVOR 565

RESULT 15

O9BK2 PRELIMINARY; PRT; 421 AA.

AC O9BK2;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, last sequence update)
DE PROBABLE FAD-DEPENDENT MONOOXYGENASE.
GN MLL1411.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RA Kaneke T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idessawa K., Ishikawa K., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.,
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
Mesorhizobium loti".
RL DNA Res. 7:331-338(2000).
DR EMBL: AB002997; BAB46792.1; -;
DR InterPro: IPR000759; Adnux_reductase.
DR InterPro: IPR001327; FAD_ox-reductase.
DR InterPro: IPR000733; Flav_monooxygenase.
DR InterPro: IPR002528; Moxy_FAD-binding.
DR InterPro: IPR001003; Fytidine_redux_2.
DR InterPro: IPR001100; Fyt_redux.
DR InterPro: IPR003042; Rng_monooxygenase.
DR Pfam: PF01494; FAD-binding_3; 1.
DR Pfam: PF01494; FAD-binding_3; 1.
DR PRINTS: PR00169; ADXPHASE.
DR PRINTS: PR00168; FADPHR.
DR PRINTS: PR00111; PRODRASE1.
DR PRINTS: PR00469; PRODRASE1.
DR PRINTS: PR00420; RKGNOXGNASE.
KW Monooxygenase; Complete proteome.
SQ SEQUENCE 421 AA; 45340 MW; ZBFLIC87476F1E CRC64;

Query Match 50.6%; Score 43; DB 16; Length 421;

Best Local Similarity 80.0%; Pred. No. 66;

Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 VGRGLAIIGD 13

DB 294 VGRRLVAVIGD 303

Search completed: September 20, 2002, 11:03:48
Job time: 1665 sec

Query Match 51.8%; Score 44; DB 16; Length 693;
Best Local Similarity 43.8%; Pred. No. 82;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
OY 2 GQVGLAIIGDINR 17

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2002, 10:35:56 ; Search time 228.86 Seconds
(without alignments)
13.104 Million cell updates/sec

Title: US-09-544-664-6
Perfect score: 135
Sequence: 1 DPASTKTKSECLKRISDELDSNMELQIR 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A.Genesec.032802.*
1: /SIDSL/gcgdata/hold-genesec/genesecp-emb1/AA1980.DAT.*
2: /SIDSL/gcgdata/hold-genesec/genesecp-emb1/AA1981.DAT.*
3: /SIDSL/gcgdata/hold-genesec/genesecp-emb1/AA1982.DAT.*
4: /SIDSL/gcgdata/hold-genesec/genesecp-emb1/AA1983.DAT.*
5: /SIDSL/gcgdata/hold-genesec/genesecp-emb1/AA1984.DAT.*
6: /SIDSL/gcgdata/hold-genesec/genesecp-emb1/AA1985.DAT.*
7: /SIDSL/gcgdata/hold-genesec/genesecp-emb1/AA1986.DAT.*
8: /SIDSL/gcgdata/hold-genesec/genesecp-emb1/AA1987.DAT.*
9: /SIDSL/gcgdata/hold-genesec/genesecp-emb1/AA1988.DAT.*
10: /SIDSL/gcgdata/hold-genesec/genesecp-emb1/AA1989.DAT.*
11: /SIDSL/gcgdata/hold-genesec/genesecp-emb1/AA1990.DAT.*
12: /SIDSL/gcgdata/hold-genesec/genesecp-emb1/AA1991.DAT.*
13: /SIDSL/gcgdata/hold-genesec/genesecp-emb1/AA1992.DAT.*
14: /SIDSL/gcgdata/hold-genesec/genesecp-emb1/AA1993.DAT.*
15: /SIDSL/gcgdata/hold-genesec/genesecp-emb1/AA1994.DAT.*
16: /SIDSL/gcgdata/hold-genesec/genesecp-emb1/AA1995.DAT.*
17: /SIDSL/gcgdata/hold-genesec/genesecp-emb1/AA1996.DAT.*
18: /SIDSL/gcgdata/hold-genesec/genesecp-emb1/AA1997.DAT.*
19: /SIDSL/gcgdata/hold-genesec/genesecp-emb1/AA1998.DAT.*
20: /SIDSL/gcgdata/hold-genesec/genesecp-emb1/AA1999.DAT.*
21: /SIDSL/gcgdata/hold-genesec/genesecp-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/hold-genesec/genesecp-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	135	100.0	27	21	AA197006 Bcl2 polyprotein B
2	135	100.0	78	21	AA197018 Human neuroprotect
3	135	100.0	131	20	AA197419 Human truncated Ba
4	135	100.0	192	16	AA197406 Human Bax protein
5	135	100.0	192	20	AA197415 Human wild-type Ba
6	135	100.0	192	20	AA197435 Human Bax protein
7	135	100.0	192	20	AA197804 Human Bcl-2 asso
8	135	100.0	192	20	AA197807 Human Bcl-2 asso
9	135	100.0	192	21	AA197827 Human Bax alpha pr
10	135	100.0	192	21	AA197827 Human Bax alpha pr
11	135	100.0	192	22	AA1974121 Human bcl-2 associ

12	135	100.0	192	22	AA1974126 Human bcl-2 associ
13	135	100.0	192	22	AA1974126 Human Bax protein
14	135	100.0	192	22	AA1974126 Human Bax protein
15	135	100.0	192	22	AA1974126 Human Bax protein
16	135	100.0	192	22	AA1974126 Human Bax protein
17	135	100.0	192	21	AA1978512 Human Bax protein
18	135	100.0	221	18	AA1978512 Human Bax protein
19	135	100.0	331	20	AA1978512 Human Bax protein
20	135	97.8	78	21	AA1978512 Human Bax protein
21	132	97.8	78	21	AA1978512 Human Bax protein
22	132	97.8	192	16	AA1974126 Human Bcl-2 asso
23	132	97.8	192	20	AA1974126 Human Bcl-2 asso
24	132	97.8	192	20	AA197805 Human Bcl-2 asso
25	132	97.8	192	21	AA197808 Human Bcl-2 asso
26	132	97.8	192	22	AA1974126 Human Bcl-2 asso
27	132	97.8	192	22	AA1974126 Human Bcl-2 asso
28	132	97.8	192	22	AA1974126 Human Bcl-2 asso
29	130	96.3	26	17	AA1974126 Human Bcl-2 asso
30	130	96.3	26	17	AA1974126 Human Bcl-2 asso
31	120	88.9	24	20	AA1974126 Human Bcl-2 asso
32	120	88.9	24	21	AA1974126 Human Bcl-2 asso
33	120	88.9	24	21	AA1974126 Human Bcl-2 asso
34	117	86.7	24	21	AA1974126 Human Bcl-2 asso
35	95	70.4	70	21	AA197816 Human Bcl-2 asso
36	92	68.1	70	21	AA197816 Human Bcl-2 asso
37	89	65.9	70	21	AA197816 Human Bcl-2 asso
38	89	65.9	70	21	AA197816 Human Bcl-2 asso
39	86	63.7	70	21	AA197816 Human Bcl-2 asso
40	86	63.7	70	21	AA197816 Human Bcl-2 asso
41	82	60.7	78	21	AA197816 Human Bcl-2 asso
42	81	60.0	16	21	AA197816 Human Bcl-2 asso
43	78	57.8	16	20	AA197816 Human Bcl-2 asso
44	78	57.8	16	21	AA197816 Human Bcl-2 asso
45	77	57.0	15	17	AA197816 Human Bcl-2 asso

ALIGNMENTS

RESULT 1

AA197006 standard: peptide: 27 AA.

AA197006:

28-FEB-2001 (first entry)

Bcl2 polyprotein BH3 domain peptide #6.

Cytostatic; neuroprotective; anti-ILV; virucide; cerebroprotective;
cardiac; Bcl-2 superfamily; BH3 domain; cell death agonist; Bcl-2
apoptosis modulation; B cell lymphoma/leukemia 2; cancer; prostate;
colorectal; gastric; non-small lung; renal; thyroid; neuroblastoma;
melanoma; lymphocytic leukemia; neurodegenerative disorder; AIDS;
stroke; myocardial infarction.

Homo sapiens.

WO200059526-A1.

12-OCT-2000.

06-APR-2000, 2000WO-US093152.

07-APR-1999, 99US-0128202.

(UNIV) UNIV JEFFERSON THOMAS.

Huang Z, Wang J, Zhang Z, Shan S, Lu Z,

WPI, 2000-679325/66.

New peptide conjugates for modulating apoptosis or for inhibiting B

cell lymphoma/leukemia 2 (Bcl-2) function, especially useful for treating neurodegenerative disorders, stroke, or cancer -

Claim 18: Page 17: 74pp: English.

The invention relates to a peptide conjugate having the formula: (R-X)n-peptide where n = 1-10; X = C=O, when the R-X group is attached to the N-terminus of the peptide, or a side chain of the peptide where the functional group of the side chain is NH₂ or OH; or X = O or NH, when the R-X group is attached to the C-terminus of the peptide, or a side chain of the peptide, where the side chain functional group is COOH or CONH₂; and R = 2-18C alkyl or alkoxy, 2-14C alkenyl optionally containing one or two double bonds, cyclobutyl, cyclopentyl, cyclohexyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, phenyl optionally monosubstituted with a 1-5C straight or branched chain alkyl group, or benzyl. The peptides AAB37001-837058 represent analogues of the peptide portion of the conjugate. The peptides represent analogues of a Bcl-2 superfamily polypeptide corresponding to amino acids 72-97 of the Bcl-2 domain of the cell death agonist Bcl. The peptide conjugate is useful for modulating apoptosis in the cells of a subject, or for reversing a cell lymphoma/leukemia 2 (Bcl-2)-mediated blockage of apoptosis in cancer cells; it is also useful for inhibiting Bcl-2 function. In particular, the peptide conjugate is useful for treating a subject afflicted with a cancer characterized by cancer cells that express Bcl-2. The cancer includes prostate, colorectal, gastric, CC non-small lung, renal or thyroid cancers, neuroblastoma, melanoma, or CC acute or chronic lymphocytic and non-lymphocytic leukemia. The peptide conjugate is also useful for treating disorders characterized by increased apoptosis, e.g. neurodegenerative disorders, acquired immunodeficiency syndrome (AIDS), stroke or myocardial infarction.

Sequence 27 AA:

Query Match 100.0%; Score 135; DB 21; Length 27;
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 OPASTKKISCELRIGDELDSNMEIQR 27
DB 1 qdasckkiscckrlrigdelidsnmeiqr 27

RESULT 2
AAV70818 standard: Protein: 78 AA.

AC AAV70818:

DT 31-JUL-2000 (first entry)

XX Human neuroprotective truncated BAX protein, tBAX78.

XX Human: truncated BAX protein; tBAX78; BAX alpha; Bcl-2 family;
KW neuron; anti-apoptotic; cerebroprotective; neuroprotective;
KW apoptosis; treatment; neurodegenerative disease; peripheral nerve injury;
XX spinal cord injury; head trauma; stroke.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Region 1..58 /note="N-terminal region of BAX alpha"

XX Domain 59..73 /label="BH3 domain"

XX WC0200023083-A1.

XX PD 27-APR-2000.

XX PF 22-OCT-1999: 99WO-US24747.

XX PR 22-OCT-1998: 98US-0177315.

XX (UNIV) UNIV WASHINGTON.

XX Johnson EM, Easton R;

XX WPI: 2000-339513/29.

XX Truncated BAX polypeptides useful for preventing apoptosis of neurons
XX for the treatment of nervous system disorders -

Claim 4: Page 33: 43pp: English.

The present sequence is a specifically claimed truncated BAX protein tBAX78 which inhibits neuronal apoptosis induced by trophic factor deprivation. The protein consists of first 78 amino acids of human BAX alpha, that includes the N-terminal region and BH3 domain. It lacks the BH1, BH2 and C-terminal transmembrane domains of the full-length BAX alpha. The tBAX protein lacking only the transmembrane domain has been shown to have anti-apoptotic activity. The present sequence is used to treat diseases associated with neuronal apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury, spinal cord injury, head trauma and stroke.

Sequence 78 AA:

Query Match 100.0%; Score 135; DB 21; Length 78;
Best Local Similarity 100.0%; Pred. No. 3.1e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 OPASTKKISCELRIGDELDSNMEIQR 27
DB 52 qdasckkiscckrlrigdelidsnmeiqr 78

RESULT 3
AAV34149 standard: Protein: 131 AA.

AC AAV34149:

DT 30-NOV-1999 (first entry)

XX Human truncated Bax protein.

XX Apoptosis; adenovirus; dimeric; Bcl-2; p53; cancer; gene therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Domain 59..101 /note="Portion of BH3 domain essential for dimerisation"

XX WC0946371-A2.

XX PD 16-SEP-1999.

XX PF 11-MAR-1999: 99WO-US05359.

XX PR 11-MAR-1998: 98US-0077541.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX McDowell TJ, Swisher SG, Fang B, Bruckheimer EM, Sarkiss MG;

XX WPI: 1999-551404/46.

XX DR N-PSDB: AA219763.

XX New adenovirus vectors, used for killing or inhibiting the growth of
XX cells and for treating cancers -

XX Claim 26: Page 148-149; 151pp; English.

CC This sequence represents a human truncated Bax protein. The cDNA
 CC contains a single base deletion relative to the wild-type (AA719/64),
 CC causing a frameshift which leads to translation of a premature stop
 CC codon, resulting in a truncated protein. However, the domain responsible
 CC for its function is still present in the truncated protein. Bax (Bcl-2
 CC associated X protein) is a proapoptotic member of the Bcl-2 gene family.
 CC Bax functions as a primary response gene in the p53-regulated apoptotic
 CC pathway. The Bax gene promoter has 4 p53 binding sites and the
 CC expression of Bax is upregulated at the transcriptional level by p53, and
 CC Bax mRNA and protein expression have been shown to increase following
 CC induction of p53. Bax protein can function as a homodimer, or it can
 CC heterodimerise with other Bcl-2 gene family members such as the
 CC antiapoptotic protein Bcl-2. Heterodimerisation of Bcl-2 family members
 CC provides a means of controlling cell death via the "rheostat" model. This
 CC model suggests that the relative amounts of Bcl-2 and Bax determine the
 CC susceptibility of a cell to undergo apoptosis. If Bcl-2 is in excess,
 CC Bcl-2/Bax heterodimers predominate and cell death is inhibited. If Bax is
 CC in excess, however, Bax homodimers predominate and the cell becomes
 CC susceptible to apoptosis following exposure to an apoptotic stimulus.
 CC Additionally, Bax can function in its monomeric form to accelerate cell
 CC death. Use of novel adenoviral vectors containing this Bax gene may
 CC augment and complement wild-type p53 gene therapy, which induces a G1
 CC cell cycle arrest and/or apoptosis in malignant cells carrying p53
 CC mutations. In addition, Bax overexpression could provide the apoptotic
 CC effect of p53 without the need for p53 itself.

XX Sequence 131 AA:

Query Match 100.0%: Score 135; DB 20; Length 131;

Best Local Similarity 100.0%: Pred. No. 5, 3e-12;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDASTKKSSECLKRIGDEDSNMLQR 27

Db 52 qdastkksseclkrigdelssmqlqr 78

RESULT 4

AA71406

AA71406

15-NOV-1995 (first entry)

Human Bax protein.

Human; bcl-2; alpha; beta; proto-oncogene; hematopoietic cell line;

apoptosis; membrane-associated cytoplasmic protein; B cell; T cell;

proliferation; cell cycle progression; Bax; apoptotic cell death;

apoptosis; cytokine; death repressor; BH1; BH2; cancer therapy;

hyperplasia; immunodeficiency disease; AIDS; neurodegeneration;

ischemic cell death.

Homo sapiens.

MO9505750-A.

02-MAR-1995.

24-AUG-1994; 94MO-US09701.

26-AUG-1993; 93US-0112208.

25-MAY-1994; 94US-0248819.

(UNIT) UNIV WASHINGTON.

Korsmeyer SJ;

WPI; 1995-106605/14.

N-PSDB; AA097606.

XX Methods for producing and identifying mutant bcl-2 proteins -
 PT that lack death repressor activity and/or lacks binding to Bax.
 XX Disclosure; Fig 3; 133pp; English.

CC This sequence represents human Bax protein. Bax is a protein which is
 CC associated with the human bcl-2 alpha and beta proteins, the sequences
 CC of which are given in AA71404-05 respectively. bcl-2 is encoded by a
 CC proto-oncogene and is capable of inhibiting apoptosis in many
 CC hematopoietic cell systems. bcl-2 is a 26 kD membrane-associated
 CC cytoplasmic protein and is thought to function by enhancing the survival
 CC of hematopoietic cells of B and T origins rather than directly promoting
 CC proliferation of these cell types. bcl-2 has not been shown to directly
 CC promote cell cycle progression nor does it necessarily alter the dose
 CC response to limiting concentrations of IL-3. bcl-2 has been shown to
 CC form heterodimers with this 21 kD protein, Bax. Overexpressed Bax
 CC accelerates apoptotic cell death induced by cytokine deprivation in an
 CC IL-3 dependent cell line, and it also acts to counter the death repressor
 CC activity of bcl-2. Therefore, the ratio between bcl-2 and Bax determines
 CC cell survival or death following an apoptotic stimulus. The invention
 CC gives a mutant form of bcl-2 in which there is at least one amino acid
 CC substitution or deletion in the BH1 or BH2 domains. This makes the
 CC mutant protein substantially incapable of binding Bax and/or incapable
 CC of death repressor activity. Down regulation of bcl-2 is useful in
 CC cancer therapy, controlling hyperplasias and eliminating self-reactive
 CC clones in autoimmunity by favouring death effector molecules. Up
 CC regulating bcl-2 is beneficial in treatment and diagnosis of immuno-
 CC deficiency diseases, including AIDS and neurodegenerative and ischemic
 CC cell death.

XX Sequence 192 AA:

Query Match 100.0%: Score 135; DB 16; Length 192;

Best Local Similarity 100.0%: Pred. No. 7, 9e-12;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDASTKKSSECLKRIGDEDSNMLQR 27

Db 52 qdastkksseclkrigdelssmqlqr 78

RESULT 5

AA734150

AA734150

30-NOV-1999 (first entry)

Human wild-type Bax protein.

Apoptosis; adenovirus; dimeric; Bcl-2; p53; cancer; gene therapy.

Homo sapiens.

MO9946371-A2.

16-SEP-1999.

11-MAR-1999; 99MO-US05359.

11-MAR-1998; 98US-0077541.

(TEXA) UNIV TEXAS SYSTEM.

McDonnell TJ, Swisher SG, Fang B, Bruckheimer EM, Sarkiss MG;

PI JI L, Roth JA;

```

XX  WPI: 1999-551404/46.
DR  N-PSDB; AA219764.
XX
XX  New adenovirus vectors, used for killing or inhibiting the growth of
PT  cells and for treating cancers
PS  Disclosure: Page 149-150; 151pp; English.
XX
XX  This sequence represents human wild-type Bax protein. A naturally
CC  occurring mutant protein (AAV34149) was also isolated. Bax (bcl-2
CC  associated x protein) is a proapoptotic member of the bcl-2 gene family.
CC  Bax functions as a primary response gene in the p53-regulated apoptotic
CC  pathway. The Bax gene promoter has 4 p53 binding sites and the
CC  expression of Bax is upregulated at the transcriptional level by p53, and
CC  Bax mRNA and protein expression have been shown to increase following
CC  induction of p53. Bax protein can function as a homodimer, or it can
CC  heterodimerize with other bcl-2 gene family members such as the
CC  antiapoptotic protein Bcl-2. Heterodimerisation of Bcl-2 family members
CC  provides a means of controlling cell death via the "rheostat" model. This
CC  model suggests that the relative amounts of Bcl-2 and Bax determine the
CC  susceptibility of a cell to undergo apoptosis. If Bcl-2 is in excess, the
CC  Bcl-2/Bax heterodimers predominate and cell death is inhibited. If Bax is
CC  in excess, however, Bax homodimers predominate and the cell becomes
CC  susceptible to apoptosis following exposure to an apoptotic stimulus.
CC  Additionally, Bax can function in its monomeric form to accelerate cell
CC  death. Use of novel adenoviral vectors containing the Bax gene may
CC  augment and complement wild-type p53 gene therapy, which induces a G1
CC  cell cycle arrest and/or apoptosis in malignant cells carrying p53
CC  mutations. In addition, Bax overexpression could provide the apoptotic
XX  effect of p53 without the need for p53 itself.
XX
XX  Sequence 192 AA:
SO

```

```

XX  WPI: 1999-255058/21.
DR
XX  Bcl homology domain 3 polypeptide
PT
XX  Disclosure: Fig 21c; 104pp; English.
XX
XX  This sequence represents the human BAX protein.
CC  The invention relates to a bcl homology domain 3 (BH3 domain),
CC  derived from a proapoptotic member of the Bcl-2 family. The
CC  BH3 polypeptide can be used in a method for promoting apoptosis in a
CC  target cell, especially where the cell is a cancer cell, a virus infected
CC  cell or an autanobody producing cell. The BH3 polypeptide can be used
CC  in therapeutic compositions for treating disease including cancer, other
CC  lymphoproliferative conditions, arthritis, inflammation, and autoimmune
CC  diseases, which may result from the down regulation of cell death
XX  regulation.
XX
XX  Sequence 192 AA:
SO

```

Query Match 100.0%; Score 135; DB 20; Length 192;
Best Local Similarity 100.0%; Pred. No. 7,9e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY  1 ODASRKSLSECLKRIQDELDSNMEIQR 27
DB  52 qdasrklsseclkrigdeldsnmelqr 78

RESULT 7
AAW87804
ID  AAW87804 standard; Protein: 192 AA.
XX
XX  AAW87804:
AC  AAW87804:
DT  10-MAR-1999 (first entry)
DE
XX  A human Bcl-2 associated protein designated Bax.
XX  Human: Bcl-2 associated protein; Bax: bcl-2; antibody; modulator;
XX  bcl-2-related function; apoptosis.
XX
XX  Homo sapiens.
XX
XX  Key Location/Qualifiers
FH  Domain 97..118
FT  /note="BH1 domain"
FT  146..168
FT  /note="BH2 domain"
XX
XX  US5856171-A.
PN  05-JAN-1999.
XX
XX  10-NOV-1994; 94US-0337646.
XX
XX  10-NOV-1994; 94US-0337646.
XX  26-AUG-1993; 93US-0112208.
XX  25-MAY-1994; 94US-0248819.
XX
XX  (UNITM ) UNIV WASHINGTON.
XX
XX  Korsmeyer SJ;
XX
XX  WPI: 1999-105119/09.
DR  N-PSDB; AAV84005.
XX
XX  DNA composition encoding bcl-2 two-hybrid and reporter system - for
PT  identifying modulators of bcl-2 function
XX
XX  Example 1: Columns 71-74; 105pp; English.
XX

```

CC The present sequence represents a human Bcl-2 associated protein
 CC designated Bax. The Bax protein is used in a composition which
 CC comprises a Bcl-2 family member polypeptide, a naturally occurring
 CC Bax polypeptide and an antibody that binds to the Bax polypeptide.
 CC The composition is used to identify modulators of bcl-2-related
 CC function, e.g. substances that inhibit binding of Bax to bcl-2,
 CC which would be potentially useful as drugs for modulating
 CC apoptosis.
 CC
 CC Sequence 192 AA:
 XX
 XX

Query Match 100.0%; Score 135; DB 20; Length 192;
 Best Local Similarity 100.0%; Pred. No. 7,9e-12;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDASTKRLSECLKRIQDELDSNMELQK 27
 |||||||
 DB 52 qdastkrlseclkrigeldsdsmelqkr 78

RESULT 8

AAM87809 standard; Protein: 192 AA.

XX AAM87809;

DT 10-MAR-1999 (first entry)

XX A human Bcl-2 associated protein designated Bax.

DE Human: Bcl-2 associated protein; Bax; bcl-2; antibody; modulator;

KW bcl-2-related function; apoptosis.

XX Homo sapiens.

OS US5856171-A.

XX 05-JAN-1999.

PF 10-NOV-1994; 94US-0337646.

XX 10-NOV-1994; 94US-0337646.

PR 26-AUG-1993; 93US-0112208.

PR 25-MAY-1994; 94US-0248819.

PA (UNIW) UNIV WASHINGTON.

PI Korsmeyer SJ;

DR WPI: 1999-105119/09.

PT DNA composition encoding bcl-2 two-hybrid and reporter system - for
 PT identifying modulators of bcl-2 function

XX Example 7; Fig 7; 105pp; English.

XX The present sequence represents a human Bcl-2 associated protein
 CC designated Bax. The Bax protein is used in a composition which
 CC comprises a Bcl-2 family member polypeptide, a naturally occurring
 CC Bax polypeptide and an antibody that binds to the Bax polypeptide.
 CC The composition is used to identify modulators of bcl-2-related
 CC function, e.g. substances that inhibit binding of Bax to bcl-2,
 CC which would be potentially useful as drugs for modulating
 CC apoptosis.
 CC
 CC Sequence 192 AA:
 XX
 XX

Query Match 100.0%; Score 135; DB 20; Length 192;
 Best Local Similarity 100.0%; Pred. No. 7,9e-12;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDASTKRLSECLKRIQDELDSNMELQK 27
 |||||||
 DB 52 qdastkrlseclkrigeldsdsmelqkr 78

RESULT 9

AAV70827 standard; Protein: 192 AA.

XX AAV70827;

DT 31-JUL-2000 (first entry)

XX Human BAX alpha protein.

DE Human: truncated BAX protein; tBAX; BAX alpha; BCL-2 family; head trauma;
 KW neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive;
 KW apoptosis; treatment; neurodegenerative disease; peripheral nerve injury;
 KW spinal cord injury; stroke; pro-apoptotic; PCPD; programmed cell death.

XX Homo sapiens.

OS Location/Qualifiers

PH Key 1..58

FT Region /label= N-terminal_region

FT Domain 59..73

FT /label= BH3 domain

FT /note= "BCL-2 Homology domain 3"

FT Domain 98..118

FT /label= BH1_domain

FT Domain 150..165

FT /label= BH2_domain

FT Domain 169..188

FT /label= Transmembrane_domain

XX WO200023083-A1.

XX 27-APR-2000.

XX 22-OCT-1999; 99WO-US24747.

XX 22-OCT-1998; 98US-0177315.

XX (UNIW) UNIV WASHINGTON.

XX Johnson EM, Easton R;

XX WPI: 2000-339513/29.

XX Truncated BAX polypeptides useful for preventing apoptosis of neurons

XX for the treatment of nervous system disorders -

XX Disclosure: Page 35-36; 43pp; English.

XX The present sequence is a human BAX alpha protein, a pro-apoptotic
 CC protein which is a member of BCL-2 family of proteins that are involved
 CC in regulation of neuronal programmed cell death. The patent discloses
 CC specific truncated proteins derived from BAX alpha which inhibit neuronal
 CC apoptosis induced by trophic factor deprivation. The anti-apoptotic
 CC truncated BAX (tBAX) proteins include tBAX70, tBAX78 and their mutants.
 CC These proteins contain the N-terminal region and at least a portion of
 CC the BH3 domain of BAX alpha and lack the BH1, BH2 and C-terminal
 CC transmembrane domains. The tBAX protein lacking only the
 CC transmembrane domain has been shown to have anti-apoptotic activity.
 CC The tBAX proteins are used to treat diseases associated with neuronal
 CC apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,
 CC spinal cord injury, head trauma and stroke.
 CC
 CC Sequence 192 AA:
 XX
 XX

Query Match 100.0%; Score 135; DB 21; Length 192;
 Best Local Similarity 100.0%; Pred. No. 7,9e-12;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ODASTRKLSRCKRIGDELDSNMETOR 27
 |||||||||||||||||||
 DB 52 qdastkkssecikrlygdeldsmeiqr 78

RESULT 10

AAI69202
 ID AAI69202 standard: peptide; 192 AA.

AAI69202:

30-MAY-2000 (first entry)

Amino acid sequence of the human Bax protein.

Pro-apoptotic peptide; Bax; BH3 domain; channel inducer; transport;
 cytochrome C transport; mitochondria; apoptosis; ion selectively;
 anti-apoptotic; bcl-2 family member; neoplasia; Epstein Barr virus;
 African Swallow fever virus; adenovirus; lymphoproliferative condition;
 chronic hepatitis; Crohn's disease; inflammation; autoimmune disease;
 immunodeficiency; senescence; neurodegenerative disease;
 reperfusion cell death; infertility; wound.

Homo sapiens.

MO200006187-A2.

10-FEB-2000.

30-JUL-1999; 99MO-US17276.

31-JUL-1998; 98US-0127048.

(UNIM) UNIV WASHINGTON.

Korameyer SJ, Schlessinger PH;

WPI: 2000-195193/17.

Modulating apoptosis in cells by modulating channel ion selectivity for

transport of cytochrome C -

Disclosure: Page 34; 57pp; English.

The present sequence represents the Bax protein. A pro-apoptotic
 peptide can be derived from the BH3 domain. The peptide is an inducer
 of formation of a channel for transport of cytochrome C out of
 mitochondria. The peptide induces apoptosis in a cell. The peptide
 changes the ion selectivity of an anti-apoptotic bcl-2 family member
 from potassium selective to chloride selective. The specification
 also describes inhibitors of apoptosis in cells. The inhibitors and
 inducers can be used to treat patients, preferably humans with a
 condition mediated by excessive down-regulation of apoptosis, or
 especially conditions chosen from neoplasia, diseases caused by
 Epstein Barr virus, African swine fever virus and adenovirus.
 CC lymphoproliferative conditions, cancer, arthritis, Crohn's disease,
 inflammation and autoimmune disease or a condition mediated by
 excessive apoptosis, especially immunodeficiency diseases, senescence,
 neurodegenerative disease, ischemic and reperfusion cell death
 infertility and wounds. The methods can also be used to identify
 apoptosis-modulating compounds.

Sequence 192 AA:

Query Match 100.0%; Score 135; DB 21; Length 192;
 Best Local Similarity 100.0%; Pred. No. 7, 9e-12;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ODASTRKLSRCKRIGDELDSNMETOR 27
 |||||||||||||||||||

DB 52 qdastkkssecikrlygdeldsmeiqr 78

RESULT 11

AAI74121
 ID AAI74121 standard: Protein; 192 AA.

AAI74121:

22-MAY-2001 (first entry)

Human bcl-2 associated X protein (Bax) #1.

Human; Bax; cytosolic; immunosuppressive; immunostimulant; infection;
 apoptosis modulator; bcl-2 associated X protein; cancer therapy; AIDS;
 autoimmunity; immunodeficiency; reperfusion injury; stroke; aging;
 myocardial infarction; traumatic brain injury; ischemia;
 neurodegenerative diseases; hepatitis; transplant rejection; toxemia;
 lymphoproliferative disease.

Homo sapiens.

US6184202-B1.

06-FEB-2001.

11-SEP-1997; 97US-0927326.

10-NOV-1994; 94US-0337646.

26-AUG-1993; 93US-0112208.

25-MAY-1994; 94US-0248819.

(UNIM) UNIV WASHINGTON.

Korameyer SJ;

WPI: 2001-256104/26.

N-PSDB; AAI77704.

Modulating apoptosis of a cell, useful in maintaining homeostasis in

adult tissues, or treating proliferative or autoimmune diseases in

PT cells administering a bcl-2 polypeptide that interacts with a 21 kD

PT bcl-2 associated X protein -

PS Claim 3; Fig 3; 105pp; English.

The present invention relates to a method of modulating apoptosis of a
 cell. The method comprises administering to the cell an agent,
 comprising a BH3 domain or BH2 domain, capable of modulating formation of
 at least one complex selected from bcl-2:bcl-2 complexes, bcl-XL:bcl-XL
 CC complexes, bcl-2-associated X protein (Bax):Bax complexes, bcl-2:Bax
 CC complexes or bcl-XL:Bax complexes. Modulating apoptosis is especially
 CC useful in cancer therapy, and treating autoimmunity, immunodeficiency
 CC diseases (e.g. AIDS), reperfusion injury, myocardial infarction, stroke,
 CC traumatic brain injury, neurodegenerative diseases, aging, ischemia,
 CC toxemia, infection, hepatitis, transplant rejection, and
 CC lymphoproliferative diseases. The present sequence is human Bax, which
 CC was used in the method of the present invention.

Sequence 192 AA:

Query Match 100.0%; Score 135; DB 22; Length 192;
 Best Local Similarity 100.0%; Pred. No. 7, 9e-12;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ODASTRKLSRCKRIGDELDSNMETOR 27
 |||||||||||||||||||
 DB 52 qdastkkssecikrlygdeldsmeiqr 78


```

ID AAB74126 standard; protein: 192 AA.
XX
AC AAB74126;
XX
DF 22-MAY-2001 (first entry)
XX
DE Human bcl-2 associated X protein (Bax) #2.
XX
KW Human; Bax; cytostatic; immunosuppressive; immunostimulant; infection;
KW apoptosis modulator; bcl-2 associated X protein; cancer therapy; AIDS;
KW autoimmunity; immunodeficiency; reperfusion injury; stroke; aging;
KW myocardial infarction; traumatic brain injury; ischemia;
KW neurodegenerative diseases; hepatitis; transplant rejection; toxemia;
KW lymphoproliferative disease.
XX
OS Homo sapiens.
XX
PN US6184202-B1.
XX
PD 06-FEB-2001.
XX
PE 11-SEP-1997; 9705-0927326.
XX
PR 10-NOV-1994; 9405-0337646.
PR 26-NOV-1993; 9305-0112208.
PR 25-MAY-1994; 9405-0248819.
XX
PA (UNITN ) UNIV WASHINGTON.
XX
PI Korsmeyer SJ;
XX
DR MPI, 2001-256104/26.
XX
PR Modulating apoptosis of a cell, useful in maintaining homeostasis in
PR adult tissues, or treating proliferative or autoimmune diseases;
PR comprises administering a bcl-2 polypeptide that interacts with a 21 kd
PR bcl-2 associated X protein -
XX
XX
XX Example 7; Fig 7; 105pp; English.
XX
XX The present invention relates to a method of modulating apoptosis of a
XX cell. The method comprises administering to the cell an agent,
XX comprising a Bhl domain or BH2 domain, capable of modulating formation of
XX at least one complex selected from bcl-2:bcl-2 complexes, bcl-XL:bcl-XL
XX complexes, bcl-2 associated X protein (Bax):Bax complexes, bcl-2:bax
XX complexes or bcl-XL:Bax complexes. Modulating apoptosis is especially
XX useful in cancer therapy, and treating autoimmunity, immunodeficiency
XX diseases (e.g. AIDS), reperfusion injury, myocardial infarction, stroke,
XX traumatic brain injury, neurodegenerative diseases, aging, ischemia,
XX toxemia, infection, hepatitis, transplant rejection, and
XX lymphoproliferative diseases. The present sequence is human Bax, which
XX was used in a sequence alignment in the present invention, with murine
XX Bax (AAB74125), human Bcl-2 (AAB74127) and murine Bcl-2 (AAB74128).
XX
XX Sequence 192 AA:
XX
XX Query Match 100.0%; Score 135; DB 22; Length 192;
XX Best Local Similarity 100.0%; Pred. No. 7.9e-12;
XX Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 ODASTKRLSECLKRIQDELDSNMEIQR 27
DB 52 qdastkrlseclkrigdeldsnmeigr 78

```

```

XX
XX Human Bax protein.
DE
XX
XX S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; 2F;
KW CUL-1; cullin; CDC53; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;
KW Bad; Bcl-2; tumour; cytosolic.
XX
XX Homo sapiens.
OS
XX
XX WO200075184-A1.
XX
XX 14-DEC-2000.
XX
XX 05-JUN-2000; 2000NO-US15449.
XX
XX 04-JUN-1999; 99US-0137494.
XX
XX (UYVA ) UNIV YALE.
XX
XX Zhang H, Tsvetkov LM, Kondo T;
XX
XX MPI: 2001-061703/07.
XX
XX N-PSDB: AAC84598.
XX
XX Modulating polypeptide levels in a cell, diagnosing and treating tumor,
XX involves altering levels of proteins such as S-phase kinase associated
XX proteins 1, 2 and cullin/CDC53 proteins -
XX
XX Claim 5; Page 100-101; 162pp; English.
XX
XX The invention relates to methods of altering the polypeptide levels in a
XX cell using proteins selected from S-phase kinase associated proteins 1
XX and 2 (SKP1, SKP2), SKP2-like proteins (2F) and CUL-1 (a member of the
XX cullin/CDC53 family of proteins). The method is useful for altering the
XX level of p27 cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2
XX polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for
XX detecting tumours and in monitoring tumor treatment in a mammal. Agents
XX that modulate interactions between SKP and target proteins are useful for
XX treating tumours.
XX
XX Sequence 192 AA:
XX
XX Query Match 100.0%; Score 135; DB 22; Length 192;
XX Best Local Similarity 100.0%; Pred. No. 7.9e-12;
XX Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 ODASTKRLSECLKRIQDELDSNMEIQR 27
DB 52 qdastkrlseclkrigdeldsnmeigr 78

```

```

RESULT 13
AAB48286
ID AAB48286 standard; protein: 192 AA.
XX
XX AAB48286;
XX
XX 02-APR-2001 (first entry)
DI

```

```

RESULT 14
AAB35129
ID AAB35129 standard; protein: 192 AA.
XX
XX AAB35129;
XX
XX 03-APR-2001 (first entry)
XX
XX Human Bax.
XX
XX Human; Bax; apoptosis modulator; BCL-2.
XX
XX Homo sapiens.
XX
XX US6165732-A.
XX
XX 26-DEC-2000.
XX
XX 31-JUL-1998; 98US-0127048.
XX
XX 14-OCT-1997; 97US-0061823.
XX

```

XX (UNITW) UNIV WASHINGTON.
 XX Kormmeyer SJ, Schlesinger PH;
 XX MPI: 2001-101692/11.
 XX
 XX Identifying apoptosis-modulating compounds by contacting the compound
 XX with lipid bilayer containing an ion channel formed by anti-apoptotic
 XX polypeptide of Bcl-2 family and determining ion selectivity of the
 XX channel.
 XX
 XX Disclosure: Fig 11; 34pp; English.
 XX
 XX The present invention describes a method for identifying modulators of
 XX apoptosis which involves contacting a compound of interest with a lipid
 XX bilayer comprising a Bcl-2 family selective channel. This channel is a
 XX member of the Bcl-2 family. Apoptosis modulators are also provided,
 XX including Bcl-2deltaITM and BaxdeltaITM.
 XX
 XX Sequence 192 AA:
 XX
 XX

Query Match 100.0%; Score 135; DB 22; Length 192;
 Best Local Similarity 100.0%; Pred. No. 7, 9e-12;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 ODASTKKISRCTARIGDELDSNMELQR 27
 Db 52 qdastkklseclkrigdeldsmeiqr 78

RESULT 15

AAAB50539
 ID AAAB50539 standard; Protein; 192 AA.

AAAB50539;

16-MAR-2001 (first entry)

Human Bax protein sequence SEQ ID NO:6.

Human: Bcl-2; Bcl-XL; Bax; VPAC; apoptosis inhibitor; detection;

apoptosis promoter; diagnosis.

Homo sapiens.

JP2000287689-A.

17-OCT-2000.

08-APR-1999; 99JP-0101888.

08-APR-1999; 99JP-0101888.

(KAGA-) KAGAKU GIYUTSU SHINKO JIGYODAN.

WPI: 2001-065575/08.

N-PSDB; AKC90811.

Screening of an apoptosis inhibitor or promoter which can be used as a
 drug and a diagnostic agent for various diseases caused by apoptosis
 inhibition or apoptosis promotion -

Claim 13; Page 17; 22pp; Japanese.

The present invention describes a method for screening for an apoptosis
 inhibitor or an apoptosis promoter in which VPAC-liposome, an index
 substance which can pass VPAC and a sample are incubated and the change
 in the concentration of the index substance during the incubation is
 detected to judge the presence of apoptosis inhibition or apoptosis
 promotion. The apoptosis inhibitor or the apoptosis promoter can be
 used as a drug and a diagnostic agent for various diseases caused by

CC apoptosis inhibition or apoptosis promotion. The present sequence
 CC represents the human Bax protein, which is an apoptosis inhibitor
 CC used in the exemplification of the present invention.
 XX
 XX Sequence 192 AA:
 XX

Query Match 100.0%; Score 135; DB 22; Length 192;
 Best Local Similarity 100.0%; Pred. No. 7, 9e-12;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 ODASTKKISRCTARIGDELDSNMELQR 27
 Db 52 qdastkklseclkrigdeldsmeiqr 78

Search completed: September 20, 2002, 10:35:57
 Job time: 425 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2002, 10:37:19 ; Search time 75.64 Seconds
(without alignments)
8.719 Million cell updates/sec

Title: US-09-544-664-6
135
Perfect score: 1 QASSTRKLSKRLIGDELDSNMEIQR 27
Sequence:

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 segs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents, AA:*
1: /cgn2.6/p10data2/1aa/5A.COMB.pep:*
2: /cgn2.6/p10data2/1aa/5B.COMB.pep:*
3: /cgn2.6/p10data2/1aa/6A.COMB.pep:*
4: /cgn2.6/p10data2/1aa/6B.COMB.pep:*
5: /cgn2.6/p10data2/1aa/PCTUS.COMB.pep:*
6: /cgn2.6/p10data2/1aa/Backtitles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	135	100.0	34	1	US-08-440-391-13
2	135	100.0	34	2	US-08-908-597A-13
3	135	100.0	34	4	US-09-236-385A-13
4	135	100.0	34	5	PCT-US96-06122-13
5	135	100.0	192	1	US-08-112-208C-9
6	135	100.0	192	1	US-08-112-208C-9
7	135	100.0	192	1	US-08-248-819A-2
8	135	100.0	192	1	US-08-248-819A-9
9	135	100.0	192	1	US-08-607-269-25
10	135	100.0	192	1	US-08-471-058-13
11	135	100.0	192	2	US-08-337-646A-2
12	135	100.0	192	2	US-08-337-646A-9
13	135	100.0	192	2	US-08-856-531-2
14	135	100.0	192	2	US-08-856-531-9
15	135	100.0	192	2	US-08-856-034-2
16	135	100.0	192	2	US-08-856-034-9
17	135	100.0	192	3	US-08-471-057-13
18	135	100.0	192	4	US-09-127-048-7
19	135	100.0	192	4	US-08-927-326-2
20	135	100.0	192	4	US-08-927-326-9
21	135	100.0	192	5	PCT-US95-04600-25
22	135	100.0	221	1	US-08-616-722A-9
23	135	100.0	221	4	US-08-037-742B-9
24	132	97.8	192	1	US-08-112-208C-3
25	132	97.8	192	1	US-08-112-208C-8
26	132	97.8	192	1	US-08-248-819A-3
27	132	97.8	192	1	US-08-248-819A-8

28	132	97.8	192	2	US-08-337-646A-3	Sequence 3, Appl1
29	132	97.8	192	2	US-08-337-646A-8	Sequence 8, Appl1
30	132	97.8	192	2	US-08-856-531-3	Sequence 3, Appl1
31	132	97.8	192	2	US-08-856-531-8	Sequence 8, Appl1
32	132	97.8	192	2	US-08-856-034-3	Sequence 3, Appl1
33	132	97.8	192	2	US-08-856-034-8	Sequence 8, Appl1
34	132	97.8	192	4	US-09-127-048-6	Sequence 6, Appl1
35	132	97.8	192	4	US-08-927-326-3	Sequence 3, Appl1
36	132	97.8	192	4	US-08-927-326-8	Sequence 8, Appl1
37	130	96.3	26	1	US-08-440-391-6	Sequence 6, Appl1
38	130	96.3	26	1	US-08-440-391-24	Sequence 24, Appl1
39	130	96.3	26	2	US-08-908-597A-6	Sequence 6, Appl1
40	130	96.3	26	2	US-08-908-597A-24	Sequence 24, Appl1
41	130	96.3	26	4	US-09-236-385A-6	Sequence 6, Appl1
42	130	96.3	26	4	US-09-236-385A-24	Sequence 24, Appl1
43	130	96.3	26	5	PCT-US96-06122-6	Sequence 6, Appl1
44	130	96.3	26	5	PCT-US96-06122-24	Sequence 24, Appl1
45	105	77.8	42	1	US-08-798-897-22	Sequence 22, Appl1

ALIGNMENTS

```
RESULT 1
US-08-440-391-13
Sequence 13, Appl1
Patent No 5656725
GENERAL INFORMATION:
APPLICANT: CITIZENDEN, Thomas D.; and
APPLICANT: LUTZ, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
TITLE OF INVENTION: MODULATE APOPTOSIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSER: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,391
FILING DATE: 12-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322,147
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8480
TELEFAX: 202-942-8484
INFORMATION FOR SPO. ID NO.: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-440-391-13

Query Match 100.0%; Score 135; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.5e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

RESULT 2
US-08-908-597A-13
Sequence 13, Application US/0808597A
Patent No. 5863795
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
APPLICANT: LUTZ, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
TITLE OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/908,597A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/440,391
FILING DATE: 12-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.147
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-908-597A-13

Query Match 100.0%; Score 135; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 1,5e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDASTKKLSCLKRIQDELDSNMELQR 27
|||||
DB 3 QDASTKKLSCLKRIQDELDSNMELQR 29

RESULT 3
US-09-236-385A-13
Sequence 13, Application US/09236385A
Patent No. 6221615
GENERAL INFORMATION:
APPLICANT: CHITTENDEN, Thomas D.; and
APPLICANT: LUTZ, Robert J.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS WHICH
MODULATE APOPTOSIS
TITLE OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/236,385A
FILING DATE: 25-Jan-1999
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
(C) ATTORNEY DOCKET NO. 104322.147CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-236-385A-13

Query Match 100.0%; Score 135; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 1,5e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDASTKKLSCLKRIQDELDSNMELQR 27
|||||
DB 3 QDASTKKLSCLKRIQDELDSNMELQR 29

RESULT 4
PCT-US96-06122-13
Sequence 13, Application PC/TUS9606122
GENERAL INFORMATION:
APPLICANT: IMMUNOGEN, INC.
TITLE OF INVENTION: NOVEL PEPTIDES AND COMPOSITIONS
WHICH MODULATE APOPTOSIS
TITLE OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06122
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/440,391
FILING DATE: 12-MAY-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WIXON, HENRY N.
REGISTRATION NUMBER: 32,073
REFERENCE/DOCKET NUMBER: 104322.147PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-942-8400
TELEFAX: 202-942-8484
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US96-06122-13

Query Match 100.0%; Score 135; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 1, 3e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QDASRKLSLSECKRIKIDELDSNMEIQR 27
|||||

DB 3 QDASRKLSLSECKRIKIDELDSNMEIQR 29

RESULT 5
US-08-112-208C-2
Sequence 2, Application US/08112208C
Patent No. 5681179
GENERAL INFORMATION:
APPLICANT: KOSMEYER, Stanley J
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/112, 208C
CLASSIFICATION: 26 59G-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30, 223
REFERENCE/DOCKET NUMBER: 15726A-000610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-112-208C-2

Query Match 100.0%; Score 135; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QDASRKLSLSECKRIKIDELDSNMEIQR 27
|||||

DB 52 QDASRKLSLSECKRIKIDELDSNMEIQR 78

RESULT 6
US-08-112-208C-9
Sequence 9, Application US/08112208C
Patent No. 5681179
GENERAL INFORMATION:
APPLICANT: KOSMEYER, Stanley J
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US

ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/112, 208C
CLASSIFICATION: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30, 223
REFERENCE/DOCKET NUMBER: 15726A-000610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-112-208C-9

Query Match 100.0%; Score 135; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QDASRKLSLSECKRIKIDELDSNMEIQR 27
|||||

DB 52 QDASRKLSLSECKRIKIDELDSNMEIQR 78

RESULT 7
US-08-248-819A-2
Sequence 2, Application US/08248819A
Patent No. 5780638
GENERAL INFORMATION:
APPLICANT: KOSMEYER, Stanley J
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Knoutie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/248, 819A
FILING DATE: 25-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112, 208
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30, 223
REFERENCE/DOCKET NUMBER: 15726A-000610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-248-819A-2

Query Match 100.0%; Score 135; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ODASTRKSLSECKLRIGDELDSNMELQ 27
DB 52 ODASTRKSLSECKLRIGDELDSNMELQ 78

RESULT 8
US-08-248-819A-9
Sequence 9, Application US/08248819A
Patent No. 5700638
GENERAL INFORMATION:

APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend Khoufie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/248,819A
FILING DATE: 25-NOV-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,208
FILING DATE: 26-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2422
TELEFAX: (415) 326-2400
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-248-819A-9

Query Match 100.0%; Score 135; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ODASTRKSLSECKLRIGDELDSNMELQ 27
DB 52 ODASTRKSLSECKLRIGDELDSNMELQ 78

RESULT 9
US-08-607-269-25
Sequence 25, Application US/08607269
Patent No. 5702897
GENERAL INFORMATION:

APPLICANT: Reed, John C.
APPLICANT: Sato, Takashi
TITLE OF INVENTION: Interaction of proteins involved in a
TITLE OF INVENTION: Cell Death Pathway
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/607,269
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/226,876
FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9882
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-607-269-25

Query Match 100.0%; Score 135; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ODASTRKSLSECKLRIGDELDSNMELQ 27
DB 52 ODASTRKSLSECKLRIGDELDSNMELQ 78

RESULT 10
US-08-471-058-13
Sequence 13, Application US/08471058
Patent No. 5720443
GENERAL INFORMATION:
APPLICANT: Kiefer, Michael C.
APPLICANT: Barr, Philip J.
TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING
TITLE OF INVENTION: PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSD for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,058


```

: FILING DATE: 06-JUN-1995
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/320,157
: FILING DATE: 07-OCT-1994
: APPLICATION NUMBER: 08/160,067
: FILING DATE: 30-NOV-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Lehnhardt, Susan K
: REGISTRATION NUMBER: 33,943
: REFERENCE/DOCKET NUMBER: 23647-20007,12
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-813-5600
: TELEFAX: 415-494-0792
: TELETYPE: 706141
: INFORMATION FOR SEQ. ID NO.: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 192 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-08-471-058-13

```

```

Query Match          100.0%; Score 135; DB 1; Length 192;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 0DASTKLSKELKRIQDELDSENMELOR 27
Db 52 0DASTKLSKELKRIQDELDSENMELOR 78

```

```

RESULT 11
US-08-337-646A-2
: Sequence 2, Application US/08337646A
: Patent No. 5856171
: GENERAL INFORMATION:
: APPLICANT: KORSMEYER, Stanley J.
: TITLE OF INVENTION: CELL DEATH REGULATORS
: NUMBER OF SEQUENCES: 78
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Hourie and Crew
: STREET: 379 Lytton Avenue
: CITY: Palo Alto
: STATE: California
: COUNTRY: US
: ZIP: 94301
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/337,646A
: FILING DATE: 10-NOV-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/248,819
: FILING DATE: 25-MAY-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/112,208
: FILING DATE: 26-AUG-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Smith, William M
: REGISTRATION NUMBER: 30,223
: REFERENCE/DOCKET NUMBER: 15726A-000620
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 326-2400
: TELEFAX: (415) 326-2422
: INFORMATION FOR SEQ. ID NO.: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 192 amino acids

```

```

: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-337-646A-2

```

```

Query Match          100.0%; Score 135; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 0DASTKLSKELKRIQDELDSENMELOR 27
Db 52 0DASTKLSKELKRIQDELDSENMELOR 78

```

```

RESULT 12
US-08-337-646A-9
: Sequence 9, Application US/08337646A
: Patent No. 5856171
: GENERAL INFORMATION:
: APPLICANT: KORSMEYER, Stanley J.
: TITLE OF INVENTION: CELL DEATH REGULATORS
: NUMBER OF SEQUENCES: 78
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Hourie and Crew
: STREET: 379 Lytton Avenue
: CITY: Palo Alto
: STATE: California
: COUNTRY: US
: ZIP: 94301
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/337,646A
: FILING DATE: 10-NOV-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/248,819
: FILING DATE: 25-MAY-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/112,208
: FILING DATE: 26-AUG-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Smith, William M
: REGISTRATION NUMBER: 30,223
: REFERENCE/DOCKET NUMBER: 15726A-000620
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 326-2400
: TELEFAX: (415) 326-2422
: INFORMATION FOR SEQ. ID NO.: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 192 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-337-646A-9

```

```

Query Match          100.0%; Score 135; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 0DASTKLSKELKRIQDELDSENMELOR 27
Db 52 0DASTKLSKELKRIQDELDSENMELOR 78

```

```

RESULT 13
US-08-856-531-2

```

```

Sequence 2, Application US/08956531
Patent No. 5942490
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howell & Haferkamp, L.C.
STREET: 7733 Forsyth Blvd., Suite 1400
CITY: St. Louis
STATE: MO USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,531
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, Donald R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 976176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..192
OTHER INFORMATION: /note="Human BAX polypeptide"

US-08-856-531-2

Query Match 100.0%; Score 135; DB 2; Length 192;
Best Local Similarity 100.0%; Pctd No. 1e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDASTKLSCLKRIQDELDSNMEIQR 27
DB 52 QDASTKLSCLKRIQDELDSNMEIQR 78

RESULT 14
US-08-856-531-9
Sequence 9, Application US/08956531
Patent No. 5942490
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howell & Haferkamp, L.C.
STREET: 7733 Forsyth Blvd., Suite 1400
CITY: St. Louis
STATE: MO USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

```

```

APPLICATION NUMBER: US/08/856,531
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, Donald R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 976176
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..192
OTHER INFORMATION: /note="Human BAX polypeptide"

US-08-856-531-9

Query Match 100.0%; Score 135; DB 2; Length 192;
Best Local Similarity 100.0%; Pctd No. 1e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDASTKLSCLKRIQDELDSNMEIQR 27
DB 52 QDASTKLSCLKRIQDELDSNMEIQR 78

RESULT 15
US-08-856-034-2
Sequence 2, Application US/08956034
Patent No. 5955595
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: CELL DEATH REGULATORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howell & Haferkamp, L.C.
STREET: 7733 Forsyth Blvd., Suite 1400
CITY: St. Louis
STATE: MO USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,034
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, Donald R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 976175
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein

```

LOCATION: 1..192
OTHER INFORMATION: /note="Human BAX polypeptide"
us-08-856-034-2

Query Match 100.0%; Score 135; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 1e-12;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ODASTKKLSECLKRIKGDELDSNMELQR 27
|||||
Db 52 ODASTKKLSECLKRIKGDELDSNMELQR 78

Search completed: September 20, 2002, 10:37:19
Job time: 407 sec

...

...

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OK protein - protein search, using sw model

Run on: September 20, 2002, 10:39:02 ; Search time 95.59 seconds

(without alignments)
27.141 Million cell updates/sec

Title: US-09-544-664-6

Sequence: 1 QDASTRKLSBCTKRIGDELDSNMELQR 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. }

SUMMARIES

Result No	Score	Query Match	Length	DB ID	Description
1	135	100.0	179	2	JC7255
2	135	100.0	192	2	A47538
3	135	100.0	218	2	B47538
4	132	97.8	192	2	D47538
5	129	95.6	133	2	T53295
6	129	95.6	145	2	F64165
7	129	95.6	145	2	D96585
8	129	95.6	145	2	S64310
9	129	95.6	145	2	A37244
10	129	95.6	145	2	H71317
11	129	95.6	145	2	S43427
12	129	95.6	145	2	G86324
13	129	95.6	145	2	A80506
14	129	95.6	145	2	T51488
15	129	95.6	145	2	T19923
16	129	95.6	145	2	P82614
17	129	95.6	145	2	A45627
18	129	95.6	145	2	A59294
19	129	95.6	145	2	S43240
20	129	95.6	145	2	JM0061
21	129	95.6	145	2	E71098
22	129	95.6	145	2	D72370
23	129	95.6	145	2	H84115
24	129	95.6	145	2	S08981
25	129	95.6	145	2	A47476
26	129	95.6	145	2	P96740
27	129	95.6	145	2	S64220
28	129	95.6	145	2	S64220
29	129	95.6	145	2	AC0941

30	47	34.8	591	2	S43428	omega-crystallin - s1
31	47	34.8	862	1	FAD0A	alpha-actinin - s1
32	47	34.8	4151	2	T13734	groovin gene prote
33	46.5	34.4	163	2	F81374	hypothetical prote
34	46.5	34.4	1736	2	F86178	hypothetical prote
35	46	34.1	98	2	D87026	hypothetical prote
36	46	34.1	186	2	T21243	hypothetical prote
37	46	34.1	455	2	H69230	NADP-dependent gly
38	46	34.1	558	2	G90300	hypothetical prote
39	46	34.1	802	2	A8754	hypothetical prote
40	46	34.1	1033	2	F88131	hypothetical prote
41	46	34.1	1094	2	S49313	protein kinase - s
42	46	34.1	1465	2	T23056	hypothetical prote
43	45.5	33.7	65	2	F97042	hypothetical prote
44	45.5	33.7	353	2	T00442	probable rRNA (ade
45	45.5	33.7	3224	1	S58884	Ran-binding protei

ALIGNMENTS

RESULT 1
JC7255
Bax-delta protein - human
C:Species: Homo sapiens (man)
C>Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 17-Nov-2000
C:Accession: JC7255
R:Schmidt, E.; Paquet, C.; Beauchemin, M.; Deyver-Bertrand, J.; Bertrand, R.
Blochem. Biophys. Res. Commun. 270, 868-879, 2000
A>Title: Characterization of Bax-delta, a cell death-inducing isoform of Bax.
A:Accession: JC7255
A:Reference number: JC7255
A:Molecule type: mRNA
A:Residues: 1-179 <SO>
A:Cross-references: GB:A247393
A:Experimental source: Cancer promyelocytic cells
C:Comment: This protein, a member of the Bcl-2 family, has a proapoptotic effect. It
activation
C:Superfamily: bcl transforming protein
C:Keywords: transmembrane protein

Query Match 100.0% Score 135; DB 2; Length 179;
Best Local Similarity 100.0% Pred. No. 2e-11; 0; indels 0; gaps 0;
Matches 27; Conservative 0; Mismatches 0;

QY 1 QDASTRKLSBCTKRIGDELDSNMELQR 27
DB 52 QDASTRKLSBCTKRIGDELDSNMELQR 78

RESULT 2
A47538
bcl-2-associated protein x, alpha splice form - human
N:Alternative names: BAX; Programmed cell death membrane protein x alpha
C:Species: Homo sapiens (man)
C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C:Accession: A47538
R:Olivia, Z. N.; Millman, C. L.; Korsmeyer, S. J.
Cell 74, 609-619, 1993
A>Title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates
A:Reference number: A47538; MIMD:93564978
A:Accession: A47538
A:Molecule type: mRNA
A:Residues: 1-192 <SO>
A:Cross-references: GB:I22473; NID:9388165; PIRN:AA03619.1; PID:9388166
A:Note: the amino end of the mature protein is blocked
C:Genetics
A:Gene: GDB:BAX
A:Cross-references: GDB:228082; OMIM:600040
A:Map position: 19q13.3-19q13.4
C:Superfamily: bcl transforming protein
C:Keywords: alternative splicing; blocked amino end; heterodimer; homodimer; transmem

F:172-191/Domain: transmembrane #status predicted <TMH1>

Query Match 100.0% Score 135; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 2, 2e-11;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ODASTKKLSECLKRTIGDELDSNMEIQR 27
|||||
DB 52 ODASTKKLSECLKRTIGDELDSNMEIQR 78

RESULT 3
bcl-2-associated protein x, beta splice form - human
N:Alternate names: BAX; programmed cell death membrane protein x beta
C:Species: Homo sapiens (man)
C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C:Accession: B47538
R:Olival, Z.N.; Millman, C.L.; Korsmeyer, S.J.
Cell 74, 609-619, 1993
A:Title: bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates F
A:Reference number: A47538; MUID:93364978
A:Accession: B47538
A:Molecule type: mRNA
A:Residues: 1-218 <OLP>
A:Cross-references: GB:L2474; NID:q388167; PIDN:AA03620.1; PID:q388168
A:Note: the amino end of the mature protein is blocked
C:Genetics:
A:Gene: GDB:BAX
A:Cross-references: GDB:228082; OMIM:600040
A:Map position: 19q13.3-19q13.4
C:Superfamily: bcl transforming protein
C:Keywords: alternative splicing; blocked amino end; cytosol; heterodimer; homodimer

Query Match 100.0% Score 135; DB 2; Length 218;
Best Local Similarity 100.0%; Pred. No. 2, 5e-11;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ODASTKKLSECLKRTIGDELDSNMEIQR 27
|||||
DB 52 ODASTKKLSECLKRTIGDELDSNMEIQR 78

RESULT 4
bcl-2-associated protein x - mouse
N:Alternate names: BAX; programmed cell death membrane protein x
C:Species: Mus musculus (house mouse)
C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 17-Nov-2000
C:Accession: B47538
R:Olival, Z.N.; Millman, C.L.; Korsmeyer, S.J.
Cell 74, 609-619, 1993
A:Title: Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that accelerates F
A:Reference number: A47538; MUID:93364978
A:Accession: B47538
A:Molecule type: mRNA
A:Residues: 1-197 <OLP>
A:Cross-references: GB:L22472
C:Genetics:
A:Gene: bax
C:Superfamily: bcl transforming protein

Query Match 97.8% Score 132; DB 2; Length 192;
Best Local Similarity 96.3%; Pred. No. 5, 7e-11;
Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ODASTKKLSECLKRTIGDELDSNMEIQR 27
|||||
DB 52 ODASTKKLSECLKRTIGDELDSNMEIQR 78

RESULT 5
153295
bcl-2-associated protein x - rat (fragment)
N:Alternate names: BAX; programmed cell death membrane protein x
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 03-Nov-2000
C:Accession: I53295
R:Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
Endocrinology 136, 232-241, 1995
A:Title: Expression of members of the bcl-2 gene family in the immature rat ovary: eq
constitutive bcl-2 and bcl-x long messenger ribonucleic acid levels.
A:Reference number: I53295; MUID:95129487
A:Accession: I53295
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-133 <RES>
A:Cross-references: EMBL:U32098; NID:q975869; PIDN:AA075200.1; PID:q975870
C:Genetics:
A:Gene: bax
C:Superfamily: bcl transforming protein

Query Match 95.6% Score 129; DB 2; Length 133;
Best Local Similarity 92.6%; Pred. No. 1e-10;
Matches 25; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 ODASTKKLSECLKRTIGDELDSNMEIQR 27
|||||
DB 16 ODASTKKLSECLKRTIGDELDSNMEIQR 42

RESULT 6
F64165
hypothetical protein H11064 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
C:Accession: F64165
R:Falschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kikness, E.F.; Kerlavage
; Gocayne, J.D.; Scott, J.; Shiley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fritchman, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Shail, K.V.; Fraser, C.M.; Smith, H.O.; Vente
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630
A:Accession: F64165
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-485 <TIOR>
A:Cross-references: GB:U32786; GB:I42023; NID:q1574605; PIDN:AA022718.1; PID:q1574615
A:Note: best homolog was a hypothetical protein from Escherichia coli
C:Genetics:
A:Start codon: GTG

Query Match 38.5% Score 52; DB 2; Length 485;
Best Local Similarity 45.5%; Pred. No. 19;
Matches 10; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 3 ASTKKLSECLKRTIGDELDSNME 24
:||| | ||| :||| :|||
DB 402 SSIKKDEFLKRVYDOLEENVK 423

RESULT 7
D96585
hypothetical protein F20D21.19 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: D96585
R:Rheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alton
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Cressy, T.H.; Dewar,

ansen, N.F.; Hughes, B.; Holzar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.B.; Li, J.H.; Li, F.; Lin, X.; Liu, Z.A.; Luos, J.S.; Malt, R.; Matzall,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Multis: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A>Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A:Reference number: A86141; MUID:21016719
 A:Accession: D96585
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-575 <STO>
 A:Cross-References: GB:AE005173; NID:94585981; PIDN:AMD2617.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: F20D21.19
 A:Map position: 1

Query Match 38.5%; Score 52; DB 2; Length 575;
 Best Local Similarity 50.0%; Pred. No. 23;
 Matches 10; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 4 STKRLSECKLRIGDELDSNM 23
 |||:||||:||||:|
 Db 508 STGKMLEALEVAGDDIDSM 527

RESULT 8
 S64310
 4-aminobutyrate transaminase (EC 2.6.1.19) - yeast (*Saccharomyces cerevisiae*)
 A:Alternate names: 4-aminobutyrate aminotransferase; gamma-aminobutyrate transaminase; F
 C:Species: *Saccharomyces cerevisiae*
 C:Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 20-Jun-2000
 C:Accession: S64310; S26708; #text_change 20-Jun-2000
 R:Rieger, M.; Mueller-Auer, S.; Brueckner, M.; Schaefer, M.
 A:Reference number: S64071
 A:Accession: S64310
 A:Molecule type: DNA
 A:Residues: 1-471 <REF>
 A:Cross-References: EMBL:272804; NID:91322986; PIDN:CAA97002.1; PID:91322987; MIPS:YGR01
 A:Experimental source: strain S288C
 R:Andre, B.; Jauniaux, J.C.
 A:Nucleic Acids Res. 18, 3049, 1990
 A>Title: Nucleotide sequence of the yeast *UCAL* gene encoding GABA transaminase.
 A:Reference number: S26708; MUID:90272415
 A:Accession: S26708
 A:Molecule type: DNA
 A:Residues: 1-239; R, 241-471 <AND1>
 A:Cross-References: EMBL:X52600; NID:914745; PIDN:CAA36833.1; PID:914746
 A:Experimental source: strain sigma 1278b
 C:Genetics:
 A:Gene: SGP:UCAL
 A:Cross-References: SGP:S0003251; MIPS:YGR019W
 A:Map position: 7R
 C:Superfamily: 4-aminobutyrate transaminase
 C:Keywords: aminotransferase; pyridoxal phosphate

Query Match 38.1%; Score 51.5; DB 2; Length 471;
 Best Local Similarity 46.4%; Pred. No. 22;
 Matches 13; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

OY 1 QDASTRKLECKLRIGDELDSNM-10R 27
 |||:||||:||||:|
 Db 367 QPISDKKLTBCGSRVGDYFKKIKGLQK 394

RESULT 9
 A37244
 nuclear autoantigen Sp-100 - human
 C:Species: *Homo sapiens* (man)

C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 05-Nov-1999
 C:Accession: A37244
 R:Stosteckl, C.; Guldner, H.H.; Netter, H.J.; Will, H.
 J. Immunol. 145, 4338-4347, 1990
 A>Title: Isolation and characterization of cDNA encoding a human nuclear antigen pred
 A:Reference number: A37244; MUID:91079525
 A:Accession: A37244
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-480 <SZO>
 A:Cross-References: GB:M60618; NID:9178688; PIDN:AAA3537.1; PID:9178689

Query Match 37.8%; Score 51; DB 2; Length 480;
 Best Local Similarity 33.3%; Pred. No. 26;
 Matches 10; Conservative 10; Mismatches 6; Indels 4; Gaps 1;

OY 2 DASTRKLECKLRIGDELDSNM-10R 27
 |||:||||:||||:|
 Db 7 DISTRKLECKLRIGDELDSNM-10R 36

RESULT 10
 H71317
 probable methyl-accepting chemotaxis protein (mcp-1) - *Syphilis spirochete*
 C:Species: *Treponema pallidum* subsp. *pallidum* (*Syphilis spirochete*)
 C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
 C:Accession: H71317
 R:Ratner, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; G
 rison, J.; Khatkhat, R.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Ullrich, T.; M
 they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
 A:Reference number: H71317
 A:Accession: H71317
 A:Molecule type: DNA
 A:Residues: 1-845 <COB>
 A:Cross-References: GB:AE00520; GB:AE00520; NID:93322775; PIDN:AA065475.1; PID:9332
 A:Experimental source: strain Nichols
 C:Genetics:
 A:Gene: TP0488

Query Match 37.8%; Score 51; DB 2; Length 845;
 Best Local Similarity 52.4%; Pred. No. 46;
 Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 3 ASTRKLECKLRIGDELDSNM 23
 |||:||||:||||:|
 Db 512 ATVGSSDDMRKIGDELDSNM 532

RESULT 11
 S43427
 Intermediate filament protein - *Sloane's squid*
 C:Species: *Octopus teledon* (Sloane's squid)
 C:Date: 07-Sep-1994 #sequence_revision 26-May-1995 #text_change 26-Aug-1999
 C:Accession: S43427
 R:Tomarev, S.I.; Zinovleva, R.D.; Piatigorsky, J.
 A:Title: Primary structure and lens-specific expression of genes for an intermediate
 A:Reference number: S43425; MUID:94060097
 A:Accession: S43427
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-614 <TOM>
 A:Cross-References: EMBL:L20112; NID:9159851; PID:9159852
 A>Note: the authors did not translate the codon for residue 1
 C:Superfamily: Intermediate filament protein A71

Query Match 37.0%; Score 50; DB 2; Length 614;

Best Local Similarity 38.1%; Pred. No. 46;
Matches 0; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy 5 TKKISECLKRTIDDELSDNML 25
Db 288 TWEIACKEIRIDEDYDQML 308

RESULT 12

hypothetical protein T2296.1 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse ear cross)
C:Date: 02-May-2001 #sequence_revision 02-May-2001 #text_change 31-Dec-2001

C:Accession: G86324
R:Medcology: A. Becker, J.R. Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chen, M.F.; Hubbard, K.; Conaway, A.B.; Conaway, A.R.; Greasy, T.H.; Dewar, K.;
Mature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maltz, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakam, H.
A:Authors: Salzberg, S.L.; Schwartz, J.P.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yi, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Accession: G86324
A:Reference number: AB6141; MIMD:21016719

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-311 <SNOS>
A:Cross-references: GB:AF005172; NID:98954052; PIDN:AF8225.1; GSPDB:GN00141
A:Genetic: 1
A:Map position: 1

Query Match 36.3%; Score 49; DB 2; Length 311;
Best Local Similarity 42.1%; Pred. No. 32;
Matches 8; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 8 LSECLKRTIDDELSDNML 26
Db 142 MDELQULMDRIDSGDLQ 160

RESULT 13

ser/thr protein kinase, probable [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001

C:Accession: A90506
R:Shen, O.; Strub, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.
arrett, R.A.; Ragan, M.A.; Senner, C.M.; Van der Oost, J.
A:Submitted to Genbank April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: A90506
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-669 <KBP>
A:Cross-references: GB:AE006641; NID:q13816645; PIDN:AKA3304.1; GSPDB:GN00155
C:Genetic: 8
A:Gene: SSO3207

Query Match 36.3%; Score 49; DB 2; Length 669;
Best Local Similarity 50.0%; Pred. No. 69;
Matches 7; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LSECLKRTIDDELSD 21
Db 175 VACMERIDDELDA 188

RESULT 14

hypothetical protein T21H9.100 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse ear cross)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000

C:Accession: T91468
R:Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asanizu, E.; Kotani, H.; Tabata, S.;
submitted to the Protein Sequence Database, August 2000
A:Reference number: Z25394
A:Accession: T91468
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-718 <SNOS>
A:Cross-references: EMBL:AL391148
A:Experimental source: cultivar Columbia; BAC clone T21H9
C:Genetic: 5
A:Map position: 27/3.381/1; 424/3; 539/3; 592/1; 650/3
A:Note: T21H9_100

Query Match 36.3%; Score 49; DB 2; Length 718;
Best Local Similarity 43.5%; Pred. No. 74;
Matches 10; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy 5 TKKISECLKRTIDDELSDNML 27
Db 571 TNEPCKRTIGKNSLVGR 593

RESULT 15

hypothetical protein C4AC10.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C:Accession: T19923
R:Coltgate, to the EMBL Data Library, February 1996
A:Reference number: Z19157
A:Accession: T19923
A:Status: preliminary; translated from GB/EMBL/DDBT
A:Molecule type: DNA
A:Residues: 1-732 <WIL>
A:Cross-references: EMBL:Z69787; PIDN:CAA93636.1; GSPDB:GN00028; CESP:C4AC10.2
A:Experimental source: clone C4AC10
A:Gene: CESP-C4AC10.2
A:Map position: X
A:Intons: 54/3; 102/3; 119/3; 388/1; 427/3; 490/3; 550/3; 619/1; 714/3

Query Match 36.3%; Score 49; DB 2; Length 732;
Best Local Similarity 42.3%; Pred. No. 76;
Matches 11; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Qy 2 DASTKISECLKRTIDDELSDNML 27
Db 154 DAKKEISEYKQLETPKNSISQR 179

Search completed: September 20, 2002, 10:39:04
Job time: 476 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2002, 11:04.28 : Search time 44.99 Seconds
(without alignments) 23.237 Million cell updates/sec

Title: US-09-544-664-6

135

Sequence: 1 QDASTKKLSECLKRIKDDELDSNMLQRLR 27

Scoring table: Biosim62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	135	100.0	192	1	BAXA_BOVIN
2	135	100.0	192	1	BAXA_HUMAN
3	135	100.0	216	1	BAXA_HUMAN
4	132	97.8	192	1	BAXA_MOUSE
5	132	97.8	192	1	BAXA_RAT
6	52	38.5	485	1	TA64_HUMAN
7	51	37.6	471	1	GAT4_YEAST
8	47.5	37.6	879	1	SP10_HUMAN
9	47.5	37.6	163	1	TPC_HUMAN
10	47	34.8	294	1	R8SK_RABCD
11	47	34.8	339	1	MDL_PETTE
12	47	34.8	350	1	MC1A_HUMAN
13	47	34.8	500	1	AROB_YEAST
14	47	34.1	862	1	ACOT1_DICDI
15	46	34.1	1033	1	YDE9_SCHPO
16	45.5	33.7	281	1	APL_BRAHE
17	45.5	33.7	3224	1	R8B2_HUMAN
18	45	33.3	417	1	T2BA_YEAST
19	45	33.3	482	1	RPOA_MOUSE
20	45	33.3	496	1	MSB1_SCHPO
21	45	33.3	522	1	CPVL_ORONI
22	45	33.3	656	1	DNKK_ALCEU
23	45	33.3	657	1	BFS1_CHICK
24	45	33.3	830	1	LEB3_HUMAN
25	45	33.3	1704	1	ABC3_HUMAN
26	44.5	33.0	1325	1	G160_MOUSE
27	44	32.6	222	1	YALV_ECOLI
28	44	32.6	281	1	KHSE_THIMA
29	44	32.6	506	1	DHA2_ALCEU
30	44	32.6	564	1	PROD_CABEL
31	44	32.6	726	1	CO3_RABIT
32	44	32.6	899	1	VP3_EBDVA
33	43.5	32.2	236	1	STX8_HUMAN

ALIGNMENTS

RESULT 1	ID	STANDARD	PRT	192 AA
BAXA_BOVIN	002703			
15-JUL-1999 (Rel. 38, Created)				
15-JUL-1999 (Rel. 38, Last sequence update)				
16-OCT-2001 (Rel. 40, Last annotation update)				
Apoptosis regulator BAX, membrane isoform alpha.				
BAX				
Bos taurus (Bovine)				
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				
Bovidae; Bos.				
NCBI-TaxID=9913;				
SEQUENCE FROM N.A.				
STRAIN=HOLSTEIN; TISSUE=Thymus;				
MEDLINE=98162580; PubMed=9501036;				
Notes R.A., Cockrell C.L.,				
Increased ratio of Bcl-2/Bax expression is associated with bovine				
leukemia virus-induced leukemogenesis in cattle.?				
Virology 242:184-192(1998).				
-1- FUNCTION: ACCELERATES PROGRAMED CELL DEATH BY BINDING TO, AND				
ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ANALOGOUS				
HOMOLOG E1B 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C,				
ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS. BAX DEFICIENCY				
LEADS TO LIVERHOLD HYPERPLASIA AND MALE STERILITY, BECAUSE OF THE				
CESSATION OF SPERM PRODUCTION (BY SIMILARITY).				
-1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,				
E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1 (BY SIMILARITY).				
-1- SUBCELLULAR LOCATION: Membrane-bound (By similarity). AND THE TWO				
ALTERNATIVE PRODUCTS: A 21 KDa MEMBRANE PROTEIN ALPHA AND THE TWO				
CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE				
SPlicing.				
-1- DOMAIN: INTERACT B33 DOMAIN IS REQUIRED BY B1X, B1D, BAK, BAD AND				
BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION				
WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.				
APOPTOTIC MEMBERS OF THE BCL-2 FAMILY (BY SIMILARITY).				
-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 1 (B1).				
-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 2 (B2).				
-1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 3 (B3).				
-1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.				
CC This SWISS-PROT entry is copyright. It is produced through a collaboration				
between the Swiss Institute of Bioinformatics and the EMBL outstation -				
the European Bioinformatics Institute. There are no restrictions on its				
use by non-profit institutions as long as its content is in no way				
modified and this statement is not removed. Usage by and for commercial				
entities requires a license agreement (See http://www.isb-sib.ch/announce/				
or send an email to license@sib-sib.ch).				
CC EMBL; 092569; AAC48806.1; ..				
CC HSPF; 007817; IMAZ.				
CC InterPro; IPR002475; BCL2_family.				
CC InterPro; IPR000712; BCL2.				
CC Pfam; PF00452; Bcl-2; 1.				

[illegible]

CC	APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC	-1 DISEASE: DEFECTS IN BAX ARE FOUND IN SOME PATIENTS WITH T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA.
CC	-1 SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 1 (BH1).
CC	-1 SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 2 (BH2).
CC	-1 SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 3 (BH3).
CC	-1 SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC	-1 SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	DR EMBL: L22473; AAA03619.1; -
DR	PIR: A47538; A47538.
DR	HSSP: Q07817; IMAZ.
DR	MIM: 600040; -
DR	InterPro: IPR002475; BCL2_family.
DR	InterPro: IPR007012; BCL2_
DR	Pfam: PF00452; Bcl-1; -
DR	SMART: SM00337; BCL2_1.
DR	PROSITE: PS50062; BCL2_FAMILY; 1.
DR	PROSITE: PS01080; BH1; 1.
DR	PROSITE: PS01258; BH2; 1.
DR	PROSITE: PS01259; BH3; 1.
KW	DOPAInsis; Transmembrane; Alternative splicing; Disease mutation.
FT	DOPAInsis 59 73 BH3.
FT	DOMAIN 98 128 BH1.
FT	DOMAIN 150 165 BH2.
FT	TRANSMEM 172 192 POTENTIAL.
FT	VARIANT 67 67 G->R (IN T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA)
FT	LEUKEMIA) /FTID=VAR_007809
SO	SEQUENCE 192 AA; 21184 MW; 6C0CD80A7DEB4994 CRC64;
Oy	1 ODASTKISSECKRIKDDELDSNMATOR 27
Db	52 ODASTKISSECKRIKDDELDSNMATOR 78
RESULT 3	
ID	BAXH.HUMAN STANDARD: PRT: 218 AA.
AC	00781d:
DT	01-FEB-1995 (Rel. 31, Created)
DT	01-FEB-1995 (Rel. 31, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
GN	Apoptosis regulator BAX, cytoplasmic isoform beta.
DN	BAX.
OS	Homo sapiens (human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBT_Taxid=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISUOE-B-cell1.
RX	MEDLINE=93364978; PubMed=9358790;
RA	Oliva J.Z.N., Millman C.L., Korsmeyer S.J.;
RT	"Bcl-2 heterodimerizes in vivo with a conserved homolog, bax, that accelerates programmed cell death.";
RL	Cell 74:609-619(1993).
CC	-1 FUNCTION: ACCELERATES PROGRAMED CELL DEATH BY BINDING TO, AND ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIUS HOMOLOG ELB 19k PROTEIN.
CC	-1 SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,

```
CC E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.
CC -1- SUBCELLULAR LOCATION: CYTOSOLASMIC.
CC -1- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOPROPH ALPHA AND THE THREE
CC CYTOSOLASMIC ISOPROPHS: BETA, GAMMA AND DELTA ARE GENERATED BY
CC ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
CC -1- DOMAIN: INTERACT BHL DOMAIN IS REQUIRED BY BIK, BID, BAX, BAD AND
CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 1 (BHL).
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 2 (BH2).
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 3 (BH3).
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L23474; AAA03620.1; .
DR PIR: B47536; B47538.
DR HSP: Q07817; LMAZ.
DR MIM: 600040; .
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR007112; Bcl_2.
DR Pfam: PF00452; Bcl-2; 1.
DR SMART: SM00337; BCL; 1.
DR PROSITE: PS01080; BHL; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS5062; BCL2_FAMILY; 1.
DR APOPTOSIS: Alternative splicing.
DR DOMAIN: 59 73 BH3.
DR DOMAIN: 98 118 BHL.
DR DOMAIN: 150 165 BH2.
DR SEQUENCE 218 AA; 24220 MW; F69DCD70F960192F CRC64;
QY 1 QDASTKRLSECLKRIQDELSDNNEIQR 27
DB 52 QDASTKRLSECLKRIQDELSDNNEIQR 78
RESULT 4
ID BAXA_MOUSE STANDARD: PRT; 192 AA.
AC Q07813;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Apoptosis regulator Bax, membrane isoform alpha.
GN BAX.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
OX NCBI_TaxID=10090;
RN [1]
RP STRAIN=C57BL/6 x DBA/2;
RX MEDLINE=93364978; PubMed=8358790;
RA Olvera L.N., Mijimnen C.L., Korsmeyer S.J.;
RT "Bcl-2 heterodimerizes in vivo with a conserved homolog, Bax, that
RL accelerates programmed cell death."
RL Cell 74:609-619(1993).
CC -1- FUNCTION: ACCELERATES PROGRAMED CELL DEATH BY BINDING TO, AND
```

```
CC ANTAGONIZING THE APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS
CC HOMOLOG E1B 19K PROTEIN, INDICES THE RELEASE OF CYTOCHROME C,
CC ACTIVITY OF CASPASE-3, AND THEREBY APOPTOSIS. BAX DEFICIENCY
CC LEADS TO LYMPHOID HYPERPLASIA AND MALE STERILITY, BECAUSE OF THE
CC CESSATION OF SPERM PRODUCTION.
CC -1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2.
CC E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.
CC -1- SUBCELLULAR LOCATION: Membrane bound.
CC -1- ALTERNATIVE PRODUCTS: A 21 KDa MEMBRANE GENERATED BY ALTERNATIVE
CC SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
CC -1- DOMAIN: INTERACT BHL DOMAIN IS REQUIRED BY BIK, BID, BAX, BAD AND
CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 1 (BHL).
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 2 (BH2).
CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 3 (BH3).
CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L23472; AAA03622.1; .
DR HSP: Q07817; LMAZ.
DR MD: MGI:99702; Bax.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR007112; Bcl_2.
DR Pfam: PF00452; Bcl-2; 1.
DR SMART: SM00337; BCL; 1.
DR PROSITE: PS01080; BHL; 1.
DR PROSITE: PS01258; BH2; 1.
DR PROSITE: PS01259; BH3; 1.
DR PROSITE: PS5062; BCL2_FAMILY; 1.
DR APOPTOSIS: Transmembrane; Alternative splicing.
DR DOMAIN: 59 73 BH3.
DR DOMAIN: 98 118 BHL.
DR DOMAIN: 150 165 BH2.
DR TRANSMEM 172 192
DR SEQUENCE 192 AA; 21394 MW; D2E0B3566579FAFF CRC64;
QY 1 QDASTKRLSECLKRIQDELSDNNEIQR 27
DB 52 QDASTKRLSECLKRIQDELSDNNEIQR 78
RESULT 5
ID BAXA_RAT STANDARD: PRT; 192 AA.
AC Q63690; Q62995; Q64383;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Apoptosis regulator Bax, membrane isoform alpha.
GN BAX.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96178771; PubMed=8600029;
```

RA Han J., Sabbatini P., Perez D., Rao L., Modha D., White E.:
 "The Bcl-2 protein blocks apoptosis by interacting with and
 inhibiting the p53-inducible and death-promoting Bax protein.";
 RL Genes Dev. 10:461-477(1996).
 RN (12)
 RN SEQUENCE OF 75-192 FROM N.A.
 RC TISSUE-BRAIN:
 RC MEDLINE-97147318; PubMed-8994223;
 RA Madison D.L., Pfeiffer S.E.:
 RA "Cloning of the 3' end of rat bax-alpha and corresponding
 RA developmental down-regulation in differentiating primary, cultured
 RA oligodendrocytes";
 RA Neurosci. Lett. 220:183-186(1996).
 RN (13)
 RP SEQUENCE OF 37-169 FROM N.A.
 RP STRAIN-SPRAGUE-DAWLEY; TISSUE-Ovary:
 RX MEDLINE-95129487; PubMed-7828536;
 RX Tilly J.L., Tilly K.L., Kenion M.L., Johnson A.L.:
 RA "Expression of members of the bcl-2 gene family in the immature rat
 RA ovary: equine chorionic gonadotropin-mediated inhibition of granulosa
 RA cell apoptosis is associated with decreased bax and constitutive
 RA bcl-2 and bcl-2 messenger ribonucleic acid levels.";
 RL Endocrinology 136:243-241(1995).
 RL "FUNCTION: ACCELERATES PROGRAMED CELL DEATH BY BINDING TO, AND
 ANTAGONIZING, APOPTOSIS REPRESSOR BCL-2 OR ITS ADENOVIRUS
 CC HOMOLOG E1B 19K PROTEIN. INDUCES THE RELEASE OF CYTOCHROME C,
 CC ACTIVATION OF CASPASE-3, AND THEREBY APOPTOSIS.
 CC -1- SUBUNIT: FORMS HOMODIMERS AND HETERODIMERS TOGETHER WITH BCL-2,
 CC E1B 19K PROTEIN, BCL-X(L), MCL-1 AND A1.
 CC -1- SUBCELLULAR LOCATION: Membrane protein and
 CC -1- ALTERNATIVE PRODUCTS: A 21 KDa MEMBRANE PROTEIN ALPHA AND THE TWO
 CC CYTOPLASMIC PROTEINS BETA AND GAMMA ARE GENERATED BY ALTERNATIVE
 CC SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES. WITH
 CC HIGHEST LEVELS IN THE TESTES AND OVARY.
 CC -1- DOMAIN: INTERACT BAX DOMAIN IS REQUIRED BY BAX, BID, BAK, BAD AND
 CC BAX FOR THEIR PRO-APOPTOTIC ACTIVITY AND FOR THEIR INTERACTION
 CC WITH ANTI-APOPTOTIC MEMBERS OF THE BCL-2 FAMILY.
 CC APOPTOTIC MEMBERS OF THE BCL-2 FAMILY
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 1 (BH1).
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG DOMAIN 2 (BH2).
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: U49729; AAC26327.1; -
 DR EMBL: U59184; AAC52988.1; -
 DR EMBL: U32098; AAC75200.1; -
 DR EMBL: S76511; AAC60700.2; -
 DR HSSP: G07817; 1MAZ.
 DR InterPro: IPR002475; BCL2_family.
 DR InterPro: IPR000712; BCL2.
 DR Pfam: PF00452; BCL-2; 1.
 DR SMART: SM00337; BCL; 1.
 DR PROSITE: PS01080; BH1; 1.
 DR PROSITE: PS01258; BH2; 1.
 DR PROSITE: PS01259; BH3; 1.
 DR PROSITE: PS50062; BCL2_FAMILY; 1.
 DR Apoptosis; Transmembrane; Alternative splicing.
 KW DOMAIN 59 73 BH3.
 FT DOMAIN 98 118 BH1.
 FT DOMAIN 150 165 BH2.
 FT TRANSMEM 172 192
 FT CONFLICT 72 72 S -> N (IN REF. 3).
 FT CONFLICT 76 76 L -> M (IN REF. 2).
 FT CONFLICT 126 126 C -> Y (IN REF. 2).

FT CONFLICT 149 149 L -> F (IN REF. 3).
 FT CONFLICT 159 159 D -> E (IN REF. 1).
 SQ SEQUENCE 192 AA; 21350 MW; 7B3CD19B56F589 CRC64;
 Query Match 97.8%; Score 132; DB 1; Length 192;
 Best Local Similarity 96.3%; Pred. No. 4, 36-11;
 Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QDASTKRLSECLRTGDELDNMELQ 27
 DB 52 QDASTKRLSECLRTGDELDNMELQ 78
 RESULT 6
 YAG4_HAEIN STANDARD; PRT; 485 AA.
 ID YAG4_HAEIN
 AC P71367;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein H11064.
 GN H11064.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellales;
 OC Haemophilus.
 NC NCBI_Taxid=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-RD / KW20 / ATCC 51907;
 RX MEDLINE-5530630; PubMed-7542800;
 RX Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RX Kerlavage A.R., Bult C.J., Tomb J.F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shiley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Uiterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Lierke L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.:
 FT "Whole-genome random sequencing and assembly of Haemophilus
 FT influenzae Rd.";
 RL Science 269:496-512(1995).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).
 CC -1- SIMILARITY: BELONGS TO THE UPF0141 FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: U32786; AAC2718.1; -
 DR DR TIGR: H11064
 DR InterPro: IPR003371; DUF146.
 DR Pfam: PF02418; DUF146; 1.
 KW Hypothetical protein; Transmembrane; Complete proteome.
 FT TRANSMEM 33 73
 FT TRANSMEM 35 75 POTENTIAL.
 FT TRANSMEM 81 101 POTENTIAL.
 FT TRANSMEM 125 145
 FT TRANSMEM 145
 SQ SEQUENCE 485 AA; 55401 MW; 3C0D8285C64D5F55 CRC64;
 Query Match 38.5%; Score 52; DB 1; Length 485;
 Best Local Similarity 45.5%; Pred. No. 8, 1;
 Matches 10; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
 QY 3 ASTRKLSCLKRTGDELDNSME 24
 DB 402 SSIRKTFEFLKRVYDQLEENVK 423

```

RESULT 7
GAP_YEAST
ID GATA_YEAST STANDARD; PRT; 471 AA.
AC F17649;
DT 01-NOV-1990 (Rel. 15, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 4-aminobutyrate aminotransferase (EC 2.6.1.19) (Gamma-amino-N-butyrate
transaminase) (GABA transaminase) (GABA aminotransferase) (GABA-AT).
GN UGAI OR YGR019W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycos.
OX NCBI_Taxid=4932;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=1278B;
RX MEDLINE=90272415; PubMed=2190186;
RA Andre B., Jaumaux J.-C.;
RT "Nucleotide sequence of the yeast UGAI gene encoding GABA
transaminase.";
RL Nucleic Acids Res. 18:3049-3049(1990).
RN 12;
RP SEQUENCE FROM N.A.
RC STRAIN=5288C;
RX MEDLINE=97435481; PubMed=9290212;
RA Rieger M., Brueckner M., Schaefer M., Mueller-Auer S.;
RT "Sequence analysis of 203 kilobases from saccharomyces cerevisiae
chromosome VII.";
RL Yeast 13:1077-1090(1997).
CC -1- CATALYTIC ACTIVITY: 4-aminobutanoate + 2-oxoglutarate -> succinate
semialdehyde + L-glutamate.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- SUBUNIT: HOMODIMER (POSSIBLE).
CC -1- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT
AMINOTRANSFERASES.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation-
at the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@sib-sib.ch).
-----
CC EMBL: X52600; CA36833.1; -
CC EMBL: Z72804; CA97002.1; -
CC FTR: S26708; S26708.
CC HSSP: P80147; IGTX.
CC SCD: S0003251; UGAI.
CC InterPro: IPR000954; Aminotran_3.
CC Pfam: PF00202; aminotran_3; 1.
CC PROSITE: PS00600; AA-TRANSFER-CLASS_3; 1.
CC Transfaser: Aminotransferase; pyridoxal phosphate.
CC BINDING 326 326 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC CONFLICT 240 240 H -> R (IN REF. 1).
CC SEQUENCE 471 AA; 52946 MW; 33D446778A91F63 CRC64;

```

```

Query Match 38.1%; Score 51.5; DB 1; Length 471;
Best Local Similarity 46.4%; Pred. No. 9.2;
Matches 13; Conservative 5; Mismatches 9; Indels 1; Gaps 1;

```

```

OY 1 ODASTFKLSPLCKRIGDELDSNNE-LOR 27
   1:| | | | | | | | | | | | | | | |
Db 367 DEISDKLTBOCSRVGYOLPKKLEGLQK 394

```

```

RESULT 8
SP10_HUMAN STANDARD; PRT; 879 AA.
ID SP10_HUMAN

```

```

AC P23497; Q13343; O75450; Q9UE32;
DT 01-NOV-1991 (Rel. 20, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Nuclear autoantigen Sp-100 (speckled 100 kDa) (Nuclear dot-associated
Sp100 protein) (Lysp100b).
GN Sp100.
OS Homo sapiens (Human).
OC Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN 1;
RP SEQUENCE FROM N.A. (ISOFORN SP100-HMG).
RC TISSUE=breast cancer;
RX MEDLINE=98301571; PubMed=9636146;
RA Seeler J.-S., Marchio A., Sitterlin D., Treacy C., Dejean A.;
RT "Interaction of Sp100 with HPI proteins: a link between the
promyelocytic leukemia-associated nuclear bodies and the chromatin
compartment.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:7316-7321(1998).
RN 12;
RP SEQUENCE FROM N.A. (ISOFORN SP100-A).
RC TISSUE=Liver, and Placenta;
RX MEDLINE=91079525; PubMed=2258622;
RA Szosteck C., Guldner H.H., Netter H.J., Will H.;
RT "Isolation and characterization of cDNA encoding a human nuclear
antigen predominantly recognized by autoantibodies from patients with
primary biliary cirrhosis.";
RL J. Immunol. 145:4338-4347(1990).
RN 13;
RP SEQUENCE FROM N.A. (ISOFORN SP100-B).
RX MEDLINE=96329378; PubMed=8695863;
RA Gent A.L., Tewdell J., Fuyton-Dullileul F., Koken M.H.M., de The H.,
RA Standt L.M.;
RT "Sp100-associated nuclear domains (LANDs): description of a new
class of subnuclear structures and their relationship to PML nuclear
bodies.";
RL Blood 88:1423-1426(1996).
RN 14;
RP SEQUENCE OF 1-10 FROM N.A.
RC TISSUE=Lymphoma;
RX MEDLINE=96411734; PubMed=8810287;
RA Groetzinger T., Jensen K., Will H.;
RT "The interferon (IFN)-stimulated gene Sp100 promoter contains an IFN-
gamma activation site and an imperfect IFN-stimulated response element
that mediate type I IFN inducibility.";
RL J. Biol. Chem. 271:25253-25260(1996).
RN 15;
RP ALTERNATIVE SPLICING (ISOFORMS SP100-B; SPALT-C AND SP100-HMG).
RC TISSUE=Cervical adenocarcinoma;
RX MEDLINE=99141186; PubMed=9973607;
RA Guldner H.H., Szosteck C., Schroeder P., Matschl U., Jensen K.,
RA Lueders C., Will H., Sternsdorf T.;
RT "Splice variants of the nuclear dot-associated Sp100 protein contain
homologues to HMG-1 and a human nuclear phosphoprotein-box motif.";
RL J. Cell Sci. 112:733-747(1999).
RN 16;
RP CHARACTERIZATION, AND COVALENT BINDING TO SUMO-1.
RX MEDLINE=99230277; PubMed=10212234;
RA Sternsdorf T., Jensen K., Reich B., Will H.;
RT "The nuclear dot protein sp100, characterization of domains necessary
for dimerization, subcellular localization, and modification by small
ubiquitin-like modifiers.";
RL J. Biol. Chem. 274:12555-12566(1999).
RN 17;
RP FUNCTION: MAY PLAY A ROLE IN THE CONTROL OF GENE EXPRESSION.
CC -1- SUBUNIT: HOMODIMER. SPLICED VARIANTS HETEROOMERIZE, INTERACT WITH
MEMBERS OF THE HPI FAMILY OF NONHISTONE CHROMOSOMAL PROTEIN, SUCH
AS HETEROCHROMATIN PROTEIN 1 ALPHA (HP1-ALPHA) AND HETEROCHROMATIN
PROTEIN 1-GAMMA (HP1-GAMMA).
CC -1- SUBCELLULAR LOCATION: NUCLEAR. FOUND IN THE NUCLEAR BODY, ALSO
KNOWN AS NUCLEAR DOMAIN 10 (ND10), PML ONCOGENIC DOMAIN (POD),
NUCLEAR DOTS, (ND) AND KR BODY. THE NUCLEAR BODY IS A NUCLEOPLASMIC
STRUCTURE OF PUNCTATE SHAPE, WHICH VARIES IN SIZE AND NUMBER.

```

FT	VARIANT	433		433	M -> V (IN HELA CELLS).
FT	VARIANT	471		471	/PIDD-VAR_005621.
FT	VARIANT	471		471	S -> P (IN HELA CELLS).
FT	CONFLICT	292		292	/PIDD-VAR_005622.
FT	CONFLICT	651		651	R -> Q (IN REF. 4).
SO	SEQUENCE	879 AA:	100416 MW;	CA55547DE21B2A10 CRC64;	A -> R (IN REF. 4).
OY	Query Match				
	Best Local Similarity 33.3%; Score 51; DB 1; Length 879;				
	Matches 10; Conservative 10; Mismatches 6; Indels 4; Gaps 1.				
Db	2 DASTKTLSECLKRIGDELDD---SNMELOR 27 :: :: :: DLSRRRLNLCISPVANENHNPRAHSIDLOR 36				
RESULT	TPC_BRALA				
ID	TPC_BRALA	STANDARD;	PRT;	163 AA.	
AC	P80322;				
DT	01-JUN-1994 (Rel. 29, Created)				
DT	01-JUN-1994 (Rel. 29, Last sequence update)				
DT	01-NOV-1997 (Rel. 35, Last annotation update)				
DE	Tropoin C.				
OS	Branchiostoma lanceolatum (Common lancelet) (Amphioxus).				
OC	Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;				
OX	Branchiostoma.				
NCBI_Taxid=740;					
LN	[1]				
RP	SEQUENCE.				
RE	TISSUE=Muscle;				
RX	MEDLINE=U4422102; PubMed=8166542;				
RA	Takagi T., Petrova T., Comte M., Kuster T., Heizmann C.W., Cox J.A.;				
CC	*Characterization and primary structure of amphioxus tropoin C.*;				
RL	Eur. J. Biochem. 221:537-546(1994).				
CC	-I- FUNCTION: TROPONIN IS THE CENTRAL REGULATORY PROTEIN OF STRIATED				
CC	MUSCLE CONTRACTION. TN CONSISTS OF THREE COMPONENTS: TN-I WHICH				
CC	IS THE INHIBITOR OF ACTOMYOSIN ATPASE. TN-T WHICH CONTAIN THE				
CC	BINDING SITE FOR TROPOMYOSIN AND TN-C. THE BINDING OF CALCIUM TO				
CC	TN-C ABOLISHES THE INHIBITORY ACTION OF TN ON ACTIN FILAMENTS.				
CC	-I- MISCELLANEOUS: THIS PROTEIN BINDS THREE CALCIUM IONS.				
CC	-I- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.				
DR	HSPG; PI0246; 1TRF.				
DR	InterPro: IPRO02048; EF-hand.				
DR	pfam: PF00036; efpnd: 4.				
DR	SMART: SMO0054; EPH: 4.				
KW	PROSITE: PS00018; EF HAND: 3.				
KW	Muscle protein; Calcium-binding; Acetylation; Methylation.				
FT	MOD_RES	1	1	20	ACETYLATION (ON THE MAJORITY OF CHAINS).
FT	MOD_RES	20	20	20	METHYLATION (MONO- AND DI-).
FT	CA_BIND	27	78	74	EF-HAND 1 (BY SIMILARITY).
FT	CA_BIND	63	74	74	EF-HAND 1 (BY SIMILARITY).
FT	CA_BIND	103	114	114	EF-HAND 2 (BY SIMILARITY).
FT	DOMAIN	140	151	151	EF-HAND 3 (BY SIMILARITY).
FT	DOMAIN	140	151	151	ANCESTRAL CALCIUM SITE 4 (POTENTIAL).
SO	SEQUENCE	163 AA;	19041 MW;	ABEF4359PBIDBA0 CRC64;	
OY	Query Match				
	Best Local Similarity 35.2%; Score 47.5; DB 1; Length 163;				
	Matches 12; Conservative 5; Mismatches 8; Indels 1; Gaps 1.				
Db	2 DASTKTLSECLKRIGDELDDSNMELOR 27 :: :: :: DISTRELTKIRKLGNST-SNEELDQ 57				
RESULT	RBSK_BACHD				
ID	RBSK_BACHD	STANDARD;	PRT;	294 AA.	
AC	O9K6K1;				
DT	01-MAR-2002 (Rel. 41, Created)				

DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Ribokinase (EC 2.7.1.15).
GN RBSK OR BH3728.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group.
OC Bacillus/Staphylococcus group; Bacillus.
OC NCBI_TaxID=86605;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C-125 / JCM 9153.
RX MEDLINE=50512582; PubMed=11058132.
RA Takami H., Nakase K., Takaki Y.,
RA Fuji F., Hirazawa C., Nakamura Y., Ogasawara N., Kubera S.,
RA Hotchkiss K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
CC -1- CATALYTIC ACTIVITY: ATP + D-ribose -> ADP + D-ribose 5-phosphate.
CC -1- PATHWAY: FIRST STEP IN RIBOSE METABOLISM.
CC -1- SUBCELLULAR LOCATION: CYTOSOL (by similarity).
CC -1- SIMILARITY: BELONGS TO THE PFKB FAMILY OF CARBOHYDRATE KINASES.
CC
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by, and for commercial entities requires a license agreement (See <http://www.isb-sdb.cn/announce/> or send an email to license@isb-sdb.cn).
CC
DR EMBL: AP001519; BAB07447.1; -
DR HSRP: P05054; 1XKD
DR InterPro: IPR002173; PFKB.
DR InterPro: IPR002139; RIBOKINASE.
DR Pfam: PR00264; PFKB; 1
DR PRINTS: PR00990; RIBOKINASE.
DR PROSITE: PS00583; PFKB_KINASES_1; 1.
DR PROSITE: PS00584; PFKB_KINASES_2; 1.
KW Transferase; kinase; Complete proteome.
KW SEQUENCE 294 AA; 31089 MW; 8C13FD0F5E89FDE CRC64;
SO
Query Match 34.8%; Score 4.7; DB 1; Length 294;
Best Local Similarity 53.3%; Pred. No.23;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
CY 9 SECTKRIQDEQDSNM 23
DB 187 NECTGAFDEPDANL 201
DB
RESULT 11
AC MDH_METPE STANDARD: PRT; 339 AA.
AC P16142;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Malate/L-sulfolactate dehydrogenase (EC 1.1.1.37) (EC 1.1.1.82).
GN MDH.
OS Methanothermus fervidus.
OC Archaea; Euryarchaeota; Methanobacteriales; Methanothermaceae;
OC Methanothermus.
OC NCBI_TaxID=2180;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-24.
RX STRAIN=V245 / DSM 2088;
RX MEDLINE=90235834; PubMed=2110059;
RA Honka E., Fabry S., Niemann T., Palm P., Hensel R.;
RT "Properties and primary structure of the L-malate dehydrogenase from the extremely thermophilic archaeobacterium Methanothermus fervidus."; Eur. J. Biochem. 188:623-632(1990).

FN [2]
 FN FUNCTION.
 RX MEDLINE=20309698; PubMed=10850983;
 RA Graupner M., Xu H., White R.H.;
 RT Identification of an archaeal 2-hydroxy acid dehydrogenase catalyzing
 RT reactions involved in coenzyme b₁₂ synthesis in methanocorphaea.¹
 RL J. Bacteriol. 182:3688-3692(2000).
 CC -1. FUNCTION: Acts on oxaloacetate, sulfofumarate but not on pyruvate.
 CC Has a higher selectivity for the coenzyme NADH than for NADPH.
 CC -1. CATALYTIC ACTIVITY: (S)-malate + NAD(P)(+) = oxaloacetate +
 CC NAD(P)H.
 CC -1. CATALYTIC ACTIVITY: (P)-sulfolactate + NAD(P)(+) = sulfofumarate +
 CC NAD(P)H.
 CC -1. SUBUNIT: Homodimer.
 CC -1. SUBCELLULAR LOCATION: CYTOSOL;Mitochondrion.
 CC -1. SIMILARITY: BELONGS TO THE Ldh2/Mdh2 OXIDOREDUCTASE FAMILY.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sdb.ch/announce/>
 CC or send an email to license@sdb-sdb.ch).
 CC -----
 DR EMBL: X51714; CAA36010.1; -
 DR EMBL: X51840; CAA38133.1; -
 DR PIR: S08689; S08689.
 DR PIR: S08581; S08581.
 DR InterPro: IPR00367; Ldh_2.
 DR Pfam: PF02615; Ldh_2; 1.
 DR OXOREDUCTASE; Hydroxybutyrate acid cycle; NAD, NADP.
 SQ SEQIDW 335 AA; 35762 MW; 23190822DB275835 CRC64.

Query Match 34.98; Score 47; DB 1; Length 339;
 Best Local Similarity 65.08; Mot 27;
 Matches 13; Conservative 1; Mismatches 4; Indels 2; Gaps 1;
 Oy 6 KSLSEKRIKDELDSDNML 25
 Db 320 KKLVEKRIADEL--NIEL 337
 ||| ||||| ||||| |||||

RESULT 12
 MCL1_HUMAN STANDARD: PRT; 350 AA.
 ID MCL1_HUMAN
 AC 007820; OGNRO3; OGNRO4;
 DT 01-FEB-1995 (Ref. 31, Created)
 DT 16-OCT-2001 (Ref. 40, Last sequence update)
 DT 16-OCT-2001 (Ref. 40, Last annotation update)
 GN Induced myeloid leukemia cell differentiation protein Mcl-1.
 GN MCL1.
 OS Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Myeloid Leukemia cells;
 RX MEDLINE=9334528; PubMed=7682708;
 RA Kozopas K.M., Yang T., Buchan H.L., Zhou P., Craig R.W.;
 RA "Mcl-1, a gene expressed in programmed myeloid cell differentiation,
 RT has sequence similarity to Bcl-2".
 RT Proc. Natl. Acad. Sci. U.S.A. 90:3516-3520(1993).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX MEDLINE=20357335; PubMed=10765760;
 RA Bingle C.D., Craig R.W., Swales B.M., Singleton A., Zhou P.,
 RA Whyte M.K.B.;
 RA "Exon skipping in Mcl-1 results in a Bcl-2 homology domain 3 only gene
 RT product that promotes cell death".
 RT J. Biol. Chem. 275:22136-22146(2000).
 RL [1]

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-slb.ch/announce/> or send an email to license@isb-slb.ch).

EMBL: Y00689; CA68685.1; -
 EMBL: X04324; CA27855.1; -
 PIR: S00103; PADOA.
 HSP: 001082; 1BR.
 DICTYDB: DP01003; abpa.
 InterPro: IPR001589; Actinin act.bind.
 InterPro: IPR001715; Calponin_hom.
 InterPro: IPR002048; EF-hand.
 InterPro: IPR002017; Spectrin.
 Pfam: PF00307; CH: 2.
 Pfam: PF00036; ethand: 2.
 Pfam: PF00435; spectrin: 4.
 SMART: SM00033; CH: 2.
 SMART: SM00054; EFb: 2.
 PROSITE: PS00019; ACTININ_1; 1.
 PROSITE: PS00020; ACTININ_2; 1.
 PROSITE: PS50021; CH: 2.
 PROSITE: PS00018; EF_HAND; 2.
 Actin-binding; Calcium-binding; Repeat.
 DOMAIN 1 240 ACTIN-BINDING.
 DOMAIN 22 128 CH 1.
 DOMAIN 137 240 CH 2.
 REPEAT 241 366 SPECTRIN 1.
 REPEAT 367 481 SPECTRIN 2.
 REPEAT 482 602 SPECTRIN 3.
 REPEAT 603 715 SPECTRIN 4.
 CA_BIND 743 754 EF-HAND 1 (BY SIMILARITY).
 CA_BIND 779 790 EF-HAND 2 (BY SIMILARITY).
 CONFLICT 360 360 T->P (IN REF. 2).
 CONFLICT 501 501 I->T (IN REF. 2).
 SEQUENCE 862 AA: 97598 MW: 15608ADB71213226 CRC64;

Query Match 34.8%; Score 47; DB 1; Length 862;
 Best Local Similarity 69.2%; Pred. No. 68;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 7 KLSCKLRIGDEL 19
 : | | | | | | | | | |
 DB 754 EFSSCKLSIGDEL 766

RESULT 15
 YDK9_SCHPO
 ID YDK9_SCHPO STANDARD: PRT: 1033 AA.
 AC PE7115;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Hypothetical 116.5 kDa protein G2068.09c in chromosome I.
 GN SPAC2068.09c.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes;
 NCBI_TaxID:4896;
 [1]
 SEQUENCE FROM N.A.
 STRAIN:972;
 RC Badcock K., Churcher C.M., Wood V., Barrell B.G., Rajandream M.A.,
 RA Submitted (May-1997) to the EMBL/GenBank/DBJ databases.
 CC -! SIMILARITY: TO YFAST YNL132W AND AN A.AMBISEXUALIS HYPOTHETICAL
 CC PROTEIN (AC P54008).
 CC -----

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-slb.ch/announce/> or send an email to license@isb-slb.ch).

EMBL: Z65334; CA80603.1; -
 KW Hypothetical protein: ATP-binding.
 NP_BIND 282 289 ATP (POTENTIAL)
 SQ SEQUENCE 1033 AA: 116463 MW: 8432B313DB1BE135 CRC64;

Query Match 34.1%; Score 46; DB 1; Length 1033;
 Best Local Similarity 52.4%; Pred. No. 11e+02;
 Matches 11; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

OY 6 KXLSCKLRIGDELSDNNELO 26
 : | | | | | | | | | |
 DB 661 KAVKSLKRIKIGDELENTNADL 681

Search completed: September 20, 2002, 11:04:30
 Job time: 1627 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2002, 11:03:36 ; Search time 172.19 Seconds
(without alignments)
27.126 Million cell updates/sec

Title: US-09-544-664-6
135
Sequence: 1 ODASTRKLSKRIKRGIDELSDNMLQK 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: SP:archae:.*
2: SP:Bacteria:.*
3: SP:fungi:.*
4: SP:human:.*
5: SP:invertebrate:.*
6: SP:mammal:.*
7: SP:mnc:.*
8: SP:organelle:.*
9: SP:phase:.*
10: SP:plant:.*
11: SP:rodent:.*
12: SP:virus:.*
13: SP:vertebrate:.*
14: SP:unclassified:.*
15: SP:ivrus:.*
16: SP:bacteriap:.*
17: SP:archaeap:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	135	100.0	149	6	O9GMG7	O9gm7 ovls aries
2	135	100.0	164	9	O9GUD6	O9gud6 homo sapien
3	135	100.0	179	4	O9NYG7	O9ny77 homo sapien
4	129	95.6	173	11	O9JRL3	O9jrl3 rattus norv
5	107	79.3	221	13	O98U13	O98u13 xenopus lae
6	83	61.5	192	13	O919N4	O919n4 brachydanto
7	66	48.0	15	4	O9UC27	O9uc27 homo sapien
8	54	40.0	1124	12	O9DVM1	O9dvm1 pluteella xy
9	53	39.3	913	5	O94893	O94893 drosophila
10	53	39.3	1861	5	O9VF02	O9vf02 drosophila
11	52	38.5	575	10	O9SL17	O9sl17 arabidopsis
12	51	37.8	427	2	O30773	O30773 treponema p
13	51	37.8	480	4	O96F70	O96f70 homo sapien
14	51	37.8	845	16	O83501	O83501 treponema p
15	51	37.8	885	4	O96F95	O96f95 homo sapien
16	51	37.8	1252	5	O9VTY9	O9vty9 drosophila

17	50	37.0	614	5	O06270	O06270 onmastrebre
18	50	37.0	948	5	O9VQ7	O9vq7 drosophila
19	50	37.0	1184	10	O9LU07	O9lu07 arabidopsis
20	50	37.0	1219	10	O9LH84	O9lh84 arabidopsis
21	49.5	36.7	675	5	O9VS46	O9vs46 drosophila
22	49.5	36.7	724	5	O961W7	O961w7 drosophila
23	49	36.3	196	10	O94B03	O94b03 arabidopsis
24	49	36.3	286	5	O27341	O27341 arabidopsis
25	49	36.3	311	10	O9LMB2	O9lmb2 arabidopsis
26	49	36.3	342	10	O9LMB3	O9lmb3 arabidopsis
27	49	36.3	527	12	O9JGP5	O9jgp5 epiloctic h
28	49	36.3	665	4	O9H9N3	O9h9n3 homo sapien
29	49	36.3	669	17	O9YU18	O9yu18 sulfolobus
30	49	36.3	718	10	O9LE10	O9le10 arabidopsis
31	49	36.3	732	5	O27480	O27480 caenorhabd
32	49	36.3	740	16	O9PC07	O9pc07 xyella fas
33	48.5	35.9	213	12	O91MS6	O91ms6 lumpy skin
34	48	35.6	126	5	O95230	O95230 plasmodium
35	48	35.6	1098	5	O9VB48	O9vb48 drosophila
36	48	35.6	1814	5	O9B1M9	O9bm9 toxocara ca
37	48	35.6	1957	5	O04009	O04009 brugia mala
38	48	35.6	1957	5	O04010	O04010 onchocerca
39	47.5	35.2	164	5	P92198	P92198 branchiosto
40	47.5	35.2	164	5	P90687	P90687 human immun
41	47	34.8	72	15	O9YR06	O9yr06 human immun
42	47	34.8	92	4	O9UHR7	O9uhr7 homo sapien
43	47	34.8	94	4	O9UHR7	O9uhr7 homo sapien
44	47	34.8	108	4	O9UHR8	O9uhr8 homo sapien
45	47	34.8	217	17	O58748	O58748 pyrococcus

ALIGNMENTS

RESULT 1

ID	OGMG7	PRELIMINARY:	PRT:	149 AA.
AC	O9GMG7			
DC	01-MAR-2001 (TREMBLrel, 16, Created)			
DT	01-MAR-2001 (TREMBLrel, 16, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel, 19, Last annotation update)			
DE	BCL2-ASSOCIATED PROTEIN BAX (FRAGMENT).			
GN	BAX.			
OS	Ovis aries (Sheep).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Caprinae; Ovis.			
OX	NCBI_TaxID=9940;			
RN	[1]_TaxID=9940;			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=OVARY;			
RA	Murray J.F., Dong Y.B., Leigh A.J., Scaramuzza R.J., Carter N.D.;			
RT	"Bax in the sheep ovary."			
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AF163774; MAF98242.1; -			
DR	HSSP: O07817; IMA2.			
DR	InterPro: IPR002475; BCL2_family.			
DR	InterPro: IPR000712; Bcl_2.			
DR	Pfam: PF00452; Bcl-2; 1.			
DR	SMART: SM00377; BCL: 1.			
DR	PROSITE: PS5062; BCL2_FAMILY; 1.			
DR	PROSITE: PS01080; BHL; 1.			
FT	NON_TER	1		
FT	NON_TER	149		
SO	SEQUENCE	149 AA; 16917 MW; ABCL0CB5C64EA2D CRC64;		

Query Match 100.0%; Score 135; DB 6; Length 149;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ODASTRKLSKRIKRGIDELSDNMLQK 27
|||||

Db 24 QDASTKRLSECLKRIGDELDSNMELOR 50

RESULT 2
ID Q90006 PRELIMINARY: PRT: 164 AA.
AC Q90006;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE BAX EPSILON.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
MEDLINE=99120940; PubMed=9920818;
RA Shi B., Trible D., Kajiji S., Iwata K.K., Bruskin A., Mahajna J.;
RT "Identification and characterization of baxepsilon, a novel bax
variant missing the BH2 and the transmembrane domains.";
RL Blochem. Biophys. Res. Commun. 254:779-785(1999).
DR EMBL: AF007826; AD22706.1; -;
DR InterPro: IPR002475; BCL2_family.
DR Pfam: PF00452; Bcl-2; 1.
DR SMART: SM00337; BCL2.
DR PROSITE: P550062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01259; BH3; 1.
SO SEQUENCE 164 AA; 18129 MW; 12C0DB8073BFA9E CRC64;

Query Match 100.0%; Score 135; DB 4; Length 164;
Best Local Similarity 100.0%; Pred. No. 2, 4e-11;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QDASTKRLSECLKRIGDELDSNMELOR 27
Db 52 QDASTKRLSECLKRIGDELDSNMELOR 78

RESULT 3
ID Q9NYG7 PRELIMINARY: PRT: 179 AA.
AC Q9NYG7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BAX-SIGMA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
MEDLINE=20237095; PubMed=10772918;
RA Schmitt E., Paquet C., Beauchemin M., Dever-Bertrand J., Bertrand R.;
RT "Characterization of bax-sigma, a cell death-inducing isoform of
Bax.";
RL Blochem. Biophys. Res. Commun. 270:868-879(2000).
DR EMBL: AF247393; AAF71267.1; -;
DR HSSP: 007817; 1MA2.
DR InterPro: IPR002475; BCL2_family.
DR Pfam: PF00452; BCL-2; 1.
DR SMART: SM00337; BCL; 1.
DR PROSITE: P550062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01259; BH3; 1.
SO SEQUENCE 179 AA; 19718 MW; 5802B0AC73B2EACE CRC64;

Query Match 100.0%; Score 135; DB 4; Length 179;
Best Local Similarity 100.0%; Pred. No. 2, 6e-11;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QDASTKRLSECLKRIGDELDSNMELOR 27
Db 52 QDASTKRLSECLKRIGDELDSNMELOR 78

RESULT 4
ID Q9JKL3 PRELIMINARY: PRT: 173 AA.
AC Q9JKL3;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BAX PROTEIN SPLICING VARIANT K.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
Jin K., He X., Greenberg D.A., Simon R.P., Graham S.H.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF235993; AAP36411.1; -;
DR HSSP: 007817; 1MA2.
DR InterPro: IPR002475; BCL2_family.
DR Pfam: PF00452; Bcl-2; 1.
DR SMART: SM00337; BCL2.
DR PROSITE: P550062; BCL2_FAMILY; 1.
DR PROSITE: PS01080; BH1; 1.
DR PROSITE: PS01259; BH2; 1.
SO SEQUENCE 173 AA; 19661 MW; F19A45BC642C34F CRC64;

Query Match 95.6%; Score 129; DB 11; Length 173;
Best Local Similarity 92.6%; Pred. No. 1, 7e-10;
Matches 25; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 QDASTKRLSECLKRIGDELDSNMELOR 27
Db 33 QDASTKRLSECLKRIGDELDSNMELOR 59

RESULT 5
ID Q98013 PRELIMINARY: PRT: 221 AA.
AC Q98013;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE BAX.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Eupidae;
OC Xenoidea; Xenopus.
RX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
MEDLINE=21107661; PubMed=1158585;
RA Finkelstein C.V., Lewellyn A.L., Waller J.L.;
RT "The mdplastula transition in xenopus embryos activates multiple
RT pathways to prevent apoptosis in response to DNA damage.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:1006-1011(2001).
DR EMBL: AF288609; AAK06406.1; -;
DR HSSP: P53563; 1AF3.
DR InterPro: IPR002475; BCL2_family.
DR InterPro: IPR000712; BCL-2; 1.
DR Pfam: PF00452; Bcl-2; 1.

DR InterPro: IPR001410: DEAD.
 DR InterPro: IPR001650: Helicase_C.
 DR InterPro: IPR000330: SNF2_N.
 DR Pfam: PF00271: helicase_C.1.
 DR Pfam: PF00176: SNF2_N.1.
 DR SMART: SM00487: DEXDC.1.
 DR SMART: SM00490: HELIC_C.1.
 KW ATP-binding; Helicase.
 FT NON_TER
 SQ SEQUENCE 913 AA: 102160 MW: 21E7E51E559F691 CRC64:

Query Match 39.3%; Score 53; DB 5; Length 913;
 Best Local Similarity 39.1%; Pred. No. 46;
 Matches 9; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

OY 1 QDASKTKSLKRLKRGDELDSNM 23
 DB 602 EDFSKHUKDCLDKDDSSASH 624

RESULT 10

ID Q9VFC2 PRELIMINARY: PRT: 1861 AA.

OS Drosophila melanogaster (Fruit fly)

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Phyllophaga; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Phoridae; Drosophilidae; Drosophila.

NCBI_TextID=7227;

SEQUENCE FROM N.A.

RP STRAIN-BERKELEY:

RC MEDLINE-20196006: PubMed-10731132;

RA Adams M.D. Ceiliker S.E. Li P.M. Hoskins R.A. Galie R.F.

RA Ananidis P.G. Scherer S.E. Li P.M. Hoskins R.A. Galie R.F.

RA George R.A. Rogers Y.-H.C. Blazej R.C. Champo O. Chen L.X.

RA Slitton G.C. Mortman J.R. Yendall M.D. Zhang S. Ashburner M. Henderson S.N.

RA Prandon R.C. Baxter E.G. Helt G. Nelson C.R. Miklos G.L.G.

RA Abell J.F. Abayanti A. An H.-J. Andrews-Pfenkoch C. Baldwin D.

RA Bellow R.M. Basu A.V. Baxendale J. Bayraktaroglu U. Beasley E.M.

RA Beeson K.V. Berman P.V. Bhanderi D. Bolshakov S.

RA Bertels K.C. Busan D.A. Butler J. Brokstein P. Brothier P.

RA Burtis J.M. Cawley S. Dahlke C. Davenport L.B. Davies P.

RA de Pablo J.M. Delcher A. Deng Z. Mays A.D. Dew I. Dietz S.M.

RA Dodson K.J. Doup L.E. Downes M. Dugan-Rocha S. Dunlop B.C. Dunn P.

RA Foadik C. Gabrielista C.C. Ferraz C. Ferreira S. Fleischmann W.

RA Glodok A. Gong P. Gorrell J.H. Gu Z. Gunn P. Harris M.

RA Hostin N.L. Harvey D. Helman T.J. Hernandez J. Honok J.

RA Jallil B.E. Kallush F. Karpen G.H. Ke Z. Kennison J.

RA Jallil B.E. Kallush F. Karpen G.H. Ke Z. Kennison J.

RA Kimmel B.M. Kodish C.D. Kraft C. Kravitz S. Kulp D. Lai Z.

RA Lasko P. Lai Y. Levitsky A.A. Li J. Li Z. Liang Y. Lin X.

RA Liu X. Matzel B. McIntosh T.C. Melrod M.P. Moberg D.

RA Morkulov G. Mikhlin N.V. Moberg C. Morris J. Moshfeghi A.

RA Mount S.M. Moy M. Murphy B. Murphy L. Muzzy J.M. Nelson D.L.

RA Palazon D.R. Nelson K.A. Nixon K. Nusslein D.R. Pichel J.M.

RA Ralston K. Remington K. Saunders R.D. Scheeler F. Shen H.

RA Shue B.C. Siden-Klimas I. Simpson M. Skupski M.P. Smith T.

RA Spiller E. Spradling A.C. Stapleton M. Strong R. Sun E.

RA Svidersky R. Tector C. Turner R. Venier L. Wang K.H. Wang X.

RA Wang Z.-Y. Wasserman D.A. Welnick K.C. Wu D. Yang S. Yoo Q.A.

RA Williams S.M. Woodruff T. Morley K.C. Wu D. Yang S. Yoo Q.A.

RA Yeh J. Yeh R.F. Zaveri J.S. Zhao M. Zhang G. Zhao Q. Zheng L.

RA Zheng X.H. Zhong F.N. Zhong M. Zhou X. Zhu S. Zhu X. Smith H.O.
 RA Gibbs R.A. Myers E.W. Rubin G.M. Venter J.C.
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003711: AAF55260.1.
 DR Flybase: FBgn0022787: hel189B.
 DR InterPro: IPR001410: DEAD.
 DR InterPro: IPR001650: Helicase_C.
 DR InterPro: IPR000330: SNF2_N.
 DR Pfam: PF00271: helicase_C.1.
 DR Pfam: PF00176: SNF2_N.1.
 DR SMART: SM00487: DEXDC.1.
 DR SMART: SM00490: HELIC_C.1.
 KW ATP-binding; Helicase.
 FT APP-BINDING
 SQ SEQUENCE 1861 AA: 206155 MW: B1B3B621807833B6 CRC64:

Query Match 39.3%; Score 53; DB 5; Length 1861;
 Best Local Similarity 39.1%; Pred. No. 46;
 Matches 9; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

OY 1 QDASKTKSLKRLKRGDELDSNM 23
 DB 1550 EDFSKHUKDCLDKDDSSASH 1572

RESULT 11

ID Q9SLJ7 PRELIMINARY: PRT: 575 AA.

OS Arabidopsis thaliana (Mouse-ear cress)

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Equisetophyta; Magnoliophyta; Eudicotyledons; Core eudicots; Rosidae;

OC Eursilic; Brassicales; Brassicaceae; Arabidopsida.

NCBI_TextID=3702;

SEQUENCE FROM N.A.

RP STRAIN-CV COLUMBIA:

RC Pedersen J.N.A. Palm C.J. Conway A.B. Conn L. Hansen N.F.

RA Altieri H. Araujo R. Guizard L. Kim C. Lanz C. Li J. Liu S.

RA Gonzalez A. Kremenetskaia I. Kim C. Lanz C. Li J. Liu S.

RA Walker M. Xu G. Ecker J. Shlim P. Tortum M. Vysotskaya V.S.

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AC005287: A025617.1.

DR InterPro: IPR000676: Nth_Exchange.

DR Pfam: PF00999: Na.H_Exchange.1.

SQ SEQUENCE 575 AA: 64043 MW: 49B2B078070EF3D1 CRC64:

Query Match 38.5%; Score 52; DB 10; Length 575;
 Best Local Similarity 50.0%; Pred. No. 39;
 Matches 10; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 4 STKRLSKLRLKRGDELDSNM 23
 DB 508 STCKRLSKLRLKRGDELDSNM 527

RESULT 12

ID Q30773 PRELIMINARY: PRT: 427 AA.

OS Arabidopsis thaliana (Mouse-ear cress)

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Equisetophyta; Magnoliophyta; Eudicotyledons; Core eudicots; Rosidae;

OC Eursilic; Brassicales; Brassicaceae; Arabidopsida.

NCBI_TextID=3702;

SEQUENCE FROM N.A.

RP STRAIN-CV COLUMBIA:

RC Pedersen J.N.A. Palm C.J. Conway A.B. Conn L. Hansen N.F.

RA Altieri H. Araujo R. Guizard L. Kim C. Lanz C. Li J. Liu S.

RA Gonzalez A. Kremenetskaia I. Kim C. Lanz C. Li J. Liu S.

RA Walker M. Xu G. Ecker J. Shlim P. Tortum M. Vysotskaya V.S.

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AC005287: A025617.1.

DR InterPro: IPR000676: Nth_Exchange.

DR Pfam: PF00999: Na.H_Exchange.1.

Fri Sep 20 11:03:25 2002

us-09-544-664-6.rpt

Page 6

Search completed: September 20, 2002, 11:03:39
Job time: 1656 sec